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(54) Title: METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BLADDER CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in bladder cancer. Also described are such genes whose expression is further up-regulated or down-regulated in drug-resistant bladder cancer cells. Related methods and compositions that can be used for diagnosis, prognosis, or treatment of bladder cancer are disclosed. Also described herein are methods that can be used to identify modulators of bladder cancer.

METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BLADDER CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/302,814, filed July 3, 2001; USSN 60/310,099, filed August 3, 2001; USSN 60/343,705, filed November 8, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2001, each of which is incorporated herein by reference.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in bladder cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of bladder cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit bladder cancer.

BACKGROUND OF THE INVENTION

In the United States, over 50,000 new cases of bladder cancer are diagnosed annually, and more than 10,000 deaths will be attributed to bladder cancer. Bladder cancer is now the fourth most common cancer among American men and the ninth most common cancer among American women. It occurs three times more frequently in men than in women, and it occurs roughly twice more frequently in white versus black men.

Bladder cancer rarely occurs in people younger than 40 years of age, being primarily a disease of older men. Nonetheless, bladder cancer is a significant cause of illness and death in the United States. The risk of bladder cancer increases steeply with age, with over half of all bladder cancer deaths occurring after age 70. In white men older than 65, the annual disease rate of bladder cancer is approximately 2 cases per 1,000 persons; this contrasts with a rate of 0.1 cases per 1,000 persons younger than 65.

Within the United States, bladder cancer rates are higher among people who reside in northern versus southern states, and is higher for people who live in urban versus rural areas. Although this difference suggests that environmental as well as genetic factors may contribute to the development and progression of the disease, other studies confirm that certain genes play a role in bladder cancer.. For example, expression of the tumor suppressor gene p53 has been associated with an adverse prognosis for patients with invasive bladder cancer. A retrospective study of 243 patients treated by radical cystectomy found that the presence of nuclear p53 was an independent predictor for recurrence among patients with mid to late stage tumors. Esrig, et al (1994) N.E.J. Med. 331:1259-64.

Urinary bladder cancers represent a spectrum of diseases that can be grouped into three general categories: superficial, invasive, and metastatic. The prognosis for treatment is highly dependent on the stage at which the tumor is first diagnosed. A unique aspect of bladder cancer treatment is that repeated surgical biopsy is an integral part of routine patient management. This has permitted the conduct of molecular genetic studies of tumors from specific stages of the disease. The results of these studies suggest that bladder cancers develop and progress along at least two discrete pathways, which may account for differences in invasiveness and metastatic potential. Incorporating molecular genetic factors into the current paradigm for diagnosis and treatment will optimize the probability of cure and allow the quality of life for bladder cancer patients to be maintained.

Early detection and treatment can prevent reoccurrence and progression of the disease to an incurable stage. Thus, the identification of novel diagnostic markers and therapeutic targets will improve the current treatment of bladder cancer patients. While industry and academia have identified novel sequences, there has not been an equal effort exerted to identify the function of these novel sequences in disease states. The elucidation of a role for novel proteins and compounds in disease states for identification of diagnostic markers and therapeutic targets is essential for improving the current treatment of bladder cancer patients. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of bladder cancer. Additionally, provided herein are molecular targets for therapeutic intervention in bladder cancer and other related bladder diseases.. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate bladder cancer.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in bladder cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate bladder cancer, such as hormones or antibodies. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

In one embodiment, the present invention provides a method of determining the level of a bladder cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-13.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat bladder cancer. In another embodiment, the patient is suspected of having metastatic bladder cancer.

In one embodiment, the patient is a human.

In one embodiment, the bladder cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of bladder cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a bladder cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic bladder cancer. In a further embodiment, the patient has a drug resistant form of bladder cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the bladder cancer-associated transcript to a level of the bladder cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate bladder cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1A-13.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-13.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting a bladder cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to bladder cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1A-13.

In another aspect, the present invention provides a method for identifying a compound that modulates a bladder cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a bladder cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of a bladder cancer-associated cell to treat bladder cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having bladder cancer or to a cell sample isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of bladder cancer.

In one embodiment, the control is a mammal with bladder cancer or a cell sample therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

In one embodiment, the test compound is administered in varying amounts or concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1A-13 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

In another aspect, the present invention provides a method for treating a mammal having bladder cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having bladder cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in a bladder cancer. In one embodiment, a gene is selected from Tables 1A-13. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate bladder cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the bladder cancer modulatory protein, or an animal lacking the bladder cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1A-13, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with bladder cancer is provided. The method comprises determining the expression of a gene of Tables 1A-13 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with bladder cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in bladder cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a bladder cancer modulating protein (bladder cancer modulatory protein) or a fragment thereof and an antibody which binds to said bladder cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining a bladder cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said bladder cancer modulatory protein or fragment thereof. The method further includes determining the binding of said bladder cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits bladder cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a bladder cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1A-13.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a bladder cancer modulating protein, preferably encoded by a nucleic acid of Tables 1A-13 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a bladder cancer modulating protein, preferably selected from the nucleic acids of Tables 1A-13, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of a bladder cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1A-13.

In another aspect of the invention, a method of treating an individual for bladder cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of a bladder cancer modulating protein. In another embodiment, the method comprises administering to a patient having bladder cancer an antibody to a bladder cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for bladder disease (BD), e.g., cancer, including metastatic bladder cancer, as well as methods for screening for compositions which modulate bladder diseases. Also provided are methods and compositions for treating bladder disease. Various related conditions where these markers may be useful also, include, e.g., carcinoma in situ, various stages of papillary carcinomas; and such conditions in different stages, layers, structural portions, etc.

Recent advances in molecular medicine, generally, have increased the interest in tumor-specific cell surface antigens that could serve as diagnostic or prognostic markers, or as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in other, e.g., normal, adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, as a physiological consequence of such expression would be limited. Examples of such antigens in cancers other than bladder cancer include Her2/neu and the B-cell antigen CD20. Humanized monclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; and Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

Definitions

The term "bladder cancer protein" or "bladder cancer polynucleotide" or "bladder cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1A-13; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1A-13, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-13 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1A-13. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "bladder cancer polypeptide" and a "bladder cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" bladder cancer protein or nucleic acid refers to a bladder cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type bladder cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of splicing, including alternative splicing, or post-translation processing.

"Biological sample" as used herein is a sample of biological tissue or fluid, e.g., that contains nucleic acids or polypeptides of a bladder cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, urine, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, or mouse; rabbit; or a bird; reptile; or fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, substitutions, naturally occurring variants, e.g., polymorphic or allelic, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison computer algorithm, test and reference sequences, subsequence coordinates, and sequence algorithm program parameters are typically designated. Default or alternative program parameters can be selected. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from about 20-600, usually about 50-200, more usually about 100-150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, by, e.g., the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l Acad. Sci. USA 85:2444-448, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

Group, 575 Science Dr., Madison, WI), or manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred algorithms suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms. See Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402; and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments typically denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which at least one amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and a non-naturally occurring amino acid polymer.

The term "amino acid" embraces naturally occurring or synthetic amino acids, amino acid analogs, and amino acid mimetics. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs include compounds that share a basic chemical structure with a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, or an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but share some basic chemical structure with a naturally occurring amino acid. Amino acid mimetics include chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to amino acid or nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Each nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another include: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M). See, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman.

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. See, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The

Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains, which are portions of a polypeptide that often form a compact unit of the polypeptide, and are typically about 25-500 amino acids long. Typical domains are made of sections of lesser organization such as stretches of β-sheet and α-helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are polymers, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds. In some cases, nucleic acid analogs are included that may have alternate backbones, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149); phosphorothioate (Mag, et al. (1991), Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048); phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-322); O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207. Other analog nucleic acids include those with positively charged backbones(Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101); non-ionic backbones (U.S. Patent Nos. 5,386,023; 5,637,684; 5,602,240; 5,216,141; and 4,469,863; Kiedrowshi, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426;

Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597-xxx; Chapters 2-3 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx); and non-ribose backbones (see U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6-7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also contemplated. See Jenkins and Turner (1995) Chem. Soc. Rev. 24:169-176. Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News. Modifications of the ribose-phosphate backbone may be made, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which include peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. The PNA backbone typically exhibits improved hybridization kinetics, exhibiting larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. And due to their non-ionic nature, hybridization of the polymers is relatively insensitive to salt concentration. In addition, PNAs are not as easily degraded by cellular enzymes, and can be more stable.

The nucleic acids may be single stranded or double stranded, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine, hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. Direct or indirect methods are comtemplated. For example, useful labels include ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the bladder cancer nucleic acids, proteins, and antibodies. Methods are well known for conjugating the antibody to the label, including those methods described by Hunter, et al. (1962) Nature 144:945-946; David, et al. (1974) Biochemistry 13:1014-021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to a target, e.g., an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds; fluorescent compounds; an enzyme or substrate; tags such as epitope tags; a toxin; activatable moieties; a chemotherapeutic agent; a lipase; an antibiotic; a radioisotope emitting "hard", e.g., beta radiation; or an attracting moiety.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which streptavidin linked label may bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operable linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Techniques in Biochemistry and Molecular Biology; vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least about two times background, preferably about 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-

65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications Academic Press NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least about twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g.,. Ausubel, et al. Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a bladder cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the bladder cancer protein or nucleic acid, e.g., a functional, physical, or chemical effect, such as the ability to decrease bladder cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cell viability, cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of bladder cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a bladder cancer protein sequence, e.g., functional, enzymatic, physical and chemical effects.

Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the bladder cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation or metabolism. Determination of the functional effect of a compound on bladder cancer can also be performed using bladder cancer assays, such as, in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of bladder cancer cells. Functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for bladder cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of bladder cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of bladder cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of bladder cancer proteins, e.g., antagonists. Antisense nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate bladder cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of bladder cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the bladder cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of bladder cancer can also be identified by incubating bladder cancer cells with the test compound and determining increases or decreases in the expression of 1 or more bladder cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more bladder cancer proteins, such as bladder cancer proteins encoded by the sequences set out in Tables 1A-13.

Samples or assays comprising bladder cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably about 50%, more preferably about 25-0%. Activation of a bladder cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably about 150%, more preferably about 200-500% (e.g., two to five fold higher relative to the control), more preferably about 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 of Freshney (1994) Culture of Animal Cells:A Manual of Basic Technique (3d ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene.

Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques can be used. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of bladder cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue (e.g., normal bladder or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the bladder, or bladder cancer tissue or metastatic bladder cancerous tissue can be compared with tissue samples of bladder and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different bladder cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in bladder cancer versus non-bladder cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate bladder cancer, and thus tumor growth or recurrence, in a particular patient; or does chemotherapy or radiation therapy induce expression of particular targets. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of bladder cancer in the tissue or origin of a primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the bladder cancer expression profile. This may be done by making biochips comprising sets of important bladder cancer genes, which can then be used in these screens. These methods can also be applied on the protein basis; that is, protein expression levels of the bladder cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the bladder cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or inhibitory nucleic acids, or the bladder cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in bladder disease or cancer relative to normal tissues and/or non-malignant bladder tissue, herein termed "bladder cancer sequences." As outlined below, bladder cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in bladder cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the bladder cancer sequences are from humans; however, as will be appreciated by those in the art, bladder cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other bladder cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets, e.g., (dogs, cats, etc.). Bladder cancer sequences from other organisms may be obtained using the techniques outlined below.

Bladder cancer sequences can include both nucleic acid and amino acid sequences. Bladder cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications. Biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the bladder cancer sequences can be generated.

A bladder cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the bladder cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying bladder cancer-associated sequences, the bladder cancer screen typically includes comparing genes identified in different tissues, e.g., normal, non-malignant, or cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing bladder cancer samples with metastatic cancer samples from other cancers, such as lung, bladder, gastrointestinal cancers, ovarian, etc. Samples of different stages of bladder cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal bladder, but also including, and not limited to lung, heart, brain, liver, bladder, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the bladder cancer screen that are expressed in a significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, e.g., not be expressed on critical organs.

In a preferred embodiment, bladder cancer sequences are those that are up-regulated in bladder cancer; that is, the expression of these genes is higher in the bladder cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and sequences of accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7 and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ).

In another preferred embodiment, bladder cancer sequences are those that are down-regulated in the bladder cancer; that is, the expression of these genes is lower in bladder cancer tissue as compared to non-cancerous tissue (see, e.g., Tables 1A-13). "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in bladder cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with bladder cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation. See Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA. Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on an electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing bladder cancer, e.g., the identification of bladder cancer-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge Univ. Press; Baxevanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Oxford Univ. Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for bladder cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of bladder cancer-associated proteins

Bladder cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the bladder cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the bladder cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Bladder cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the bladder cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g, secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Bladder cancer proteins that are secreted or released proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or urine tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of bladder cancer nucleic acids

As described above, bladder cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the bladder cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The bladder cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-13, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the bladder cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a bladder cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire bladder cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant bladder cancer nucleic acid can be further-used as a probe to identify and isolate other bladder cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant bladder cancer nucleic acids and proteins.

The bladder cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the bladder cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense/inhibition applications. Alternatively, the bladder cancer nucleic acids that include coding regions of bladder cancer proteins can be put into expression vectors for the expression of bladder cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to bladder cancer nucleic acids (both the nucleic acid sequences outlined in the tables and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the bladder cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be a number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See WO 00/55627.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of bladder cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a bladder cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of bladder cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative

PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification. See, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com.

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1080; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, and linker adapter PCR, etc.

Expression of bladder cancer proteins from nucleic acids

In a preferred embodiment, bladder cancer nucleic acids, e.g., encoding bladder cancer proteins, are used to make a variety of expression vectors to express bladder cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the bladder cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; two sequences may be operably linked if they are physically linked on a single polynucleotide. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the bladder cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are useful in the present invention.

In addition, an expression vector may comprise additional elements. The expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and replication. For integrating expression vectors, the expression vector may contain at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known (e.g., Fernandez and Hoeffler, supra).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The bladder cancer proteins of the present invention may be produced by culturing a host cell transformed with an expression vector under the appropriate conditions to induce or cause expression of the bladder cancer protein. Conditions appropriate for bladder cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will typically require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter typically requires identifying the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, insect, and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the bladder cancer proteins are expressed in mammalian cells. Mammalian expression systems include retroviral and adenoviral systems. Retroviral vector systems are described in PCT/US97/01019 and PCT/US97/01048. Of particular use are promoters from mammalian viral genes, since viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlyation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian and other hosts are well known, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In another embodiment, bladder cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. Synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. A bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. Often an efficient ribosome binding site is desirable. The expression vector may include a signal peptide sequence that provides for secretion of the bladder cancer protein. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs, e.g., ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline, or biosynthetic genes, e.g., those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using, e.g., calcium chloride treatment, electroporation, and other methods.

Bladder cancer proteins can also be produced in insect cells. See, e.g., Miller, et al. (1997) Baculovirus Expression Vectors: A Laboratory Manual Oxford Books; ISBN: 0716770172; and Makrides (1999) Prot. Expr. Purif. 17:183-202.

Bladder cancer protein may be produced in yeast cells. Yeast expression systems exist with expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis and K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica. See, e.g., Jones, et al. (eds. 1993) The Molecular and Cellular Biology of the Yeast Saccharomyces: Gene Expression CSH Press; ISBN: 0879693657.

The bladder cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the bladder cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the bladder cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the bladder cancer protein is a bladder cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression or purification purposes.

The bladder cancer protein is typically purified or isolated after expression. Bladder cancer proteins may be isolated or purified in a variety of ways, depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, reverse-phase HPLC chromatography, and chromatofocusing. The bladder cancer protein may be purified using a standard anti-bladder cancer protein antibody affinity column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see, e.g., Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the bladder cancer protein. In some instances no purification will be necessary, which may depend on the intended use.

Once expressed and purified, if necessary, the bladder cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of bladder cancer proteins

In one embodiment, the bladder cancer proteins are derivative or variant bladder cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative bladder cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most residues within the bladder cancer peptide.

Certain embodiments of bladder cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the bladder cancer protein, using cassette or PCR, mutagenesis, or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant bladder cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are often characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the bladder cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. To optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed bladder cancer variants screened for the optimal combination of desired activities. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is performed using assays of bladder cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combinations thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the bladder cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the bladder cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the bladder cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. Substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, e.g., the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic acid or aspartic acid; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

Covalent modifications of bladder cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a bladder cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a bladder cancer polypeptide. Derivatization with bifunctional agents is useful, e.g., for crosslinking bladder cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-bladder cancer polypeptide antibodies or screening assays. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamic and aspartic residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (pp. 79-86, Creighton (1984) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the bladder cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence bladder cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence bladder cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express bladder cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to bladder cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence bladder cancer polypeptide (for O-linked glycosylation sites). The bladder cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the bladder cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the bladder cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide.

Such methods are described in the art, e.g., in WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the bladder cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art. See, e.g., Hakimuddin, et al. (1987) Arch. Biochem. Biophys. 259:52-57; and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of bladder cancer comprises linking the bladder cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Bladder cancer polypeptides of the present invention may also be modified to form chimeric molecules comprising a bladder cancer polypeptide fused to a heterologous polypeptide or amino acid sequence. In one embodiment, a chimeric molecule comprises a fusion of a bladder cancer polypeptide with an epitope tag. The epitope tag is generally placed at the amino-or carboxyl-terminus of the bladder cancer polypeptide. The presence of such epitope-tagged forms of a bladder cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the bladder cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a bladder cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616);

and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other bladder cancer proteins of the bladder cancer family, and bladder cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related bladder cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the bladder cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known. See, e.g., Innis (1990) PCR Protocols, supra.

Antibodies to bladder cancer proteins

In a preferred embodiment, when the bladder cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the bladder cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller bladder cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known (see, e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the tables or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected as appropriate.

The antibodies may be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1A-13 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (pp. 59-103, Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Tables 1A-13 or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to bladder cancer protein are capable of reducing or eliminating a biological function of a bladder cancer protein, as is described below. That is, the addition of anti-bladder cancer protein antibodies (either polyclonal or preferably monoclonal) to bladder cancer tissue (or cells containing bladder cancer) may reduce or eliminate the bladder cancer. Generally, at least about 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred, and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the bladder cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. See Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596. Humanization can be performed, e.g., following the method of Winter and co-workers (see Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or of human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996) Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of bladder cancer with an antibody raised against bladder cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient), which may be used to target a label or toxin. Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the bladder cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted bladder cancer protein.

In another preferred embodiment, the bladder cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the bladder cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane bladder cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the bladder cancer protein. The antibody is also an antagonist of the bladder cancer protein. Further, the antibody prevents activation of the transmembrane bladder cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the bladder cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, bladder cancer is treated by administering to a patient antibodies directed against the transmembrane bladder cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be a number of molecules, including labelling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the bladder cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the bladder cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with bladder cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to bladder cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with bladder cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against bladder cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane bladder cancer proteins not only serves to increase the local concentration of therapeutic moiety in the bladder cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the bladder cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the bladder cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The bladder cancer antibodies of the invention specifically bind to bladder cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μM, preferably at least about 0.1 μM or better, and most preferably, 0.01 μM or better. Selectivity of binding is also important.

Detection of bladder cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the bladder cancer phenotype. Expression levels of genes in normal tissue (e.g., not experiencing bladder cancer) and in bladder cancer tissue (and in some cases, for varying severities of bladder cancer that relate to prognosis, as outlined below), or in non-malignant disease, are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus bladder cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from about 300-1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the bladder cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to bladder cancer genes, e.g., those identified as being important in a bladder cancer or disease phenotype, can be evaluated in a bladder cancer diagnostic test.

In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In this embodiment, the bladder cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of bladder cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the bladder cancer protein are detected. Although DNA or RNA encoding the bladder cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a bladder cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example, a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a bladder cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, bladder cancer proteins, including intracellular, transmembrane or secreted proteins, find use as diagnostic or prognostic markers of bladder cancer, or to assist in selecting therpay based on expression profile and archival data. Detection of these proteins in putative bladder cancer tissue allows for detection or diagnosis of bladder cancer. In one embodiment, antibodies are used to detect bladder cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the bladder cancer protein is detected, e.g., by immunoblotting with antibodies raised against the bladder cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the bladder cancer protein find use in in situ imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) "Antibodies in Cell Biology" Methods in Cell Biology (vol. 37). In this method cells are contacted with from one to many antibodies to the bladder cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the bladder cancer protein(s) contains a detectable label, e.g. an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of bladder cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing bladder cancer from blood, serum, plasma, stool, urine, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of bladder cancer proteins. Antibodies can be used to detect a bladder cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous bladder cancer protein.

In a preferred embodiment, in situ hybridization of labeled bladder cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including bladder cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to bladder cancer, clinical, pathological, or other information, e.g., in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, bladder cancer probes may be attached to biochips for the detection and quantification of bladder cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR methods may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified bladder cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the bladder cancer phenotype or an identified physiological function of a bladder cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in bladder cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the bladder cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing bladder cancer, with changes of at least about 10%, preferably about 50%, more preferably about 100-300%, and in some embodiments about 300-1000% or greater. Thus, if a gene exhibits about 4-fold increase in bladder cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, about 10-fold decrease in bladder cancer tissue compared to normal tissue often provides a target value of about 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the bladder cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein..

In this embodiment, the bladder cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of bladder cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more bladder cancer-associated sequences, e.g., a polynucleotide sequence set out inTables 1A-13. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate bladder cancer, modulate bladder cancer proteins, bind to a bladder cancer protein, or interfere with the binding of a bladder cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the bladder cancer phenotype or the expression of a bladder cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a bladder cancer phenotype, e.g., to a normal tissue or non-malignant fingerprint. In another embodiment, a modulator induced a bladder cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than about 100 and less than about 2,500 daltons. Preferred small molecules are less than about 2000, or less than about 1500 or less than about 1000 or less than about 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl, or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a bladder cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a bladder cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88); peptoids (PCT Publication No WO 91/19735); encoded peptides (PCT Publication WO 93/20242); random bio-oligomers (PCT Publication WO 92/00091); benzodiazepines (U.S. Pat. No. 5,288,514); diversomers such as hydantoins, benzodiazepines, and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-6913); vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-6570); nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218); analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-2662); oligocarbamates (Cho, et al. (1993) Science 261:1303-1305); and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Strategene, Corp.); peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083); antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14:309-314, and PCT/US96/10287);

carbohydrate libraries (Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853); and small organic molecule libraries (see, e.g., benzodiazepines, Baum (p. 33, Jan 18, 1993) C&E News); isoprenoid (U.S. Patent No. 5,569,588); thiazolidinones and metathiazanones (U.S. Patent No. 5,549,974); pyrrolidines (U.S. Patent Nos. 5,525,735 and 5,519,134); morpholino compounds (U.S. Patent No. 5,506,337); benzodiazepines (U.S. Patent No. 5,288,514); and the like.

Devices for the preparation of combinatorial libraries are commercially available. See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; and 9050 Plus, Millipore, Bedford, MA.

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, NJ; Asinex, Moscow, Ru; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of bladder cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA; etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate nucleotide or amino acid substitutions. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of bladder cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the bladder cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a bladder cancer expression pattern leading to a normal expression pattern, or to modulate a single bladder cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated bladder cancer tissue reveals genes that are not expressed in normal tissue or bladder cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for bladder cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated bladder cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of bladder cancer cells, that have an associated bladder cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., bladder cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the bladder cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on bladder cancer activity. By defining such a signature for the bladder cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "bladder cancer proteins" or a "bladder cancer modulatory protein". The bladder cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables 1A-13. Preferably, the bladder cancer modulatory protein is a fragment. In a preferred embodiment, the bladder cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of Tables 1A-13. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of Tables 1A-13. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the bladder cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the bladder cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the bladder cancer protein is conjugated to BSA.

Measurements of bladder cancer polypeptide activity, or of bladder cancer or the bladder cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the bladder cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of bladder cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian bladder cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a bladder cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the bladder cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the bladder cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the bladder cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β-gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "bladder cancer proteins." The bladder cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the bladder cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a bladder cancer protein and a candidate compound, and determining the binding of the compound to the bladder cancer protein. Preferred embodiments utilize the human bladder cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative bladder cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the bladder cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the bladder cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the bladder cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the bladder cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the bladder cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., a bladder cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the bladder cancer protein and thus is capable of binding to, and potentially modulating, the activity of the bladder cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the bladder cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the bladder cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the bladder cancer proteins. In this embodiment, the methods comprise combining a bladder cancer protein and a competitor in a first sample. A second sample comprises a test compound, a bladder cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the bladder cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the bladder cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native bladder cancer protein, but cannot bind to modified bladder cancer proteins. The structure of the bladder cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a bladder cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a bladder cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising bladder cancer proteins. Many different cell types may be transfected to contain a recombinant nucleic acid that encodes a bladder cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, and pharmacological agents including, e.g., chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In one example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate bladder cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the bladder cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting bladder cancer cell division is provided. The method comprises administration of a bladder cancer inhibitor. In another embodiment, a method of inhibiting bladder cancer is provided. The method comprises administration of a bladder cancer inhibitor. In a further embodiment, methods of treating cells or individuals with bladder cancer are provided. The method comprises administration of a bladder cancer inhibitor. In one embodiment, a bladder cancer inhibitor is an antibody as discussed above. In another embodiment, the bladder cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of bladder cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^{3}H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^{3}H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a bladder cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^{3}H)-thymidine is determined autoradiographically. See, Freshney (1994), supra.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Nat'l Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879; Freshney (1994), supra). This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells. See, e.g., "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), supra. See also, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer, Plenum; and Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate bladder cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1984), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (2000), supra.

Tumor growth in vivo

Effects of bladder cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the bladder cancer gene is disrupted or in which a bladder cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous bladder cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous bladder cancer gene with a mutated version of the bladder cancer gene, or by mutating the endogenous bladder cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be made. See Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Nat'l Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a bladder cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of bladder cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a bladder cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a bladder cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the bladder cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for bladder cancer molecules. A preferred antisense molecule is for a bladder cancer sequences in Tables 1A-13, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999)

Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of bladder cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes. See, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes.

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing them are well known. See, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al.(1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of bladder cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of bladder cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating bladder cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-bladder cancer antibody that reduces or eliminates the biological activity of an endogenous bladder cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a bladder cancer protein. This may be accomplished in many ways. In a preferred embodiment, e.g., when the bladder cancer sequence is down-regulated in bladder cancer, such state may be reversed by increasing the amount of bladder cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous bladder cancer gene or administering a gene encoding the bladder cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the bladder cancer sequence is up-regulated in bladder cancer, the activity of the endogenous bladder cancer gene is decreased, e.g., by the administration of a bladder cancer antisense nucleic acid.

In one embodiment, the bladder cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to bladder cancer proteins. Similarly, the bladder cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify bladder cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a bladder cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The bladder cancer antibodies may be coupled to standard affinity chromatography columns and used to purify bladder cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the bladder cancer protein.

Methods of identifying variant bladder cancer-associated sequences

Without being bound by theory, expression of various bladder cancer sequences is correlated with bladder cancer. Accordingly, disorders based on mutant or variant bladder cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant bladder cancer genes, e.g., determining all or part of the sequence of at least one endogenous bladder cancer genes in a cell. This may be accomplished using many sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the bladder cancer genotype of an individual, e.g., determining all or part of the sequence of at least one bladder cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced bladder cancer gene to a known bladder cancer gene, e.g., a wild-type gene.

The sequence of all or part of the bladder cancer gene can then be compared to the sequence of a known bladder cancer gene to determine if differences exist. This can be done using many known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the bladder cancer gene of the patient and the known bladder cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the bladder cancer genes are used as probes to determine the number of copies of the bladder cancer gene in the genome.

In another preferred embodiment, the bladder cancer genes are used as probes to determine the chromosomal localization of the bladder cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the bladder cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a bladder cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharma. Assn.; and Pickar (1999) Dosage Calculations Thomson. As is known in the art, adjustments for bladder cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. USSN 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in bladder cancer and is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the bladder cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the bladder cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a bladder cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like.

"Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that bladder cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a bladder cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacologial Basis of Therapeutics McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1-10 mg per patient per day. Dosages from about 0.1-100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman: The Pharmacologial Basis of Therapeutics, supra.

The compositions containing modulators of bladder cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. The composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present bladder cancer protein-modulating compounds can be administered alone or in combination with additional bladder cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1A-13, such as antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of bladder cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo, or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols in Molecular Biology Lippincott; and Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, bladder cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, bladder cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the bladder cancer coding regions) can be administered in a gene therapy application. These bladder cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Bladder cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (Vitiello, et al. (1995) J. Clin. Invest. 95:341-349); peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres

(Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681); peptide compositions contained in immune stimulating complexes (ISCOMS) (Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243); multiple antigen peptide systems (MAPs) (Tam (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32); peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al. in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-547; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al. in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc., Needham, MA, may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides;

polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et al. (1990) Science 247:1465-1468 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode bladder cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a bladder cancer gene or portion of a bladder cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a bladder cancer patient. The bladder cancer gene used for DNA vaccines can encode full-length bladder cancer proteins, but more preferably encodes portions of the bladder cancer proteins including peptides derived from the bladder cancer protein. In one embodiment, a patient is immunized with a

DNA vaccine comprising a plurality of nucleotide sequences derived from a bladder cancer gene. For example, bladder cancer-associated genes or sequence encoding subfragments of a bladder cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the bladder cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment bladder cancer genes find use in generating animal models of bladder cancer. When the bladder cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the bladder cancer gene will also diminish or repress expression of the gene. Animal models of bladder cancer find use in screening for modulators of a bladder cancer-associated sequence or modulators of bladder cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the bladder cancer protein. When desired, tissue-specific expression or knockout of the bladder cancer protein may be necessary.

It is also possible that the bladder cancer protein is overexpressed in bladder cancer. As such, transgenic animals can be generated that overexpress the bladder cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of bladder cancer and are additionally useful in screening for modulators to treat bladder cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include one or more of the following: assay reagents, buffers, bladder cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense or inhibitory polynucleotides, ribozymes, dominant negative bladder cancer polypeptides or polynucleotides, small molecules inhibitors of bladder cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of bladder cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a bladder cancer-associated polypeptide or polynucleotide, control positive or negative samples, reaction tubes, and instructions for testing bladder cancer-associated activity. Optionally, the kit contains biologically active bladder cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

TABLE DESCRIPTIONS

Table 1A shows about 3413 that exhibit increased or decreased expression in bladder cancer samples. See USSN 60/302,814.

Table 2A shows about 485 genes overexpressed in bladder tumors relative to normal tissues as analyzed using the Affymetrix/Eos Hu03 GeneChip array. See USSN 60/343,705.

Table 3A shows about 414 genes upregulated in bladder cancer relative to normal body tissues and preferred for utility as small molecule, antibody, DNA vaccine targets for the therapy of bladder cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 4A shows about 129 genes upregulated in bladder cancer relative to normal body tissues and preferred for utility as diagnostics of bladder cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 5A shows about 149 genes upregulated in bladder cancer relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 6A shows about 199 genes upregulated in bladder cancer relative to normal bladder tissue. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 7A shows about 63 genes downregulated in bladder tumors relative to normal bladder. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 8A shows about 1440 genes upregulated in Ta or T1 bladder tumors from patients who later presented with muscle-invasive bladder tumors (stage T2-T4). Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 9A shows about 1200 genes upregulated in Ta or T1 tumors of patients who later presented with either more Ta tumors or no tumors at all. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 10A shows about 65 genes upregulated in non-invasive exophytic Ta bladder tumors relative to T2-T4 muscle-invasive tumors. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 11A shows about 106 genes upregulated in muscle-invasive T2-T4 bladder tumors relative to non-invasive exophytic Ta bladder tumors. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 12A shows the Pkey, ExAccn, UnigeneID, and Unigene Title for all of the sequences in Table 13. Seq ID No. is used to link Table 12A to table 13.

Tables 1B-12B show the accession numbers for those Pkey's lacking UnigeneID's for tables 1A –12A, respectively. For each probeset is listed a gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 1C-12C show genomic positioning for Pkey's lacking Unigene ID's and accession numbers for tables 1A –12A, respectively. For each predicted exon, is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 1A:

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	please refer to original application
R2:	please refer to original application
Target Type:	downregulate stage if target is downregulated in bladder tumors relative to normal bladder or

early stage if target is an earl stage (Ta) bladder tumor marker or
late stage if target is a late stage (T2-T4) bladder tumor marker or
T2-T4 grade 3 papilloma marker or T2-T4 grade 3 solid tumor marker or Upregulate stage

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	Target Type
400440	X83957	Hs.83870	*nebulin*	0.17	2.05	downregulate stage
400888				0.24	1.97	downregulate stage
401566				0.19	4.06	downregulate stage
401669				0.2	2.05	downregulate stage
401691				0.04	10.13	downregulate stage
401905				0.3	1.87	downregulate stage
402076				0.06	6.51	downregulate stage
402110				0.43	2.35	downregulate stage
402271	NM_002197	Hs.154721	aconitase 1, soluble	0.21	2.16	downregulate stage
403362				0.18	4.44	downregulate stage
403687				0.32	1.91	downregulate stage
403959				0.14	2.27	downregulate stage
404015				0.2	2.48	downregulate stage
404059				0.36	1.84	downregulate stage
404152				0.32	1.85	downregulate stage
404498				0.14	2.18	downregulate stage
404819				0.19	5.25	downregulate stage
405001	U58196	Hs.296281	interleukin enhancer binding factor 1	0.16	2.92	downregulate stage
405349				0.18	3.8	downregulate stage
405390				0.3	2.54	downregulate stage
405735				0.13	2.44	downregulate stage
405968				0.26	1.85	downregulate stage
406017				0.32	2.28	downregulate stage
406305	BE261320	Hs.297096	transcriptional adaptor 3 (ADA3, yeast h	0.42	1.93	downregulate stage
406320				0.37	2.01	downregulate stage
406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.3	2.84	downregulate stage
406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	0.14	7.4	downregulate stage
406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	0.05	12.51	downregulate stage
407013	U35637		gb:Human nebulin mRNA, partial cds	0.14	2.17	downregulate stage
407245	X90568	Hs.172004	titin	0.02	15.21	downregulate stage
407330	AA582607		gb:nn51b05.s1 NCI_CGAP_Kid6 Homo sapiens	0.42	1.87	downregulate stage
407571	AI446183	Hs.9572	ESTs	0.38	2.13	downregulate stage
407682	AL035858	Hs.3807	FXYD domain-containing ion transport reg	0.34	2.56	downregulate stage
407815	AW373860	Hs.301716	ESTs	0.31	2.44	downregulate stage
407834	AW084991	Hs.26100	ESTs	0.15	2.98	downregulate stage
407891	AA486620	Hs.41135	endomucin-2	0.15	3.33	downregulate stage
407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	0.12	8.05	downregulate stage
407938	AA905097	Hs.85050	phospholamban	0.08	8.77	downregulate stage
407965	W21483	Hs.41707	heat shock 27kD protein 3	0.26	2.29	downregulate stage
408009	AF020498	Hs.41735	purinergic receptor P2X, ligand-gated io	0.49	1.91	downregulate stage
408139	AA451966	Hs.43005	RAB9-like protein	0.41	1.88	downregulate stage
408221	AA912183	Hs.47447	ESTs	0.04	24.1	downregulate stage
408374	AW025430	Hs.155591	forkhead box F1	0.35	2.85	downregulate stage
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	0.09	9.04	downregulate stage
408508	AI806109	Hs.135736	KIAA1580 protein	0.45	2.2	downregulate stage
408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (f	0.13	5.48	downregulate stage
408652	R43409	Hs.6829	ESTs	0.33	2.5	downregulate stage
408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	0.05	6.94	downregulate stage
408896	AI610447	Hs.48778	niban protein	0.39	2.01	downregulate stage
409277	T05558	Hs.156880	ESTs	0.18	2.75	downregulate stage
410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	0.07	2.7	downregulate stage
410036	R57171	Hs.57975	calsequestrin 2, cardiac muscle	0.09	5.23	downregulate stage
410132	NM_003480	Hs.58882	Microfibril-associated glycoprotein-2	0.24	2.34	downregulate stage
410168	AW834050	Hs.9973	tensin	0.39	2.17	downregulate stage
410243	D83402	Hs.289006	ESTs, Weakly similar to alternatively sp	0.11	2.82	downregulate stage
410339	AI916499	Hs.298258	ESTs	0.15	2.16	downregulate stage
410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	0.32	2.65	downregulate stage
410868	T06529	Hs.98518	Homo sapiens cDNA FLJ11490 fis, clone HE	0.2	2.74	downregulate stage
411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	0.2	1.92	downregulate stage
411067	AI681006	Hs.301543	ESTs	0.11	3.41	downregulate stage
411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	0.17	5.8	downregulate stage
411644	H92064	Hs.301548	ESTs	0.06	13.8	downregulate stage
411741	AW859650		gb:RC0-CT0358-071299-011-d03 CT0358 Homo	0.36	2.5	downregulate stage
412047	AA934589	Hs.49696	ESTs	0.18	3.57	downregulate stage
412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	0.32	1.89	downregulate stage
412389	AW947655		gb:RC0-MT0003-140300-031-b07 MT0003 Homo	0.38	2.6	downregulate stage
412442	AI983730	Hs.26530	serum deprivation response (phosphatidyl	0.12	3.67	downregulate stage
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	0.24	1.86	downregulate stage
412622	AW664708	Hs.171959	ESTs	0.06	5.45	downregulate stage
412649	NM_002206	Hs.74369	integrin, alpha 7	0.29	2.95	downregulate stage
412659	AW753865	Hs.74376	olfactomedin related ER localized protei	0.18	2.06	downregulate stage
412758	Y07818	Hs.74566	dihydropyrimidinase-like 3	0.3	2.23	downregulate stage

412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	0.11	2.71	downregulate stage
412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, S	0.44	2.03	downregulate stage
413074	AI871368	Hs.8417	ESTs	0.47	1.91	downregulate stage
413272	AA127923	Hs.293256	ESTs	0.09	4.44	downregulate stage
413276	Z24725	Hs.75260	mitogen inducible 2	0.23	2.48	downregulate stage
413508	BE145364		gb:IL0-HT0198-151099-125-e05 HT0198 Homo	0.31	2.53	downregulate stage
413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hevin)	0.33	2.17	downregulate stage
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	0.33	2.63	downregulate stage
414063	H26904	Hs.75736	apolipoprotein D	0.42	1.85	downregulate stage
414241	AA425085	Hs.4007	Sarcolemmal-associated protein	0.16	2.22	downregulate stage
414290	AI568801	Hs.71721	ESTs	0.02	10	downregulate stage
414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	0.13	4.14	downregulate stage
414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	0.33	2.14	downregulate stage
414712	N88858	Hs.77039	ribosomal protein S3A	0.4	2.5	downregulate stage
414903	AA451700	Hs.85835	Homo sapiens cDNA: FLJ22841 fis, clone K	0.3	3.3	downregulate stage
415165	AW887604	Hs.78065	complement component 7	0.04	3.41	downregulate stage
415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	0.2	3.29	downregulate stage
415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	0.15	6.55	downregulate stage
415672	N53097	Hs.193579	ESTs	0.28	3.55	downregulate stage
415934	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)	0.34	2.64	downregulate stage
416127	N49843	Hs.79022	GTP-binding protein overexpressed in ske	0.3	1.98	downregulate stage
416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	0.41	1.96	downregulate stage
416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	0.02	49.3	downregulate stage
416854	H40164	Hs.80296	Purkinje cell protein 4	0.02	7.55	downregulate stage
416941	BE000150	Hs.48778	niban protein	0.27	2.16	downregulate stage
416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	0.29	2.43	downregulate stage
417011	F08212	Hs.234898	ESTs	0.41	2.06	downregulate stage
417298	AW665639	Hs.37958	ESTs	0.27	3.7	downregulate stage
417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig),	0.39	2.08	downregulate stage
417553	L09190	Hs.82276	trichohyalin	0.29	2.59	downregulate stage
417987	AA210872	Hs.50133	ESTs	0.22	2.09	downregulate stage
418297	R91254		gb:yp94e12.s1 Soares fetal liver spleen	0.28	1.9	downregulate stage
418332	R34976	Hs.78293	ESTs	0.2	3.9	downregulate stage
418391	NM_003281	Hs.84673	troponin I, skeletal, slow	0.35	2.02	downregulate stage
418409	AA219332	Hs.120869	ESTs, Weakly similar to AF092922 1 retin	0.21	3.8	downregulate stage
418421	R58620	Hs.85050	phospholamban	0.2	2.08	downregulate stage
418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.05	21.55	downregulate stage
418533	NM_004533	Hs.85937	myosin-binding protein C, fast-type	0.42	1.95	downregulate stage
418787	AW296134	Hs.86999	ESTs	0.48	1.87	downregulate stage
418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	0.26	2.43	downregulate stage
418947	W52990	Hs.22860	ESTs	0.13	7.18	downregulate stage
419037	R39895	Hs.7864	ESTs	0.27	2	downregulate stage
419441	AW023731	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586I1524 (f	0.19	5.25	downregulate stage
419535	AW139550	Hs.115173	ESTs	0.31	2.59	downregulate stage
419682	H13139	Hs.92282	paired-like homeodomain transcription fa	0.28	2.38	downregulate stage
419685	W76083	Hs.173077	ESTs	0.4	2.21	downregulate stage
419703	AI793257	Hs.128151	ESTs	0.09	3.52	downregulate stage
419942	U25138	Hs.93841	potassium large conductance calcium-acti	0.28	2.96	downregulate stage
420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.3	2.09	downregulate stage
420195	N44348	Hs.300794	ESTs	0.22	2.79	downregulate stage
420261	AW206093	Hs.748	fibroblast growth factor receptor 1 (fms	0.35	1.98	downregulate stage
420674	NM_000055	Hs.1327	butyrylcholinesterase	0.29	3.5	downregulate stage
421296	NM_002666	Hs.103253	perilipin	0.36	2.11	downregulate stage
421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDN	0.13	4.3	downregulate stage
421763	AW163500	Hs.108080	cysteine and glycine-rich protein 1	0.26	3.49	downregulate stage
421853	AL117472	Hs.108924	DKFZP586P1422 protein	0.14	5	downregulate stage
422103	AA984330	Hs.111676	protein kinase H11; small stress protein	0.2	2.29	downregulate stage
422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	0.27	2.58	downregulate stage
422320	AI745249	Hs.23650	ESTs, Weakly similar to AAB47496 NG5 [H.	0.24	2.95	downregulate stage
422633	X56832	Hs.118804	enolase 3, (beta, muscle)	0.23	3.57	downregulate stage
422639	AI929377	Hs.173724	creatine kinase, brain	0.39	1.97	downregulate stage
423334	AK000906	Hs.127273	hypothetical protein FLJ10044	0.37	2.29	downregulate stage
423587	AA328074	Hs.284256	hypothetical protein FLJ14033 similar to	0.37	2.47	downregulate stage
423889	AL035447	Hs.134594	hypothetical protein LOC57158	0.24	2.43	downregulate stage
424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	0.27	2.28	downregulate stage
424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	0.3	2.59	downregulate stage
424479	AF064238	Hs.149098	smoothelin	0.26	3.29	downregulate stage
424580	AA446539	Hs.35092	ESTs	0.15	2.57	downregulate stage
424846	AU077324	Hs.1832	neuropeptide Y	0.4	2.04	downregulate stage
424938	AW102607	Hs.245233	ESTs	0.29	2.16	downregulate stage
424982	U94777	Hs.154084	phosphorylase, glycogen; muscle (McArdle	0.42	1.89	downregulate stage
425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	0.14	1.86	downregulate stage
425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	0.03	13.25	downregulate stage
425622	AW360847	Hs.16578	ESTs	0.3	2.19	downregulate stage
425751	T19239	Hs.1940	crystallin, alpha B	0.47	1.92	downregulate stage
425869	AA524547	Hs.160318	FXYD domain-containing ion transport reg	0.45	1.85	downregulate stage
425887	AL049443	Hs.161283	Homo sapiens mRNA; cDNA DKFZp586N2020 (f	0.19	2.85	downregulate stage

425932	M81650	Hs.1968	semenogelin I	0.02	16.3	downregulate stage
426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	0.27	2.52	downregulate stage
426429	X73114	Hs.169849	myosin-binding protein C, slow-type	0.1	10.3	downregulate stage
426752	X69490	Hs.172004	titin	0.03	31.3	downregulate stage
426809	BE313114	Hs.29706	ESTs	0.34	2.95	downregulate stage
427078	AI676062	Hs.111902	ESTs	0.22	2.11	downregulate stage
427136	AL117415	Hs.173716	Homo sapiens mRNA; cDNA DKFZp434K0521 (f	0.37	2.33	downregulate stage
427164	AB037721	Hs.173871	KIAA1300 protein	0.12	5.47	downregulate stage
427185	AA398930	Hs.186674	ESTs	0.22	4.65	downregulate stage
427373	AB007972	Hs.177533	Homo sapiens mRNA; cDNA DKFZp586N0318 (f	0.22	3.18	downregulate stage
427393	AB029018	Hs.177635	KIAA1095 protein	0.27	2.13	downregulate stage
427665	AF134803	Hs.180141	cofilin 2 (muscle)	0.05	4	downregulate stage
427676	AA394062	Hs.180266	tropomyosin 2 (beta)	0.45	1.87	downregulate stage
427888	AA417088	Hs.137598	ESTs	0.36	2.04	downregulate stage
427980	AA418305		gb:zv96g05.s1 Soares_NhHMPu_S1 Homo sapi	0.32	2.39	downregulate stage
428087	AA100573	Hs.182421	troponin C2, fast	0.17	4.37	downregulate stage
428138	AA773842	Hs.293799	ESTs	0.45	2.2	downregulate stage
428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase of f	0.23	3.36	downregulate stage
428329	AA426091	Hs.98453	ESTs	0.21	2.09	downregulate stage
428409	AW117207	Hs.98523	ESTs	0.1	7.63	downregulate stage
428411	AW291464	Hs.10338	ESTs	0.32	1.98	downregulate stage
428648	AF052728	Hs.188021	potassium voltage-gated channel, subfami	0.08	2.99	downregulate stage
428649	AL045716	Hs.188228	Homo sapiens cDNA FLJ11003 fis, clone PL	0.11	2.07	downregulate stage
428899	AA744610	Hs.194431	palladin	0.42	1.84	downregulate stage
429350	AI754634	Hs.131987	ESTs	0.06	4.73	downregulate stage
429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	0.18	2.31	downregulate stage
429545	AI824164	Hs.77667	lymphocyte antigen 6 complex, locus E	0.31	2.07	downregulate stage
429655	U48959	Hs.211582	myosin, light polypeptide kinase	0.33	2.18	downregulate stage
429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	0.36	2.17	downregulate stage
429930	AI580809	Hs.99569	ESTs	0.18	5.6	downregulate stage
429956	AI374651	Hs.22542	ESTs	0.22	4.45	downregulate stage
430013	AA463833	Hs.151275	ESTs	0.21	3.03	downregulate stage
430271	T06199	Hs.237506	heat shock cognate 40	0.47	1.85	downregulate stage
430310	U60115	Hs.239069	four and a half LIM domains 1	0.18	3.44	downregulate stage
430418	R98852	Hs.36029	heart and neural crest derivatives expre	0.38	2.26	downregulate stage
430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	0.16	2.52	downregulate stage
430712	AW044647	Hs.196284	ESTs	0.29	1.94	downregulate stage
430778	D90337	Hs.247916	natriuretic peptide precursor C	0.14	4.48	downregulate stage
430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.35	1.87	downregulate stage
432247	AA531287	Hs.105805	ESTs	0.21	3.99	downregulate stage
432689	AB018320	Hs.278626	Arg/Abl-interacting protein ArgBP2	0.11	1.98	downregulate stage
432792	AA448114	Hs.278950	protocadherin beta 1	0.22	2.93	downregulate stage
433142	AL120697	Hs.110640	ESTs	0.21	2.18	downregulate stage
433633	AI880516	Hs.84630	ESTs	0.34	2.67	downregulate stage
433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	0.35	2.27	downregulate stage
433826	AA609938	Hs.144492	ESTs	0.24	1.91	downregulate stage
434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	0.07	3.46	downregulate stage
434160	BE551196	Hs.114275	ESTs	0.5	2	downregulate stage
434352	AF129505	Hs.86492	small muscle protein, X-linked	0.34	2.13	downregulate stage
434361	AF129755	Hs.117772	ESTs	0.03	31.3	downregulate stage
435731	AA699581	Hs.186811	ESTs	0.31	3.25	downregulate stage
435869	AF255910	Hs.54650	vascular endothelial junction-associated	0.21	3.73	downregulate stage
435978	AF272899	Hs.135118	Homo sapiens PR-domain zinc finger prote	0.35	2.25	downregulate stage
436359	Z83806		gb:H.sapiens mRNA for axonemal dynein he	0.24	3.28	downregulate stage
436638	AI271945	Hs.134984	ESTs	0.36	1.87	downregulate stage
436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	0.14	6.95	downregulate stage
437176	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	0.32	2.19	downregulate stage
437233	D81448	Hs.153961	ARP1 (actin-related protein 1, yeast) ho	0.27	2.38	downregulate stage
438619	AB032773	Hs.6341	TU12B1-TY protein	0.19	2.69	downregulate stage
438666	AW014493	Hs.126727	ESTs	0.16	1.98	downregulate stage
439231	AW581935	Hs.141480	ESTs	0.1	3.9	downregulate stage
439973	AI733308	Hs.124663	ESTs	0.16	6.2	downregulate stage
440172	AA868584	Hs.126154	ESTs	0.24	2.34	downregulate stage
440274	R24595	Hs.7122	scrapie responsive protein 1	0.11	3.02	downregulate stage
440687	AL080222	Hs.7358	hypothetical protein FLJ13110	0.19	2.95	downregulate stage
440700	AW952281	Hs.296184	ESTs, Highly similar to GB01_HUMAN GUANI	0.13	2.69	downregulate stage
440737	AI375167	Hs.132221	Homo sapiens cDNA FLJ12401 fis, clone MA	0.5	2	downregulate stage
441805	AA285136	Hs.7974	neuronal specific transcription factor D	0.07	13.55	downregulate stage
441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.38	1.86	downregulate stage
442109	BE218975	Hs.212395	ESTs	0.24	2.86	downregulate stage
442985	AI025984	Hs.55467	ESTs	0.19	2	downregulate stage
443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	0.09	3.66	downregulate stage
443164	AI038503	Hs.55780	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.2	1.86	downregulate stage
443476	AW068594	Hs.133878	ESTs, Weakly similar to AF151889 1 CGI-1	0.11	2.79	downregulate stage
443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	0.24	3.41	downregulate stage
443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chai	0.28	3.6	downregulate stage
443932	AW888222	Hs.9973	tensin	0.32	2.57	downregulate stage

444195	AB002351	Hs.10587	KIAA0353 protein	0.19	4.04	downregulate stage
444484	AK002126	Hs.11260	hypothetical protein FLJ11264	0.38	2.04	downregulate stage
444684	AW044070	Hs.147037	ESTs	0.36	2.25	downregulate stage
444793	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	0.29	2.19	downregulate stage
444938	AW470690	Hs.148814	ESTs	0.43	2.3	downregulate stage
445230	U97018	Hs.12451	echinoderm microtubule-associated protei	0.13	2.64	downregulate stage
445235	AI564022	Hs.138207	ESTs	0.13	2.4	downregulate stage
445621	AI733818	Hs.145549	ESTs	0.25	1.91	downregulate stage
445687	W80382	Hs.149297	ESTs	0.2	3.5	downregulate stage
445850	AI262049	Hs.145560	ESTs	0.53	1.9	downregulate stage
446406	AI553681	Hs.25248	ESTs	0.07	3.25	downregulate stage
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	0.33	1.9	downregulate stage
447595	AW379130	Hs.18953	phosphodiesterase 9A	0.28	1.85	downregulate stage
447918	AI129320	Hs.16930	ESTs	0.29	2.46	downregulate stage
448076	AJ133123	Hs.20196	adenylate cyclase 9	0.2	2.27	downregulate stage
448283	AI340462	Hs.182979	ribosomal protein L12	0.53	1.9	downregulate stage
448303	BE622468	Hs.11924	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.39	1.84	downregulate stage
448425	AI500359	Hs.233401	ESTs	0.16	1.97	downregulate stage
448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	0.12	5.43	downregulate stage
448555	AI536697	Hs.159863	ESTs	0.32	2.86	downregulate stage
448901	AK001021	Hs.22505	hypothetical protein FLJ10159	0.17	2.66	downregulate stage
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	0.24	1.86	downregulate stage
449226	AB002365	Hs.23311	KIAA0367 protein	0.1	4.96	downregulate stage
449238	AA428229	Hs.85524	muscle-specific RING-finger protein homo	0.14	2.53	downregulate stage
449422	AA001373	Hs.59821	ESTs	0.43	2.3	downregulate stage
449690	AA002140	Hs.33024	ESTs	0.5	2	downregulate stage
449874	AA135688	Hs.10083	ESTs	0.33	2.7	downregulate stage
449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	0.11	5.57	downregulate stage
450300	AL041440	Hs.58210	ESTs	0.41	2.13	downregulate stage
450578	AI971773	Hs.232268	ESTs	0.44	2.25	downregulate stage
450810	BE207588	Hs.25511	transforming growth factor beta 1 induce	0.51	1.86	downregulate stage
450831	R37974	Hs.25255	ESTs	0.23	1.96	downregulate stage
451331	AK002039	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	0.37	2.18	downregulate stage
451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.1	9.36	downregulate stage
451782	AF233588	Hs.27018	Ris	0.35	2.43	downregulate stage
451948	AW452473	Hs.211125	ESTs	0.43	1.88	downregulate stage
452422	AA521416	Hs.22701	ESTs	0.41	1.85	downregulate stage
452463	R36452	Hs.300817	ESTs	0.09	4.05	downregulate stage
452776	AA194540	Hs.13522	ESTs	0.36	2.16	downregulate stage
452814	AI092790	Hs.55016	hypothetical protein FLJ21935	0.06	4.7	downregulate stage
453064	R40334	Hs.301395	Homo sapiens cDNA: FLJ21204 fis, clone C	0.07	4.47	downregulate stage
453351	AI625721	Hs.61814	Homo sapiens cDNA: FLJ22750 fis, clone K	0.33	3.05	downregulate stage
453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	0.03	7.14	downregulate stage
453359	AA448787	Hs.24872	ESTs, Weakly similar to aortic carboxype	0.4	1.92	downregulate stage
453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	0.24	3.29	downregulate stage
453500	AI478427	Hs.43125	ESTs	0.02	11.41	downregulate stage
453582	AW854339	Hs.33476	hypothetical protein FLJ11937	0.39	2.04	downregulate stage
453586	AA248089	Hs.50841	ESTs, Weakly similar to tuftelin [M.musc	0.43	1.86	downregulate stage
453666	AW015681	Hs.135229	ESTs, Moderately similar to AF107203 1 a	0.28	2.42	downregulate stage
453698	AA037615	Hs.42746	ESTs	0.2	1.88	downregulate stage
453702	AA037637	Hs.42128	ESTs	0.32	2.42	downregulate stage
453725	W28543		gb:48c5 Human retina cDNA randomly prime	0.2	2.06	downregulate stage
453950	AA156998	Hs.211568	eukaryotic translation initiation factor	0.07	7.86	downregulate stage
454078	AA601518	Hs.22209	secreted modular calcium-binding protein	0.16	2.49	downregulate stage
454471	AW902125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	0.41	2.45	downregulate stage
454637	AW811613		gb:CM3-ST0157-300999-017-f06 ST0157 Homo	0.18	2.2	downregulate stage
454750	AW866285		gb:QV4-SN0024-080400-167-a09 SN0024 Homo	0.49	2.05	downregulate stage
455073	AW854829		gb:QV2-CT0261-201099-011-f01 CT0261 Homo	0.27	2.09	downregulate stage
455485	AA102287	Hs.26756	Homo sapiens cDNA: FLJ20896 fis, clone A	0.32	2.07	downregulate stage
455611	L06419	Hs.75093	procollagen-lysine, 2-oxoglutarate 5-dio	0.15	2.87	downregulate stage
456100	AI983981	Hs.189114	ESTs	0.4	2.5	downregulate stage
456841	AA875863	Hs.152345	poliovirus receptor-related 1 (herpesvir	0.35	1.9	downregulate stage
457064	AA776743	Hs.191589	ESTs	0.17	2.34	downregulate stage
457108	N74724	Hs.108479	ESTs	0.48	2.1	downregulate stage
457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	0.29	2.59	downregulate stage
457625	T10073		gb:seq1293 b4HB3MA Cot8-HAP-Ft Homo sapi	0.29	3.45	downregulate stage
458482	AV648858	Hs.29488	ESTs	0.26	2.17	downregulate stage
458622	AA972412	Hs.13755	f-box and WD-40 domain protein 2	0.51	1.95	downregulate stage
458841	W28965		gb:54d10 Human retina cDNA randomly prim	0.32	3.1	downregulate stage
459037	AW439497	Hs.290656	EST	0.43	2.35	downregulate stage
400762				0.71	0.4	early stage
400937				1.2	0.26	early stage
400977				0.63	0.48	early stage
401024				0.8	0.3	early stage
401048				1.9	0.22	early stage
401537				1.3	0.2	early stage
401619				3.5	0.19	early stage

402089				0.39	0.55	early stage
402176				0.35	0.91	early stage
402407				1	0.15	early stage
402430				0.28	1.25	early stage
402435				2.15	0.21	early stage
402522				1.8	0.14	early stage
402546				0.17	1.66	early stage
402604				0.41	0.66	early stage
402716				0.14	0.86	early stage
402846				0.61	0.52	early stage
402922				0.14	0.83	early stage
403567				0.44	0.49	early stage
403590				1	0.34	early stage
404336				0.49	0.44	early stage
404345	AA730407	Hs.159156	protocadherin 11	0.38	0.4	early stage
404501	AW247252	Hs.75514	nucleoside phosphorylase	0.32	0.8	early stage
404594				0.37	0.91	early stage
404874				1.87	0.26	early stage
404881				0.36	0.5	early stage
404896	NM_000429	Hs.106845	methionine adenosyltransferase I, alpha	1	0.36	early stage
404999	U58196	Hs.296281	interleukin enhancer binding factor 1	0.19	1.06	early stage
405071				0.19	0.77	early stage
405308				0.4	0.55	early stage
405463				0.41	1	early stage
405580				1.89	0.19	early stage
405600				0.22	0.63	early stage
405720				0.37	0.61	early stage
405863				0.53	0.26	early stage
405867				0.24	1.1	early stage
405920				0.39	1.15	early stage
406036				2.15	0.17	early stage
406243				0.32	1.23	early stage
406367				0.38	0.76	early stage
406834	AI318680		gb:ta49g09.x1 NCI_CGAP_Lu25 Homo sapiens	0.4	0.67	early stage
406881	D16154		gb:Human gene for cytochrome P-450c11, e	0.14	1.55	early stage
407411	AF060170		gb:Homo sapiens AS12 protein mRNA, parti	0.39	0.69	early stage
407639	AW205369	Hs.252936	ESTs	0.61	0.34	early stage
408112	AW451982	Hs.248613	ESTs	0.2	0.54	early stage
408732	AL117490	Hs.47225	Homo sapiens mRNA; cDNA DKFZp434N211 (fr	1	0.32	early stage
409103	AF251237	Hs.112208	XAGE-1 protein	0.33	1.03	early stage
409840	AW502122		gb:UI-HF-BR0p-ajr-c-08-0-UI.r1 NIH_MGC_5	0.56	0.28	early stage
410128	AW904599		gb:RC1-NN1063-260400-011-h05 NN1063 Homo	1.26	0.37	early stage
411474	AW848427		gb:IL3-CT0214-150200-075-H10 CT0214 Homo	1	0.14	early stage
412564	X83703	Hs.74019	cardiac ankyrin repeat protein	0.36	0.44	early stage
413266	BE300352		gb:600944231F1 NIH_MGC_17 Homo sapiens c	1.46	0.25	early stage
413341	H78472	Hs.191325	ESTs, Weakly similar to cDNA EST yk414c9	0.41	0.48	early stage
414055	AW818687	Hs.5366	Homo sapiens cDNA: FLJ21522 fis, clone C	0.33	0.67	early stage
414170	AA335996	Hs.3743	matrix metalloproteinase 24 (membrane-in	1.15	0.21	early stage
414220	BE298094		gb:601118231F1 NIH_MGC_17 Homo sapiens c	0.16	0.52	early stage
414276	BE297862		gb:601174780F1 NIH_MGC_17 Homo sapiens c	1.75	0.2	early stage
414327	BE408145	Hs.185254	ESTs, Moderately similar to NAC-1 protei	0.1	0.99	early stage
414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	1	0.31	early stage
414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [	0.18	0.96	early stage
414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	0.48	0.67	early stage
415199	AA161125	Hs.57893	ESTs	0.75	0.72	early stage
417304	H15635		gb:ym27h06.r1 Soares infant brain 1NIB H	0.6	0.58	early stage
417371	N74613	Hs.269149	ESTs	0.3	0.58	early stage
418133	R43504	Hs.6181	ESTs	1.28	0.29	early stage
419273	BE271180	Hs.293490	ESTs	0.54	0.28	early stage
419716	AA953770		gb:on89e04.s1 Soares_NFL_T_GBC_S1 Homo s	0.45	0.66	early stage
420390	AA330047	Hs.191187	ESTs	1.45	0.12	early stage
421745	AF205849	Hs.107740	Kruppel-like factor 2 (lung)	0.33	0.71	early stage
421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Brn52 Homo sapien	0.52	0.67	early stage
422669	H12402	Hs.119122	ribosomal protein L13a	1	0.26	early stage
422743	BE304678	Hs.119598	ribosomal protein L3	0.2	0.57	early stage
422760	BE409561		gb:601299865F1 NIH_MGC_21 Homo sapiens c	0.41	0.64	early stage
422880	AF228704	Hs.121524	glutathione reductase	3.75	0.1	early stage
423457	F08208	Hs.155606	paired mesoderm homeo box 1	0.55	0.54	early stage
425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1	0.21	early stage
425360	BE547704		gb:601076309F1 NIH_MGC_12 Homo sapiens c	0.28	0.85	early stage
426356	BE536836		gb:601064837F1 NIH_MGC_10 Homo sapiens c	0.31	0.69	early stage
426521	AF161445	Hs.170219	hypothetical protein	0.11	0.69	early stage
426670	AA383047	Hs.193718	ESTs	1	0.55	early stage
426699	AA383337	Hs.121269	ESTs	0.33	0.71	early stage
427827	AA416577	Hs.189105	ESTs	1.16	0.41	early stage
428651	AF196478	Hs.188401	annexin A10	1.85	0.24	early stage
430727	X75917	Hs.2654	MHC binding factor, beta	0.78	0.46	early stage

430750	AI650360	Hs.100256	ESTs	2.15	0.17	early stage
430795	AW971398		gb:EST383487 MAGE resequences, MAGL Homo	1.95	0.21	early stage
431900	AW972048	Hs.192534	ESTs	0.36	0.73	early stage
432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	1.8	0.17	early stage
432791	NM_014554	Hs.278949	sentrin/SUMO-specific protease	2.8	0.15	early stage
433404	T32982	Hs.102720	ESTs	2.2	0.13	early stage
433782	AF090945		gb:Homo sapiens clone HQ0670	3.3	0.15	early stage
433877	BE146567	Hs.257475	ESTs	0.65	0.7	early stage
434483	AA223646	Hs.57222	nurim (nuclear envelope membrane protein	0.38	0.49	early stage
435752	AF230801	Hs.125180	growth hormone receptor	0.52	0.4	early stage
436178	BE152396	Hs.21590	Homo sapiens HSPC304 mRNA, partial cds	1.65	0.14	early stage
436391	AJ227892	Hs.146274	ESTs	1.35	0.16	early stage
436602	AI793222	Hs.166817	ESTs	0.17	1.46	early stage
436777	AA731199	Hs.293130	ESTs	1	0.2	early stage
436813	AW975714	Hs.129004	ESTs	0.19	1.45	early stage
436869	NM_014867	Hs.297661	Homo sapiens YAC clone 377A1 unknown mRN	0.96	0.2	early stage
437169	AA309612	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	0.07	1.8	early stage
438649	AA813136	Hs.143014	ESTs	1.38	0.19	early stage
438681	AW384815	Hs.149208	KIAA1555 protein	0.25	0.54	early stage
438802	AA825976	Hs.136954	ESTs	1.8	0.14	early stage
438887	R68857	Hs.265499	ESTs	1.05	0.32	early stage
440128	AA962623	Hs.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	1	0.19	early stage
440397	AA884448	Hs.157239	ESTs	0.59	0.38	early stage
440509	BE410132	Hs.134202	ESTs, Weakly similar to B41182 collagen	0.26	0.9	early stage
440605	Z40094	Hs.185698	ESTs	0.51	0.43	early stage
442238	AW135374	Hs.270949	ESTs	1	0.18	early stage
443258	AF169301	Hs.9098	sulfate transporter 1	0.85	0.49	early stage
445739	AW136354	Hs.145303	ESTs	0.88	0.4	early stage
447306	AI373163	Hs.170333	ESTs	0.15	0.8	early stage
447346	AI525135	Hs.210507	ESTs	1.35	0.27	early stage
448265	N46272	Hs.26812	ESTs	0.47	0.26	early stage
448678	AI560776	Hs.199854	ESTs	0.19	0.68	early stage
448778	AF074913		gb:Homo sapiens transcription factor Pax	0.57	0.53	early stage
448871	BE616709		gb:601279937F1 NIH_MGC_39 Homo sapiens c	0.26	0.94	early stage
449180	AI633836	Hs.195649	ESTs	0.46	0.45	early stage
449213	BE616861		gb:601279056F1 NIH_MGC_39 Homo sapiens c	0.73	0.56	early stage
449231	BE410360		gb:601302340F1 NIH_MGC_21 Homo sapiens c	0.27	0.76	early stage
449450	AL039852	Hs.256990	ESTs, Moderately similar to ALU7_HUMAN A	1	0.26	early stage
449815	AI671000	Hs.199739	ESTs	1.2	0.15	early stage
450972	AW967906	Hs.194617	ESTs	0.28	0.83	early stage
451236	AI767406	Hs.207026	ESTs, Weakly similar to B56205 transcrip	0.35	0.77	early stage
451283	H83979		gb:ys93d11.r1 Soares retina N2b5HR Homo	1	0.23	early stage
451375	AI792066	Hs.283902	Homo sapiens BAC clone RP11-481J13 from	0.16	1.37	early stage
452530	AI905518		gb:RC-BT091-210199-098 BT091 Homo sapien	1.35	0.21	early stage
452550	AA026735		gb:ze93d05.r1 Soares_fetal_heart_NbHH19W	0.44	0.6	early stage
454121	AW090524	Hs.244967	ESTs	2.85	0.17	early stage
454554	AW847505		gb:RC0-CT0210-280999-021-c10 CT0210 Homo	0.36	0.5	early stage
454697	AW813728	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC0	0.43	0.6	early stage
454851	AW835127		gb:RC4-LT0011-100100-012-c07 LT0011 Homo	0.77	0.32	early stage
455040	AW852286		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	0.26	0.52	early stage
455225	AW996689		gb:QV3-BN0046-150400-151-g09 BN0046 Homo	1.7	0.18	early stage
455970	AI733857	Hs.71483	ESTs	0.66	0.45	early stage
456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	0.64	0.43	early stage
456450	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	0.38	0.76	early stage
456526	AA782222	Hs.192008	ESTs	0.63	0.43	early stage
456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.49	0.46	early stage
456983	AI081687	Hs.170225	thymopoietin	0.27	0.75	early stage
457089	AA416556	Hs.98234	ESTs	0.34	0.48	early stage
458198	AI286100	Hs.192739	ESTs	0.47	0.48	early stage
458425	AI084057	Hs.301149	ESTs	0.4	0.37	early stage
458660	AI299739	Hs.99601	Homo sapiens cDNA FLJ12553 fis, clone NT	0.79	0.68	early stage
458703	AW749121	Hs.282901	ESTs	1	0.23	early stage
458767	T97083	Hs.148355	ESTs	1	0.17	early stage
459399	BE407712		gb:601299745F1 NIH_MGC_21 Homo sapiens c	0.68	0.56	early stage
400860				4.9	0.08	late stage
408190	AB032963	Hs.43577	ATPase, Class I, type 8B, member 2	0.58	0.84	late stage
408558	AW015759	Hs.235709	ESTs	1.26	0.45	late stage
410077	AF097645	Hs.58570	deleted in cancer 1; RNA helicase HDB/DI	6.2	0.12	late stage
410295	AA741357	Hs.62041	nidogen (enactin)	0.77	0.86	late stage
410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	1.45	0.27	late stage
410614	AI091195	Hs.65029	growth arrest-specific 1	0.4	1.12	late stage
410867	X63556	Hs.750	fibrillin 1 (Marfan syndrome)	0.71	1.07	late stage
411573	AB029000	Hs.70823	KIAA1077 protein	3.64	0.19	late stage
412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	5.18	0.13	late stage
412178	AW898526		gb:RC6-NN0072-040500-011-E05 NN0072 Homo	7.55	0.08	late stage
412429	AV650262	Hs.75765	GRO2 oncogene	3.37	0.15	late stage
412652	AI801777	Hs.6774	ESTs	0.49	1.24	late stage

412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	3.6	0.11	late stage
414020	NM_002984	Hs.75703	*small inducible cytokine A4 (homologous*	4.62	0.14	late stage
414183	AW957446	Hs.301711	ESTs	3.18	0.16	late stage
414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	0.81	0.73	late stage
414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	0.37	0.99	late stage
414504	AW069181	Hs.293523	ESTs, Weakly similar to transformation-r	0.97	0.65	late stage
414812	X72755	Hs.77367	monokine induced by gamma interferon	3.84	0.1	late stage
415116	AA160363	Hs.269956	ESTs	7.45	0.07	late stage
415714	NM_002290	Hs.78672	laminin, alpha 4	0.49	1.39	late stage
415822	D59243		gb:HUM526E07B Clontech human placenta po	8.15	0.09	late stage
415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	0.48	1.46	late stage
417059	AL037672	Hs.81071	extracellular matrix protein 1	1.52	0.44	late stage
417259	AW903838	Hs.81800	*chondroitin sulfate proteoglycan 2 (vers*	2	0.39	late stage
417733	AL048678	Hs.82503	syntaphilin	0.2	2.67	late stage
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	4.56	0.12	late stage
417849	AW291587	Hs.82733	nidogen 2	1.81	0.38	late stage
418005	AI186220	Hs.83164	collagen, type XV, alpha 1	0.97	0.74	late stage
418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	1.21	0.56	late stage
418875	W19971	Hs.233459	ESTs	2.63	0.33	late stage
419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	7.65	0.07	late stage
419925	AA159850	Hs.93765	lipoma HMGIC fusion partner	0.91	0.82	late stage
420411	AI581085	Hs.24678	ESTs	7.3	0.1	late stage
420943	AI718702	Hs.105341	ESTs	7.05	0.07	late stage
421116	T19132	Hs.101850	retinol-binding protein 1, cellular	0.99	0.42	late stage
421684	BE281591	Hs.106768	hypothetical protein FLJ10511	8.1	0.08	late stage
421786	AI188653	Hs.21351	ESTs	8.15	0.08	late stage
422414	AW875237	Hs.13701	ESTs	1.05	0.69	late stage
422550	BE297626	Hs.296049	microfibrillar-associated protein 4	0.28	1.53	late stage
422790	AA809875	Hs.25933	ESTs	2.59	0.28	late stage
423057	AW961597	Hs.130816	ESTs	7.55	0.08	late stage
423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone C	1.24	0.61	late stage
423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	2.12	0.24	late stage
423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	0.29	2.45	late stage
423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	4.47	0.17	late stage
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	2.44	0.26	late stage
424839	AA740632	Hs.120850	ESTs	2.74	0.23	late stage
426780	BE242284	Hs.172199	adenylate cyclase 7	8.55	0.09	late stage
426974	AB002298	Hs.173035	KIAA0300 protein	1.56	0.36	late stage
427055	AI301740	Hs.173381	dihydropyrimidinase-like 2	0.72	1	late stage
427882	AA640987	Hs.193767	ESTs	2.25	0.29	late stage
428065	AI634046	Hs.157313	ESTs	6.19	0.1	late stage
428147	AW629965	Hs.234983	ESTs	8.42	0.08	late stage
428585	AB007863	Hs.185140	KIAA0403 protein	6.85	0.08	late stage
428825	AI084336	Hs.128783	ESTs	0.9	0.8	late stage
429490	AI971131	Hs.293684	ESTs, Weakly similar to alternatively sp	1.59	0.39	late stage
429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	0.77	0.49	late stage
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.92	0.3	late stage
431319	AA873350		gb:oh64h02.s1 NCI_CGAP_Kid5 Homo sapiens	1.36	0.44	late stage
431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.69	0.17	late stage
432314	AA533447	Hs.285173	ESTs	1.75	0.31	late stage
432331	W37862	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586I1524 (f	0.35	1.58	late stage
432559	AW452948	Hs.257631	ESTs	1.37	0.49	late stage
433470	AW960564	Hs.3337	*transmembrane 4 superfamily member 1*	2.58	0.24	late stage
433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	5.06	0.11	late stage
436428	AW246900	Hs.283712	hypothetical protein	8.25	0.09	late stage
436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	1.6	0.26	late stage
438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.15	0.08	late stage
439584	AA838114	Hs.221612	ESTs	8.6	0.09	late stage
439653	AW021103	Hs.6631	hypothetical protein FLJ20373	2.21	0.27	late stage
440524	R71264	Hs.16798	ESTs	3.44	0.21	late stage
440624	AF017987	Hs.7306	secreted frizzled-related protein 1	0.42	0.63	late stage
441976	AA428403	Hs.106131	ESTs	8.5	0.09	late stage
442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	7.95	0.06	late stage
443852	AI679966	Hs.150603	ESTs	6.84	0.12	late stage
443896	AI680242	Hs.271687	Homo sapiens cDNA FLJ13527 fis, clone PL	7.95	0.08	late stage
444212	AW503976	Hs.10649	basement membrane-induced gene	2.31	0.28	late stage
444331	AW193342	Hs.24144	ESTs	0.32	1.64	late stage
445142	AW978484	Hs.93842	Homo sapiens cDNA: FLJ22554 fis, clone H	2.52	0.24	late stage
445701	AF055581	Hs.13131	lymphocyte adaptor protein	1.43	0.47	late stage
446584	U53445	Hs.15432	downregulated in ovarian cancer 1	0.54	1.39	late stage
447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte ch	1.43	0.43	late stage
447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgra	1.35	0.26	late stage
447818	W79940	Hs.21906	ESTs	6.63	0.13	late stage
449567	AI990790	Hs.188614	ESTs	4.7	0.13	late stage
450455	AL117424	Hs.25035	chloride intracellular channel 4	0.64	1.31	late stage
452239	AW379378	Hs.170121	protein tyrosine phosphatase, receptor t	0.59	1.18	late stage
452698	NM_001295	Hs.301921	ESTs	2.31	0.26	late stage

453212	H15416	Hs.21865	ESTs	2.51	0.26	late stage
455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio	8.6	0.06	late stage
400775	R58624	Hs.2186	eukaryotic translation elongation factor	1	1	T2-T4 grade 3 papilloma marker
401508				1	1	T2-T4 grade 3 papilloma marker
403092				1	1	T2-T4 grade 3 papilloma marker
404232				1	1	T2-T4 grade 3 papilloma marker
407020	U49973		gb:Human Tigger1 transposable element, c	1	1	T2-T4 grade 3 papilloma marker
407345	AI053836	Hs.169365	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	1	T2-T4 grade 3 papilloma marker
407420	AF084362		gb:Homo sapiens lipoate-protein ligase B	1	1	T2-T4 grade 3 papilloma marker
407577	AW131324	Hs.246759	ESTs, Weakly similar to KIAA1074 protein	1	1	T2-T4 grade 3 papilloma marker
407666	AF071107	Hs.37501	MAD (mothers against decapentaplegic, Dr	1	1	T2-T4 grade 3 papilloma marker
407916	L09234	Hs.603	ATPase, H+ transporting, lysosomal (vacu	1	1	T2-T4 grade 3 papilloma marker
407936	AW118147	Hs.270935	ESTs	1	1	T2-T4 grade 3 papilloma marker
408186	AW168847	Hs.250156	ESTs	1	1	T2-T4 grade 3 papilloma marker
408950	AA707814	Hs.7396	ESTs	1	1	T2-T4 grade 3 papilloma marker
409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.2	0.12	T2-T4 grade 3 papilloma marker
409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	1	1	T2-T4 grade 3 papilloma marker
409196	NM_001874	Hs.169765	carboxypeptidase M	1	1	T2-T4 grade 3 papilloma marker
409281	AA069998		gb:zm67b03.r1 Stratagene neuroepithelium	1	1	T2-T4 grade 3 papilloma marker
410010	AW572853	Hs.257683	ESTs, Weakly similar to ALU3_HUMAN ALU S	1	0.5	T2-T4 grade 3 papilloma marker
410157	AW593277	Hs.225056	ESTs	1	0.69	T2-T4 grade 3 papilloma marker
411112	AW818158		gb:CM1-ST0277-161299-070-g07 ST0277 Homo	1	1	T2-T4 grade 3 papilloma marker
411336	AW837675		gb:QV2-LT0039-260300-107-b04 LT0039 Homo	1	1	T2-T4 grade 3 papilloma marker
412051	T15872	Hs.268713	ESTs, Weakly similar to hypothetical pro	1	1	T2-T4 grade 3 papilloma marker
413485	N52628		gb:yv37g11.s1 Soares fetal liver spleen	1	1	T2-T4 grade 3 papilloma marker
413574	BE149158	Hs.129998	Homo sapiens cDNA FLJ14267 fis, clone PL	1	1	T2-T4 grade 3 papilloma marker
413782	BE546104		gb:601072642F1 NIH_MGC_12 Homo sapiens c	1	1	T2-T4 grade 3 papilloma marker
414749	H94622	Hs.193358	ESTs, Moderately similar to diabetes mel	1	1	T2-T4 grade 3 papilloma marker
415293	R49462	Hs.106541	ESTs	1	1	T2-T4 grade 3 papilloma marker
415442	F12963	Hs.7045	GL004 protein	1	1	T2-T4 grade 3 papilloma marker
416255	T87587	Hs.272082	ESTs	1	1	T2-T4 grade 3 papilloma marker
417047	AA192640	Hs.1526	ATPase, Ca++ transporting, cardiac muscl	1	1	T2-T4 grade 3 papilloma marker
417181	L10123	Hs.1071	surfactant protein A binding protein	1	1	T2-T4 grade 3 papilloma marker
417367	N73877	Hs.171815	ESTs	1	1	T2-T4 grade 3 papilloma marker
419721	NM_001650	Hs.288650	aquaporin 4	1	1	T2-T4 grade 3 papilloma marker
420294	AA808259	Hs.196716	ESTs	1	0.65	T2-T4 grade 3 papilloma marker
423589	AA328082	Hs.209569	ESTs, Weakly similar to thrombospondin t	1	1	T2-T4 grade 3 papilloma marker
424549	AI873205	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	1	1	T2-T4 grade 3 papilloma marker
425458	H89317	Hs.182889	ESTs	1	1	T2-T4 grade 3 papilloma marker
426475	AL134728		gb:DKFZp547A1890_r1 547 (synonym: hfbr1)	1	1	T2-T4 grade 3 papilloma marker
429453	AA453195	Hs.124222	ESTs	1	1	T2-T4 grade 3 papilloma marker
431200	AF044923	Hs.250752	hook1 protein	1	1	T2-T4 grade 3 papilloma marker
431938	AA938471	Hs.115242	developmentally regulated GTP-binding pr	1	1	T2-T4 grade 3 papilloma marker
431944	AI360891	Hs.143619	ESTs	1	1	T2-T4 grade 3 papilloma marker
432021	AA524470	Hs.58753	ESTs	1	1	T2-T4 grade 3 papilloma marker
432205	AI806583	Hs.125291	ESTs	1	0.31	T2-T4 grade 3 papilloma marker
432527	AW975028	Hs.102754	ESTs	1	1	T2-T4 grade 3 papilloma marker
434069	AF116651	Hs.283058	hypothetical protein PRO0800	1	0.41	T2-T4 grade 3 papilloma marker
435278	AW994242	Hs.173495	ESTs	1	1	T2-T4 grade 3 papilloma marker
435965	AI034368	Hs.132650	ESTs	1	0.36	T2-T4 grade 3 papilloma marker
436227	AA706937	Hs.120802	ESTs, Moderately similar to A26641 Na+/K	1	1	T2-T4 grade 3 papilloma marker
436635	AW104325	Hs.272093	ESTs, Weakly similar to STK2_HUMAN SERIN	1	0.74	T2-T4 grade 3 papilloma marker
436640	AA724411	Hs.156065	ESTs	1	1	T2-T4 grade 3 papilloma marker
436884	BE046657		gb:hn42e02.x1 NCI_CGAP_RDF2 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
437251	AW976082		gb:EST388191 MAGE resequences, MAGN Homo	1	1	T2-T4 grade 3 papilloma marker
437348	AA749149	Hs.163114	ESTs	1	1	T2-T4 grade 3 papilloma marker
437769	AA767853	Hs.122895	ESTs	1	1	T2-T4 grade 3 papilloma marker
437771	AA811071	Hs.123349	ESTs	1	1	T2-T4 grade 3 papilloma marker
438347	AA909686	Hs.293397	ESTs	1	1	T2-T4 grade 3 papilloma marker
439171	AA831133	Hs.294128	ESTs	1	0.95	T2-T4 grade 3 papilloma marker
439914	AA854066	Hs.145394	ESTs	1	1	T2-T4 grade 3 papilloma marker
440399	AI215527	Hs.125589	ESTs	1	1	T2-T4 grade 3 papilloma marker
440972	BE044588	Hs.276158	ESTs	1	1	T2-T4 grade 3 papilloma marker
442004	AA973568	Hs.128317	ESTs	1	1	T2-T4 grade 3 papilloma marker
442270	BE565699	Hs.62005	ESTs	1	1	T2-T4 grade 3 papilloma marker
443413	AI056457	Hs.221642	ESTs	1	1	T2-T4 grade 3 papilloma marker
443927	AW016726	Hs.134860	ESTs	1	1	T2-T4 grade 3 papilloma marker
445442	N20392	Hs.42846	ESTs	1	1	T2-T4 grade 3 papilloma marker
445611	AW418497	Hs.145583	ESTs	1	0.49	T2-T4 grade 3 papilloma marker
445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	1	1	T2-T4 grade 3 papilloma marker
446552	AW470827	Hs.156241	ESTs	1	1	T2-T4 grade 3 papilloma marker
447399	AI815401	Hs.251967	Homo sapiens clone 785627 unknown mRNA	2.9	0.14	T2-T4 grade 3 papilloma marker
449111	T83109	Hs.196180	ESTs	1	1	T2-T4 grade 3 papilloma marker
449232	AW192780	Hs.196080	ESTs	1	0.8	T2-T4 grade 3 papilloma marker
451373	AI792030		gb:os03e11.y5 NCI_CGAP_Lu5 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	1	1	T2-T4 grade 3 papilloma marker
452534	AW083022	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1	0.67	T2-T4 grade 3 papilloma marker

452536	BE063380		gb:PM0-BT0275-291099-002-g10 BT0275 Homo	1.65	0.26	T2-T4 grade 3 papilloma marker
452640	AA027115	Hs.100206	ESTs, Weakly similar to AAAD_HUMAN ARYLA	1	1	T2-T4 grade 3 papilloma marker
452645	AI911325	Hs.212049	EST	1	1	T2-T4 grade 3 papilloma marker
453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1	1	T2-T4 grade 3 papilloma marker
453472	AL037925		gb:DKFZp564M037_r1 564 (synonym: hfbr2)	1	0.8	T2-T4 grade 3 papilloma marker
453609	AL045301	Hs.13427	ESTs	1	1	T2-T4 grade 3 papilloma marker
453677	AL079389		gb:DKFZp434E2116_r1 434 (synonym: htes3)	1	0.77	T2-T4 grade 3 papilloma marker
453704	R41806	Hs.100884	ESTs	1	1	T2-T4 grade 3 papilloma marker
455267	AW880861		gb:QV0-OT0033-070300-152-c12 OT0033 Homo	1	1	T2-T4 grade 3 papilloma marker
455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	1	1	T2-T4 grade 3 papilloma marker
456520	AW835416	Hs.29417	HCF-binding transcription factor Zhangfe	1	1	T2-T4 grade 3 papilloma marker
456763	AJ271351	Hs.128180	B-cell translocation gene 4	1	0.71	T2-T4 grade 3 papilloma marker
456912	AI458843	Hs.158112	protein tyrosine phosphatase, receptor t	1	1	T2-T4 grade 3 papilloma marker
457018	AA761820	Hs.250965	ESTs	1	1	T2-T4 grade 3 papilloma marker
457323	AW967813	Hs.201064	ESTs	1	1	T2-T4 grade 3 papilloma marker
457339	AW971949	Hs.291252	ESTs	1	1	T2-T4 grade 3 papilloma marker
457340	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
457507	AW300248	Hs.181693	ESTs	1	1	T2-T4 grade 3 papilloma marker
458106	AF086561	Hs.37	acetyl-Coenzyme A acetyltransferase 1 (a	1	1	T2-T4 grade 3 papilloma marker
458624	AI362790	Hs.181801	ESTs	1	0.34	T2-T4 grade 3 papilloma marker
459396	AI907536	Hs.103869	ESTs	1	1	T2-T4 grade 3 papilloma marker
401002				1	1	T2-T4 grade 3 solid tumor marker
401866				1.35	0.14	T2-T4 grade 3 solid tumor marker
403615				1	1	T2-T4 grade 3 solid tumor marker
403776				1	1	T2-T4 grade 3 solid tumor marker
404113				1	0.43	T2-T4 grade 3 solid tumor marker
404488				1	0.17	T2-T4 grade 3 solid tumor marker
404653				1	1	T2-T4 grade 3 solid tumor marker
406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	1	0.24	T2-T4 grade 3 solid tumor marker
406471				1	0.42	T2-T4 grade 3 solid tumor marker
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	2.75	0.05	T2-T4 grade 3 solid tumor marker
407624	AW157431	Hs.248941	ESTs	3.05	0.15	T2-T4 grade 3 solid tumor marker
409153	W03754	Hs.50813	hypothetical protein FLJ20022	3.85	0.03	T2-T4 grade 3 solid tumor marker
409464	X69115	Hs.54488	zinc finger protein 37a (KOX 21)	1.15	0.29	T2-T4 grade 3 solid tumor marker
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	1	0.24	T2-T4 grade 3 solid tumor marker
410025	BE220489	Hs.113592	ESTs	1	0.3	T2-T4 grade 3 solid tumor marker
410589	AW770768	Hs.266717	ESTs	1	0.28	T2-T4 grade 3 solid tumor marker
411840	AW866330		gb:QV4-SN0024-080400-167-e01 SN0024 Homo	1.05	0.15	T2-T4 grade 3 solid tumor marker
412198	AA937111	Hs.69165	ESTs	1	0.26	T2-T4 grade 3 solid tumor marker
412305	AW936369		gb:QV4-DT0021-301299-071-d07 DT0021 Homo	1	0.53	T2-T4 grade 3 solid tumor marker
412753	AI065016	Hs.6390	ESTs	1	0.33	T2-T4 grade 3 solid tumor marker
413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	1	0.69	T2-T4 grade 3 solid tumor marker
413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	1	0.29	T2-T4 grade 3 solid tumor marker
415027	D31010		gb:HUML12147 Human fetal lung Homo sapie	1	1	T2-T4 grade 3 solid tumor marker
416099	H18626	Hs.22634	ESTs	1	0.74	T2-T4 grade 3 solid tumor marker
416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8	0.12	T2-T4 grade 3 solid tumor marker
418329	AW247430	Hs.84152	cystathionine-beta-synthase	2.85	0.08	T2-T4 grade 3 solid tumor marker
420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	1	0.2	T2-T4 grade 3 solid tumor marker
421243	AW873803	Hs.102876	pancreatic lipase	1	0.38	T2-T4 grade 3 solid tumor marker
422660	AW297582	Hs.237062	ESTs	1.05	0.32	T2-T4 grade 3 solid tumor marker
422834	AA318334		gb:EST20402 Retina II Homo sapiens cDNA	1	0.38	T2-T4 grade 3 solid tumor marker
422972	N59319	Hs.145404	ESTs	1	0.61	T2-T4 grade 3 solid tumor marker
423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	2.95	0.12	T2-T4 grade 3 solid tumor marker
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	1	0.05	T2-T4 grade 3 solid tumor marker
424268	AA397653	Hs.144339	Human DNA sequence from clone 495O10 on	1	0.35	T2-T4 grade 3 solid tumor marker
425196	AL037915	Hs.155097	carbonic anhydrase II	2.75	0.05	T2-T4 grade 3 solid tumor marker
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1	0.09	T2-T4 grade 3 solid tumor marker
430300	U60805	Hs.238648	oncostatin M receptor	1	0.25	T2-T4 grade 3 solid tumor marker
431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoisoadenylate	1	0.28	T2-T4 grade 3 solid tumor marker
431277	AA501806	Hs.249965	ESTs	1	0.22	T2-T4 grade 3 solid tumor marker
431750	AA514986	Hs.283705	ESTs	1	1	T2-T4 grade 3 solid tumor marker
434273	AA913143	Hs.26303	ESTs	1	0.41	T2-T4 grade 3 solid tumor marker
435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.8	0.19	T2-T4 grade 3 solid tumor marker
436281	AW411194	Hs.120051	ESTs	2.05	0.14	T2-T4 grade 3 solid tumor marker
437010	AA741368	Hs.291434	ESTs	2.4	0.17	T2-T4 grade 3 solid tumor marker
437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.8	0.13	T2-T4 grade 3 solid tumor marker
438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	1	0.3	T2-T4 grade 3 solid tumor marker
438376	BE541211	Hs.34804	Homo sapiens cDNA FLJ11472 fis, clone HE	1	0.57	T2-T4 grade 3 solid tumor marker
439370	AW274369	Hs.158853	ESTs	1	0.17	T2-T4 grade 3 solid tumor marker
440021	AW025498	Hs.270842	ESTs, Weakly similar to ALU8_HUMAN ALU S	1	0.65	T2-T4 grade 3 solid tumor marker
440404	AI015881	Hs.125616	ESTs	1	0.26	T2-T4 grade 3 solid tumor marker
441523	AW514263	Hs.168872	ESTs, Weakly similar to ALUF_HUMAN !!!!	1	1	T2-T4 grade 3 solid tumor marker
442277	AW448914	Hs.202391	ESTs	2.4	0.15	T2-T4 grade 3 solid tumor marker
442738	AW002370	Hs.131055	ESTs	1	0.29	T2-T4 grade 3 solid tumor marker
443297	AI049864	Hs.133029	ESTs	1	1	T2-T4 grade 3 solid tumor marker
444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	1	0.61	T2-T4 grade 3 solid tumor marker
445550	AI242754	Hs.137306	ESTs	1	0.5	T2-T4 grade 3 solid tumor marker

446149	BE242960	Hs.203181	ESTs	1	0.25	T2-T4 grade 3 solid tumor marker
446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1	0.21	T2-T4 grade 3 solid tumor marker
446434	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5)	1	1	T2-T4 grade 3 solid tumor marker
446928	AI694493	Hs.246916	ESTs	1	0.31	T2-T4 grade 3 solid tumor marker
448591	AI540111	Hs.171261	ESTs	1	1	T2-T4 grade 3 solid tumor marker
449121	AI915858	Hs.194980	ESTs	1	1	T2-T4 grade 3 solid tumor marker
449539	W80363	Hs.58446	ESTs	1	0.33	T2-T4 grade 3 solid tumor marker
450451	AW591528	Hs.202072	ESTs	1	0.59	T2-T4 grade 3 solid tumor marker
450469	AI955049	Hs.281326	ESTs	1	0.43	T2-T4 grade 3 solid tumor marker
450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1	0.05	T2-T4 grade 3 solid tumor marker
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	1.55	0.11	T2-T4 grade 3 solid tumor marker
451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	1	0.95	T2-T4 grade 3 solid tumor marker
451130	AI762250	Hs.211347	ESTs	3.65	0.15	T2-T4 grade 3 solid tumor marker
451412	AW136378	Hs.208060	ESTs	1	1	T2-T4 grade 3 solid tumor marker
451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	1.35	0.22	T2-T4 grade 3 solid tumor marker
452114	N22687	Hs.8236	ESTs	1	0.19	T2-T4 grade 3 solid tumor marker
452743	AW965082	Hs.61455	ESTs	1	0.44	T2-T4 grade 3 solid tumor marker
454622	U70071		gb:HSU70071 Human Homo sapiens cDNA clon	1	1	T2-T4 grade 3 solid tumor marker
455235	AW875951		gb:CM1-PT0013-131299-067-f09 PT0013 Homo	1	0.31	T2-T4 grade 3 solid tumor marker
457792	AL046988	Hs.268677	ESTs, Moderately similar to ALU7_HUMAN A	1	0.24	T2-T4 grade 3 solid tumor marker
100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	20.531	0.036	upregulate stage
101193	L20861	Hs.152213	"wingless-type MMTV integration site fam	1	0.526	upregulate stage
101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	20.67	0.037	upregulate stage
101809	M86849	"Hs.323733	"gap junction protein, beta 2, 26kD (con	20.78	0.019	upregulate stage
102154	U17760	Hs.75517	"laminin, beta 3 (nicein (125kD), kalini	18.848	0.042	upregulate stage
102211	U23070	Hs.78776	putative transmembrane protein	2.092	0.28	upregulate stage
102623	U66083	Hs.37110	"melanoma antigen, family A, 9"	1	0.306	upregulate stage
102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.27	0.041	upregulate stage
103036	X54925	"Hs.83169	matrix metalloproteinase 1 (interstitial	13.63	0.034	upregulate stage
103119	X63629	Hs.2877	"cadherin 3, type 1, P-cadherin (placent	7.296	0.054	upregulate stage
103312	X82693	Hs.3185	"lymphocyte antigen 6 complex, locus D"	0.908	0.485	upregulate stage
103478	Y07755	Hs.38991	S100 calcium-binding protein A2	2.928	0.219	upregulate stage
103587	Z29083	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.156	0.16	upregulate stage
106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	1.642	0.516	upregulate stage
107151	AA621169	Hs.8687	ESTs	2.421	0.174	upregulate stage
107901	AA026418	"Hs.111758	keratin 6A	1.259	0.343	upregulate stage
107922	AA028028	Hs.61460	"Homo sapiens Ig superfamily receptor LN	14.22	0.049	upregulate stage
109166	AA179845	Hs.73625	"RAB6 interacting, kinesin-like (rabkine	11.13	0.039	upregulate stage
109424	AA227919	"Hs.85962	hyaluronan synthase 3	1.737	0.518	upregulate stage
110906	N39584	Hs.17404	ESTs	20.93	0.021	upregulate stage
112244	R51309	Hs.70823	KIAA1077 protein	3.941	0.181	upregulate stage
115060	AA253214	Hs.198249	"gap junction protein, beta 5 (connexin	1.932	0.502	upregulate stage
115697	AA411502	Hs.63325	"transmembrane protease, serine 4"	7.394	0.101	upregulate stage
115978	AA447522	"Hs.69517	"Homo sapiens, clone MGC:5257, mRNA, com	1.667	0.445	upregulate stage
116335	AA495830	Hs.41690	desmocollin 3	4.899	0.154	upregulate stage
118314	N63402	Hs.46692	ESTs	9.75	0.069	upregulate stage
118336	N63604	Hs.47166	HT021	4.601	0.197	upregulate stage
119845	W79920	Hs.58561	G protein-coupled receptor 87	1.95	0.123	upregulate stage
120486	AA253400	Hs.137569	tumor protein 63 kDa with strong homolog	4.191	0.211	upregulate stage
121027	AA398470	Hs.99785	"Homo sapiens cDNA: FLJ21245 fis, clone	14.25	0.058	upregulate stage
124059	F13673	Hs.283713	"ESTs, Weakly similar to ORF YGL050w [S.	4.99	0.168	upregulate stage
128595	U31875	"Hs.152677	"Homo sapiens cDNA FLJ20338 fis, clone H	2.433	0.306	upregulate stage
128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	4.34	0.14	upregulate stage
129041	H58873	"Hs.169902	"solute carrier family 2 (facilitated gl	2.003	0.455	upregulate stage
129468	L42583	"Hs.111758	keratin 6A	11.584	0.042	upregulate stage
130627	L23808	Hs.1695	matrix metalloproteinase 12 (macrophage	2.376	0.233	upregulate stage
132349	Y00705	"Hs.181286	"serine protease inhibitor, Kazal type 1	5.4	0.132	upregulate stage
132710	W93726	Hs.55279	"serine (or cysteine) proteinase inhibit	3.888	0.187	upregulate stage
133391	X57579	Hs.727	"inhibin, beta A (activin A, activin AB	1.517	0.334	upregulate stage
134110	AA242758	"Hs.79136	"LIV-1 protein, estrogen regulated"	2.221	0.387	upregulate stage
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.85	0.03	upregulate stage
400297	AI127076	Hs.288381	hypothetical protein DKFZp564O1278	3.54	0.13	upregulate stage
400346	AB041269	Hs.272263	Homo sapiens mRNA for keratin 19, partia	8.95	0.07	upregulate stage
400419	AF084545	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	10.7	0.06	upregulate stage
400495				1	0.56	upregulate stage
400509	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	1.52	0.51	upregulate stage
400528				3.47	0.23	upregulate stage
400577				1	0.29	upregulate stage
400608				7.2	0.08	upregulate stage
400644				1	1	upregulate stage
400666				1.42	0.43	upregulate stage
400750				8.7	0.1	upregulate stage
400773				1.11	0.51	upregulate stage
400844				9.65	0.04	upregulate stage
400845				2.3	0.28	upregulate stage
400846				1.34	0.5	upregulate stage
400880				9.4	0.06	upregulate stage

400887				1	1	upregulate stage
401086				1	0.51	upregulate stage
401093				7	0.08	upregulate stage
401101				1	0.17	upregulate stage
401197				5.18	0.14	upregulate stage
401262				1	1	upregulate stage
401271				1	1	upregulate stage
401279				9.1	0.06	upregulate stage
401342				1.42	0.5	upregulate stage
401345	M83738	Hs.147663	protein tyrosine phosphatase, non-recept	1	0.33	upregulate stage
401365				6.5	0.11	upregulate stage
401395				1	0.31	upregulate stage
401420				1	1	upregulate stage
401439				2.65	0.17	upregulate stage
401451				12	0.05	upregulate stage
401599	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	9.15	0.08	upregulate stage
401600	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	8.75	0.09	upregulate stage
401694				1	1	upregulate stage
401747				29.75	0.02	upregulate stage
401759				11.35	0.06	upregulate stage
401780				6.15	0.07	upregulate stage
401868	AC005261	Hs.98338	serine/threonine kinase 13 (aurora/IPL1-	1	0.69	upregulate stage
401994				3.15	0.15	upregulate stage
402001				4.4	0.14	upregulate stage
402230				8.75	0.06	upregulate stage
402325				1	0.36	upregulate stage
402408				5.15	0.1	upregulate stage
402472				9.05	0.08	upregulate stage
402480				1	1	upregulate stage
402490				9.6	0.07	upregulate stage
402553				9.85	0.09	upregulate stage
402889				9.4	0.09	upregulate stage
402901				1.07	0.65	upregulate stage
402938				1	1	upregulate stage
402995				9.6	0.06	upregulate stage
403005				1.5	0.21	upregulate stage
403020				5.15	0.12	upregulate stage
403052	R58624	Hs.2186	eukaryotic translation elongation factor	1	1	upregulate stage
403053	R58624	Hs.2186	eukaryotic translation elongation factor	1.5	0.28	upregulate stage
403073				1	0.37	upregulate stage
403085				1	0.43	upregulate stage
403106				1.12	0.57	upregulate stage
403152	AA576664	Hs.37078	v-crk avian sarcoma virus CT10 oncogene	0.86	1.08	upregulate stage
403172				7.7	0.09	upregulate stage
403212				1.18	0.62	upregulate stage
403214				6.05	0.1	upregulate stage
403277				4.5	0.11	upregulate stage
403331				3.2	0.13	upregulate stage
403381				10.7	0.05	upregulate stage
403485				10.35	0.08	upregulate stage
403588				1	1	upregulate stage
403851				2.45	0.34	upregulate stage
403860				1	1	upregulate stage
403894				4.45	0.14	upregulate stage
403903				1.39	0.58	upregulate stage
403954	W28077	Hs.79389	nel (chicken)-like 2	1	1	upregulate stage
404148				9.15	0.08	upregulate stage
404229				1	1	upregulate stage
404268				1	1	upregulate stage
404274				1.3	0.2	upregulate stage
404288				1	0.39	upregulate stage
404403				1	0.28	upregulate stage
404440				7.05	0.06	upregulate stage
404507				1	0.33	upregulate stage
404516				1	1	upregulate stage
404639				1	1	upregulate stage
404684				0.89	0.9	upregulate stage
404685				2.74	0.26	upregulate stage
404704				9.35	0.08	upregulate stage
404829				1	0.24	upregulate stage
404860				3.65	0.15	upregulate stage
404894				2.05	0.16	upregulate stage
404939				1	1	upregulate stage
405034	AL035754	Hs.2474	toll-like receptor 1	1	0.18	upregulate stage
405059				1	0.56	upregulate stage
405064				1	0.22	upregulate stage
405102				9.65	0.08	upregulate stage

405167				1	0.67	upregulate stage
405170				1	0.48	upregulate stage
405177				1	0.22	upregulate stage
405186				3.75	0.1	upregulate stage
405258				8.85	0.09	upregulate stage
405281				1	1	upregulate stage
405379				1	0.87	upregulate stage
405494				5	0.13	upregulate stage
405520				1	0.95	upregulate stage
405526				8.96	0.08	upregulate stage
405725				3.3	0.12	upregulate stage
405738				0.86	0.69	upregulate stage
405809				2.4	0.18	upregulate stage
405838				1	0.22	upregulate stage
405906				2.6	0.12	upregulate stage
406137				1.54	0.52	upregulate stage
406187				3.2	0.14	upregulate stage
406322				3.95	0.12	upregulate stage
406360				4.1	0.1	upregulate stage
406397				1	0.24	upregulate stage
406434				7.4	0.07	upregulate stage
406467				9.1	0.07	upregulate stage
406511				1	1	upregulate stage
406517	W28077	Hs.79389	nel (chicken)-like 2	1	1	upregulate stage
406588				0.93	0.91	upregulate stage
406651	AI559224	Hs.277477	major histocompatibility complex, class	10.1	0.07	upregulate stage
406665	U22961	Hs.75442	albumin	1.08	0.81	upregulate stage
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	5.7	0.12	upregulate stage
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	1.95	0.3	upregulate stage
406732	AA487229	Hs.2064	vimentin	1	0.77	upregulate stage
406747	AI925153	Hs.217493	annexin A2	3.6	0.14	upregulate stage
406753	AA505665	Hs.217493	annexin A2	5.45	0.13	upregulate stage
406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	3.65	0.09	upregulate stage
406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.29	0.62	upregulate stage
406892	D55643		gb:Human spleen PABL (pseudoautosomal bo	1	1	upregulate stage
406944	J04742	Hs.247945	Human autonomous replicating sequence H1	1	1	upregulate stage
406950	L17325	Hs.278	pre-T/NK cell associated protein	1	0.36	upregulate stage
406961	L77563		gb:Homo sapiens DGS-F partial mRNA.	1	1	upregulate stage
406964	M21305	Hs.247946	Human alpha satellite and satellite 3 ju	42.25	0.01	upregulate stage
406993	S83249		gb:NG-TRA=transporter protein/putative h	1	1	upregulate stage
407017	U48697		gb:Human mariner-like element-containing	1	1	upregulate stage
407073	Y10510		gb:H.sapiens mRNA for CD67S protein.	1	0.53	upregulate stage
407105	S64699	Hs.663	cystic fibrosis transmembrane conductanc	1	1	upregulate stage
407128	R83312	Hs.237260	EST	1	1	upregulate stage
407132	T02871	Hs.228523	EST	1	0.45	upregulate stage
407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	14.3	0.05	upregulate stage
407158	N49839		gb:yz08b10.s1 Soares_multiple_sclerosis_	1	0.57	upregulate stage
407175	T86603		gb:yd87d12.s1 Soares fetal liver spleen	1	0.31	upregulate stage
407186	AA435610		gb:zt74b11.s1 Soares_testis_NHT Homo sap	1	1	upregulate stage
407189	AA598927		gb:ae37e03.s1 Gessler Wilms tumor Homo s	1	1	upregulate stage
407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	6.05	0.12	upregulate stage
407195	C21124		gb:HUMGS0002072 Human adult (K.Okubo) Ho	1	1	upregulate stage
407202	N58172	Hs.109370	ESTs	3.7	0.16	upregulate stage
407204	R41933	Hs.140237	ESTs, Weakly similar to AF119917 13 PRO1	10.2	0.06	upregulate stage
407205	R78910	Hs.272620	pregnancy specific beta-1-glycoprotein 9	1.9	0.22	upregulate stage
407211	T95828	Hs.230070	EST	1	0.59	upregulate stage
407346	AI090210	Hs.264106	ESTs	1	1	upregulate stage
407422	AF116633		gb:Homo sapiens PRO1318 mRNA, complete c	1	0.22	upregulate stage
407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	4.1	0.13	upregulate stage
407547	Y10259		gb:H.sapiens ACTH receptor mRNA 3'UTR.	2.45	0.19	upregulate stage
407564	AA042860	Hs.103005	ESTs	1	1	upregulate stage
407603	AW955705	Hs.62604	ESTs	1.18	0.73	upregulate stage
407634	AW016569	Hs.301280	ESTs, Highly similar to AF241831 1 intra	9.6	0.06	upregulate stage
407668	BE161086	Hs.279817	ESTs	1	0.39	upregulate stage
407709	AA456135	Hs.23023	ESTs	6.8	0.12	upregulate stage
407710	AW022727	Hs.23616	ESTs	3.9	0.14	upregulate stage
407725	BE388094	Hs.21857	ESTs	9.97	0.07	upregulate stage
407729	T40707	Hs.270862	ESTs	9.2	0.09	upregulate stage
407774	AA084958		gb:zn13d12.r1 Stratagene hNT neuron (937	2.65	0.22	upregulate stage
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.1	0.34	upregulate stage
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	8.45	0.06	upregulate stage
407813	AL120247	Hs.40109	KIAA0872 protein	9.1	0.08	upregulate stage
407833	AW955632	Hs.66666	ESTs	9.2	0.07	upregulate stage
407839	AA045144	Hs.161566	ESTs	2.11	0.25	upregulate stage
407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	1	0.34	upregulate stage
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	3.52	0.18	upregulate stage
407882	AI241264	Hs.62772	ESTs	1	0.26	upregulate stage

407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	13.6	0.05	upregulate stage
407911	AF104922	Hs.41565	growth differentiation factor 8	1	1	upregulate stage
407912	AW104401	Hs.243489	ESTs, Weakly similar to AF151881 1 CGI-1	10.35	0.07	upregulate stage
407935	U31986	Hs.41683	cartilage paired-class homeoprotein 1	4.25	0.12	upregulate stage
407939	W05608		gb:za85e07.r1 Soares_fetal_lung_NbHL19W	8.75	0.09	upregulate stage
407944	R34008	Hs.239727	desmocollin 2	9.2	0.06	upregulate stage
407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	1.45	0.25	upregulate stage
407946	AA226495	Hs.154292	ESTs	9.4	0.07	upregulate stage
407949	W21874	Hs.247057	ESTs	3.32	0.2	upregulate stage
407974	AW968123	Hs.146401	small inducible cytokine subfamily E, me	3.55	0.14	upregulate stage
407983	U40371	Hs.41718	phosphodiesterase 1C, calmodulin-depende	8.95	0.07	upregulate stage
407994	AW135309	Hs.244331	ESTs	4.5	0.12	upregulate stage
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	2.89	0.19	upregulate stage
408014	AA723782	Hs.41749	protein kinase, cGMP-dependent, type II	1.31	0.53	upregulate stage
408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	3.6	0.17	upregulate stage
408046	AW139121	Hs.183643	ESTs	1	0.36	upregulate stage
408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	10.75	0.05	upregulate stage
408092	NM_007057	Hs.42650	ZW10 interactor	4.7	0.13	upregulate stage
408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.5	0.14	upregulate stage
408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic b	4.4	0.13	upregulate stage
408170	AW204516	Hs.31835	ESTs	5.85	0.13	upregulate stage
408184	AW168741	Hs.22249	ESTs	1	1	upregulate stage
408224	AW175997		gb:QV0-BT0078-190899-005-E02 BT0078 Homo	1	0.44	upregulate stage
408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.95	0.04	upregulate stage
408241	AW176546		gb:MR0-CT0063-200899-001-a01 CT0063 Homo	2.8	0.17	upregulate stage
408268	AL138247		gb:DKFZp547D237_r1 547 (synonym: hfbr1)	1	0.61	upregulate stage
408277	AW177959		gb:IL3-HT0060-200899-008-D03 HT0060 Homo	1	1	upregulate stage
408306	BE141991		gb:PM2-HT0134-220999-002-d10 HT0134 Homo	1	1	upregulate stage
408352	AA053875	Hs.95310	ESTs	1	1	upregulate stage
408360	AI806090	Hs.44344	hypothetical protein FLJ20534	9.15	0.08	upregulate stage
408393	AW015318	Hs.23165	ESTs	9.35	0.07	upregulate stage
408396	AA330496	Hs.40840	ESTs	1	0.61	upregulate stage
408442	R59608	Hs.21435	ESTs	1	1	upregulate stage
408514	AW206559	Hs.255903	ESTs	1	0.34	upregulate stage
408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1	0.33	upregulate stage
408617	R61736	Hs.124128	ESTs	2.75	0.14	upregulate stage
408633	AW963372	Hs.46677	PRO2000 protein	3.14	0.25	upregulate stage
408706	AW438503	Hs.256935	ESTs	8.45	0.09	upregulate stage
408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	2.81	0.21	upregulate stage
408725	AA131539	Hs.15669	ESTs	9.1	0.08	upregulate stage
408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.1	0.11	upregulate stage
408738	NM_014785	Hs.47313	KIAA0258 gene product	4.4	0.13	upregulate stage
408739	W01556	Hs.238797	ESTs	5.65	0.11	upregulate stage
408754	N31256	Hs.161623	ESTs	1	1	upregulate stage
408765	AA057268	Hs.146013	ESTs	8.75	0.09	upregulate stage
408805	H69912	Hs.48269	vaccinia related kinase 1	4.95	0.12	upregulate stage
408813	AI580090	Hs.48295	RNA helicase family	3.65	0.17	upregulate stage
408817	AA524525	Hs.279864	PRO1996 protein	6.15	0.12	upregulate stage
408849	BE219451	Hs.254919	ESTs	1	0.32	upregulate stage
408902	AW014869	Hs.5510	ESTs	3.3	0.15	upregulate stage
408908	BE296227	Hs.48915	serine/threonine kinase 15	5.65	0.1	upregulate stage
408916	AW295232	Hs.22893	ESTs	10	0.08	upregulate stage
408933	AA058979	Hs.182133	ESTs, Highly similar to ADP-ribosylation	1	0.91	upregulate stage
408943	NM_007070	Hs.49105	FKBP-associated protein	3.45	0.16	upregulate stage
408960	BE158389	Hs.300976	ESTs	6.3	0.1	upregulate stage
409032	AW301807	Hs.297260	ESTs	8.4	0.08	upregulate stage
409093	BE243834	Hs.50441	CGI-04 protein	1.71	0.49	upregulate stage
409099	AK000725	Hs.50579	hypothetical protein FLJ20718	10.1	0.07	upregulate stage
409142	AL136877	Hs.50758	chromosome-associated polypeptide C	11.85	0.05	upregulate stage
409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	2.83	0.24	upregulate stage
409231	AA446644	Hs.692	tumor-associated calcium signal transduc	9.34	0.08	upregulate stage
409262	AK000631	Hs.52256	hypothetical protein FLJ20624	8.7	0.09	upregulate stage
409357	M73628	Hs.54415	casein, kappa	1.6	0.2	upregulate stage
409402	AF208234	Hs.695	cystatin B (stefin B)	1.57	0.56	upregulate stage
409405	AA075869	Hs.126400	ESTs, Highly similar to RL39_HUMAN 60S R	2.6	0.12	upregulate stage
409408	AW387837		gb:MR4-ST0118-021299-021-f08 ST0118 Homo	4.3	0.15	upregulate stage
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	8.28	0.06	upregulate stage
409509	AL036923	Hs.127006	ESTs	10.2	0.06	upregulate stage
409566	AA078899		gb:zm94b01.r1 Stratagene colon HT29 (937	1	0.56	upregulate stage
409575	AW419225	Hs.256247	ESTs	2.15	0.14	upregulate stage
409582	R27430	Hs.271565	ESTs	7.3	0.07	upregulate stage
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	3.78	0.19	upregulate stage
409642	AW450809	Hs.257347	ESTs	9.55	0.07	upregulate stage
409674	AI935146	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1	0.29	upregulate stage
409691	T89983	Hs.246042	ESTs	1	1	upregulate stage
409703	NM_006187	Hs.56009	2'-5'oligoadenylate synthetase 3	2.22	0.36	upregulate stage
409727	N63786	Hs.94149	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.57	upregulate stage

409760	AA302840		gb:EST10534 Adipose tissue, white I Homo	9.95	0.06	upregulate stage
409789	BE256027	Hs.180946	ribosomal protein L5	1	0.83	upregulate stage
409794	AW885691		gb:RC4-OT0071-240300-013-b04 OT0071 Homo	1	1	upregulate stage
409977	AW805510	Hs.97056	hypothetical protein FLJ21634	9.65	0.07	upregulate stage
409985	AW291944	Hs.122139	ESTs	4.35	0.14	upregulate stage
409989	R37868	Hs.13333	ESTs	1	0.21	upregulate stage
409995	AW960597	Hs.30164	ESTs	5.05	0.12	upregulate stage
410013	AF067173	Hs.57904	mago-nashi (Drosophila) homolog, prolife	3.05	0.26	upregulate stage
410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	3.15	0.09	upregulate stage
410071	AW582568		gb:RC1-ST0278-080100-011-h04 ST0278 Homo	2.5	0.18	upregulate stage
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	8	0.06	upregulate stage
410114	AW590540	Hs.271280	ESTs	5.1	0.14	upregulate stage
410117	AK001586	Hs.58650	hypothetical protein FLJ10724	1	1	upregulate stage
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	4.7	0.11	upregulate stage
410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	1	0.23	upregulate stage
410196	AI936442	Hs.59838	hypothetical protein FLJ10808	6.05	0.09	upregulate stage
410252	AW821182	Hs.61418	microfibrillar-associated protein 1	5.55	0.12	upregulate stage
410259	AK000337	Hs.61485	hypothetical protein	10.1	0.07	upregulate stage
410276	AI554545	Hs.68301	ESTs	2.98	0.25	upregulate stage
410278	AW614396	Hs.282230	ESTs	1	0.28	upregulate stage
410325	AB023154	Hs.62264	KIAA0937 protein	6.85	0.13	upregulate stage
410356	BE244668	Hs.62643	dual adaptor of phosphotyrosine and 3-ph	1	1	upregulate stage
410388	AA831460	Hs.22039	hepatocyte nuclear factor 3, alpha	1	0.33	upregulate stage
410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific	1.07	0.78	upregulate stage
410420	AA224053	Hs.172405	ESTs, Moderately similar to I52835 H-NUC	1	0.14	upregulate stage
410429	AA310600	Hs.63657	hypothetical protein FLJ11005	11.25	0.07	upregulate stage
410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	9.6	0.08	upregulate stage
410475	AW749927		gb:QV0-BT0537-231299-049-f03 BT0537 Homo	9.8	0.08	upregulate stage
410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	11.3	0.06	upregulate stage
410501	AI675688	Hs.83286	ESTs	4.75	0.1	upregulate stage
410503	AW975746	Hs.188662	Homo sapiens cDNA: FLJ23421 fis, clone H	6.5	0.1	upregulate stage
410520	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	1	1	upregulate stage
410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	3.1	0.16	upregulate stage
410537	AW753108		gb:PM1-CT0247-080100-008-e10 CT0247 Homo	10.35	0.08	upregulate stage
410553	AW016824	Hs.68784	ESTs	1.67	0.41	upregulate stage
410560	N29220		gb:yx43b05.r1 Soares melanocyte 2NbHM Ho	9	0.07	upregulate stage
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	6.2	0.11	upregulate stage
410562	AW858528		gb:CM3-CT0341-150300-119-h11 CT0341 Homo	1	1	upregulate stage
410579	AK001628	Hs.64691	KIAA0483 protein	11.1	0.06	upregulate stage
410634	AW888653	Hs.266859	ESTs	1	1	upregulate stage
410664	NM_006033	Hs.65370	lipase, endothelial	3.95	0.1	upregulate stage
410668	BE379794	Hs.65403	hypothetical protein	1.82	0.41	upregulate stage
410730	AW368860	Hs.293950	ESTs	9.25	0.07	upregulate stage
410751	AA357918		gb:EST66726 Fetal lung III Homo sapiens	1	1	upregulate stage
410754	T63840		gb:yc16b10.s1 Stratagene lung (937210) H	3.1	0.14	upregulate stage
410762	AF226053	Hs.66170	HSKM-B protein	5.55	0.1	upregulate stage
410764	AW978159	Hs.250164	ESTs, Weakly similar to coded for by C.	1	0.2	upregulate stage
410782	AW504860	Hs.288836	Homo sapiens cDNA FLJ12673 fis, clone NT	1.75	0.25	upregulate stage
410794	AA248010	Hs.154669	ESTs	1	0.67	upregulate stage
410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.2	0.17	upregulate stage
410844	AW807073		gb:MR4-ST0062-031199-018-d06 ST0062 Homo	1	0.8	upregulate stage
410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	6.5	0.12	upregulate stage
410910	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	9.35	0.08	upregulate stage
410973	AW812278		gb:RC0-ST0174-211099-011-h12 ST0174 Homo	1	1	upregulate stage
410976	R36207	Hs.25092	ESTs	8.35	0.1	upregulate stage
410997	AW812877		gb:RC3-ST0186-300100-017-e04 ST0186 Homo	1	1	upregulate stage
410998	W28247	Hs.82007	KIAA0094 protein	2.45	0.18	upregulate stage
411036	AA857218	Hs.297007	ESTs	4.05	0.14	upregulate stage
411110	H93000		gb:yv07f01.s1 Soares fetal liver spleen	1	0.36	upregulate stage
411132	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	1	1	upregulate stage
411137	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	3.65	0.18	upregulate stage
411157	AW819867		gb:QV0-ST0294-070300-151-f02 ST0294 Homo	3.2	0.2	upregulate stage
411159	AW820178		gb:QV0-ST0294-100400-185-e07 ST0294 Homo	1	0.27	upregulate stage
411170	AW820503		gb:QV2-ST0298-140200-042-b05 ST0298 Homo	1	1	upregulate stage
411193	AW821484		gb:IL2-ST0311-211299-028-F12 ST0311 Homo	1	0.24	upregulate stage
411242	BE146808		gb:QV4-HT0222-181099-013-g03 HT0222 Homo	2.55	0.26	upregulate stage
411245	AW833441		gb:QV4-TT0008-271099-020-g01 TT0008 Homo	9.62	0.09	upregulate stage
411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.4	0.32	upregulate stage
411282	AW995011		gb:QV0-BN0040-170300-161-d07 BN0040 Homo	1	1	upregulate stage
411284	N28519	Hs.135191	ESTs, Weakly similar to unnamed protein	3.25	0.12	upregulate stage
411294	AW859729	Hs.42680	ESTs	1	1	upregulate stage
411327	AW836922		gb:QV1-LT0036-150200-074-h06 LT0036 Homo	1	0.37	upregulate stage
411338	AW731782	Hs.116122	ESTs, Weakly similar to unnamed protein	5	0.13	upregulate stage
411339	BE164598		gb:RC3-HT0470-120200-013-b10 HT0470 Homo	1	0.25	upregulate stage
411383	AA001394	Hs.69749	KIAA0087 gene product	3.6	0.18	upregulate stage
411387	AW842339	Hs.130815	hypothetical protein FLJ21870	8.75	0.09	upregulate stage
411400	AA311919	Hs.69851	GAR1 protein	12.1	0.07	upregulate stage

411425	AW846012		gb:RC2-CT0163-230999-003-E01 CT0163 Homo	1	0.74	upregulate stage
411461	AW847937		gb:IL3-CT0213-210200-042-D02 CT0213 Homo	1	1	upregulate stage
411526	AW850327		gb:IL3-CT0219-221199-029-D08 CT0219 Homo	1	1	upregulate stage
411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo	2.8	0.17	upregulate stage
411568	BE144593		gb:MR0-HT0167-141199-002-f04 HT0167 Homo	1	1	upregulate stage
411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.55	0.14	upregulate stage
411605	AW006831	Hs.20479	ESTs	9.6	0.08	upregulate stage
411626	AW793453	Hs.71109	KIAA1229 protein	1	1	upregulate stage
411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	4.1	0.11	upregulate stage
411643	AI924519	Hs.192570	Homo sapiens cDNA: FLJ22028 fis, clone H	1	0.28	upregulate stage
411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	8.9	0.08	upregulate stage
411727	AW858443		gb:CM0-CT0341-260100-160-f10 CT0341 Homo	1	1	upregulate stage
411771	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	2.6	0.14	upregulate stage
411787	AW863568		gb:MR3-SN0010-240300-102-c10 SN0010 Homo	1	1	upregulate stage
411788	AW897793		gb:CM1-NN0063-280400-203-f07 NN0063 Homo	3.7	0.15	upregulate stage
411826	AW947946		gb:PM0-MT0011-240300-001-a09 MT0011 Homo	3.25	0.13	upregulate stage
411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	1	1	upregulate stage
411860	T89420		gb:yd98f04.s1 Soares fetal liver spleen	1	0.22	upregulate stage
411874	AA096106	Hs.20403	ESTs	5.75	0.11	upregulate stage
411917	AW876360	Hs.3592	Homo sapiens cDNA: FLJ22555 fis, clone H	1	0.33	upregulate stage
411928	AA888624	Hs.19121	adaptor-related protein complex 2, alpha	4.75	0.12	upregulate stage
411932	AW876548		gb:RC3-PT0028-190100-012-h02 PT0028 Homo	1	0.38	upregulate stage
411943	BE502436	Hs.7962	ESTs, Weakly similar to putative [C.eleg	3.82	0.23	upregulate stage
411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	4.65	0.15	upregulate stage
411991	X58822	Hs.73010	interferon, omega 1	2.45	0.14	upregulate stage
412040	D86519	Hs.73086	neuropeptide Y receptor Y6 (pseudogene)	4.6	0.14	upregulate stage
412088	AI689496	Hs.108932	ESTs	2.82	0.18	upregulate stage
412134	AW895560		gb:QV4-NN0038-270400-187-g08 NN0038 Homo	6.4	0.1	upregulate stage
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	17.05	0.04	upregulate stage
412231	AW902491	Hs.289088	heat shock 90kD protein 1, alpha	1	0.91	upregulate stage
412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	1	1	upregulate stage
412327	AW937355		gb:QV3-DT0043-211299-044-a06 DT0043 Homo	1	1	upregulate stage
412357	AW939537		gb:QV1-DT0072-110200-066-f05 DT0072 Homo	1	0.24	upregulate stage
412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	1	0.41	upregulate stage
412367	AW945964		gb:QV0-ET0001-050500-228-e09 ET0001 Homo	1	0.22	upregulate stage
412529	BE271224	Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	4.45	0.14	upregulate stage
412530	AA766268	Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	9.3	0.08	upregulate stage
412537	AL031778	Hs.797	nuclear transcription factor Y, alpha	4.25	0.14	upregulate stage
412547	W27161		gb:23a12 Human retina cDNA randomly prim	1	1	upregulate stage
412559	T31474		gb:EST33147 Human Embryo Homo sapiens cD	1	0.26	upregulate stage
412636	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	12.05	0.05	upregulate stage
412648	AA115211	Hs.69658	EST	1	0.28	upregulate stage
412668	AA456195	Hs.10056	ESTs	10.75	0.07	upregulate stage
412671	AW977734		gb:EST389963 MAGE resequences, MAGO Homo	2.65	0.3	upregulate stage
412673	AL042957	Hs.31845	ESTs	4.6	0.11	upregulate stage
412723	AA648459	Hs.179912	ESTs	2.55	0.11	upregulate stage
412739	AA116018	Hs.271809	Homo sapiens cDNA: FLJ22406 fis, clone H	1.6	0.24	upregulate stage
412744	N31101		gb:yx52a03.r1 Soares melanocyte 2NbHM Ho	2	0.23	upregulate stage
412778	AA120882	Hs.159244	ESTs	1	1	upregulate stage
412811	H06382	Hs.21400	ESTs	1	0.49	upregulate stage
412838	D61870		gb:HUM218F11B Clontech human aorta polyA	1	0.34	upregulate stage
412854	BE004149	Hs.31161	ESTs	1	1	upregulate stage
413075	D59828	Hs.70953	ESTs	1	0.77	upregulate stage
413109	AW389845	Hs.110855	ESTs	3.93	0.1	upregulate stage
413117	BE066107	Hs.138484	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.22	upregulate stage
413119	BE065941		gb:RC3-BT0319-100100-012-d12 BT0319 Homo	1	0.87	upregulate stage
413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	5.45	0.12	upregulate stage
413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PL	2.54	0.19	upregulate stage
413228	AA127518	Hs.195870	ESTs	1	1	upregulate stage
413273	U75679	Hs.75257	Hairpin binding protein, histone	5.05	0.11	upregulate stage
413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.45	0.5	upregulate stage
413294	BE144034		gb:MR0-HT0165-191199-004-a02 HT0165 Homo	1	1	upregulate stage
413324	V00571	Hs.75294	corticotropin releasing hormone	6.95	0.03	upregulate stage
413342	AA128535		gb:zl24e04.r1 Soares_pregnant_uterus_NbH	1	1	upregulate stage
413430	R22479	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT	3	0.18	upregulate stage
413707	BE158679		gb:CM0-HT0395-280100-169-c04 HT0395 Homo	1	0.28	upregulate stage
413743	BE161004		gb:PM0-HT0425-170100-002-h03 HT0425 Homo	1	1	upregulate stage
413753	U17760	Hs.301103	Human DNA sequence from clone 272L16 on	22.7	0.03	upregulate stage
413786	AW613780	Hs.13500	ESTs	9.9	0.07	upregulate stage
413792	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	1	1	upregulate stage
413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	0.99	0.75	upregulate stage
413833	Z15005	Hs.75573	centromere protein E (312kD)	2.55	0.17	upregulate stage
413854	BE174300	Hs.44581	heat shock protein hsp70-related protein	1.25	0.24	upregulate stage
413918	AW015898	Hs.71245	ESTs	4	0.11	upregulate stage
413968	AW500374	Hs.64056	ESTs	10.85	0.07	upregulate stage
414091	T83742		gb:yd67g02.s1 Soares fetal liver spleen	8.9	0.1	upregulate stage
414099	U11313	Hs.75760	sterol carrier protein 2	10.3	0.06	upregulate stage

414116	AA587370	Hs.71584	ESTs	1	1	upregulate stage
414127	AI431863	Hs.135270	ESTs	2.85	0.13	upregulate stage
414169	AA136169	Hs.149335	ESTs	8.95	0.09	upregulate stage
414275	AW970254	Hs.889	Charot-Leyden crystal protein	7.05	0.05	upregulate stage
414304	AI621276	Hs.165998	DKFZP564M2423 protein	1	0.24	upregulate stage
414338	N80751	Hs.301471	ESTs	10.3	0.08	upregulate stage
414447	AA147549	Hs.109909	ESTs	3.4	0.16	upregulate stage
414494	AA768491	Hs.6783	Homo sapiens cDNA: FLJ22724 fis, clone H	3.4	0.18	upregulate stage
414520	AA148806	Hs.204046	ESTs	1	0.21	upregulate stage
414569	AF109298	Hs.118258	prostate cancer associated protein 1	3.1	0.18	upregulate stage
414575	H11257	Hs.295233	ESTs	3.1	0.15	upregulate stage
414597	H67472	Hs.34274	ESTs	4.6	0.11	upregulate stage
414643	H46177	Hs.119316	ESTs	1	0.28	upregulate stage
414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD)	7.75	0.08	upregulate stage
414661	T97401	Hs.21929	ESTs	1	0.26	upregulate stage
414683	S78296	Hs.76888	internexin neuronal intermediate filamen	2.72	0.25	upregulate stage
414735	BE468016	Hs.281904	ESTs	1	0.38	upregulate stage
414737	AI160386	Hs.125087	ESTs	5.5	0.1	upregulate stage
414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	3.19	0.24	upregulate stage
414774	X02419	Hs.77274	plasminogen activator, urokinase	1.45	0.49	upregulate stage
414783	AW069569	Hs.75839	zinc finger protein 6 (CMPX1)	4.65	0.13	upregulate stage
414799	AI752416	Hs.77326	insulin-like growth factor binding prote	1.7	0.46	upregulate stage
414833	T07114		gb:EST05003 Fetal brain, Stratagene (cat	4.5	0.13	upregulate stage
414883	AA926960	Hs.77550	CDC28 protein kinase 1	3.36	0.22	upregulate stage
414885	AA157531	Hs.269276	ESTs	2.7	0.21	upregulate stage
414918	AI219207	Hs.72222	Homo sapiens cDNA FLJ13459 fis, clone PL	0.87	0.69	upregulate stage
414985	C17372		gb:C17372 Clontech human aorta polyA+ mR	1	0.42	upregulate stage
415025	AW207091	Hs.72307	ESTs	5.3	0.06	upregulate stage
415033	D31476	Hs.301448	Homo sapiens cDNA FLJ12152 fis, clone MA	1	1	upregulate stage
415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	6.05	0.1	upregulate stage
415068	Z19448	Hs.131887	ESTs, Weakly similar to ORF YNL227c (S.c	4.5	0.13	upregulate stage
415095	D59592	Hs.34745	ESTs	1	0.44	upregulate stage
415099	AI492170	Hs.77917	ubiquitin carboxyl-terminal esterase L3	2.27	0.29	upregulate stage
415104	D60076		gb:HUM084E10A Clontech human fetal brain	3.95	0.13	upregulate stage
415114	D60468		gb:HUM111A06B Clontech human fetal brain	2.05	0.2	upregulate stage
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	5.8	0.05	upregulate stage
415139	AW975942	Hs.48524	ESTs	1.15	0.21	upregulate stage
415148	Z36953	Hs.48527	ESTs	2.5	0.2	upregulate stage
415153	C03508	Hs.7000	ESTs	8.95	0.09	upregulate stage
415178	D80503		gb:HUM080A02B Human fetal brain (TFujiwa	1	0.15	upregulate stage
415217	H23983	Hs.26922	ESTs	1	0.31	upregulate stage
415227	AW821113	Hs.72402	ESTs	6.3	0.11	upregulate stage
415238	R37780	Hs.21422	ESTs	1	1	upregulate stage
415241	F02208	Hs.27214	ESTs	1	1	upregulate stage
415295	R41450	Hs.6546	ESTs	1	0.63	upregulate stage
415296	F05086		gb:HSC01A011 normalized infant brain cDN	5.65	0.1	upregulate stage
415327	H22769	Hs.1861	membrane protein, palmitoylated 1 (55kD)	8.15	0.09	upregulate stage
415330	Z44693	Hs.21422	ESTs	3	0.2	upregulate stage
415336	T77664	Hs.78362	Human clone 23839 mRNA sequence	1	0.87	upregulate stage
415337	Z44881	Hs.9012	ESTs	8.8	0.07	upregulate stage
415352	F06565		gb:HSC1CG051 normalized infant brain cDN	1	1	upregulate stage
415364	F06771		gb:HSC1KD031 normalized infant brain cDN	1	1	upregulate stage
415371	R15239		gb:yf89b02.r1 Soares infant brain 1NIB H	5.1	0.13	upregulate stage
415412	F08049	Hs.52132	ESTs	4.25	0.16	upregulate stage
415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.1	0.15	upregulate stage
415462	R52692	Hs.12698	ESTs	4.65	0.11	upregulate stage
415496	R37637	Hs.12286	ESTs	5.4	0.13	upregulate stage
415509	R40000	Hs.91968	ESTs	1	0.44	upregulate stage
415511	AI732617	Hs.182362	ESTs	9.3	0.03	upregulate stage
415542	R13474	Hs.290263	ESTs	9.7	0.08	upregulate stage
415569	Z43930		gb:HSC1OH121 normalized infant brain cDN	1	0.74	upregulate stage
415600	F12664		gb:HSC3CG021 normalized infant brain cDN	1	0.43	upregulate stage
415616	F12945	Hs.12294	ESTs	1	1	upregulate stage
415626	Z43847		gb:HSC1MC051 normalized infant brain cDN	1	1	upregulate stage
415635	F13168		gb:HSC3JF101 normalized infant brain cDN	1	0.26	upregulate stage
415750	AA167712		gb:zq39g08.s1 Stratagene hNT neuron (937	1	0.83	upregulate stage
415786	AW419196	Hs.257924	Homo sapiens cDNA FLJ13782 fis, clone PL	9	0.08	upregulate stage
415788	AW628686	Hs.78851	KIAA0217 protein	5.2	0.11	upregulate stage
415790	R23574	Hs.23545	ESTs	1	1	upregulate stage
415799	AA653718	Hs.225841	DKFZP434D193 protein	4.25	0.12	upregulate stage
415837	H05279	Hs.21758	ESTs	1	0.57	upregulate stage
415857	AA866115	Hs.301646	Homo sapiens cDNA FLJ11381 fis, clone HE	8.05	0.07	upregulate stage
415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	12.2	0.06	upregulate stage
415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	12.2	0.06	upregulate stage
415948	AA262226		gb:zs24h06.r1 NCI_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
415979	H16427	Hs.271501	ESTs	4.85	0.13	upregulate stage
415989	AI267700	Hs.111128	ESTs	4.45	0.08	upregulate stage

416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	1	1	upregulate stage
416052	R12816	Hs.21164	ESTs	1.45	0.24	upregulate stage
416053	H16359	Hs.130648	ESTs	4.35	0.14	upregulate stage
416061	R45516	Hs.26119	ESTs	1	1	upregulate stage
416065	BE267931	Hs.78996	proliferating cell nuclear antigen	4.72	0.17	upregulate stage
416097	BE387371	Hs.301304	Homo sapiens cDNA: FLJ21017 fis, clone C	5.75	0.11	upregulate stage
416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	8.4	0.09	upregulate stage
416135	AW473656	Hs.45119	ESTs	2.29	0.2	upregulate stage
416155	AI807264	Hs.205442	ESTs, Weakly similar to AF117610 1 inner	5.1	0.13	upregulate stage
416173	R52782		gb:yg99d09.r1 Soares infant brain 1NIB H	3.7	0.12	upregulate stage
416195	AW131940	Hs.104030	ESTs	1.1	0.16	upregulate stage
416196	W51955	Hs.73372	ESTs	3.25	0.14	upregulate stage
416203	H27794	Hs.269055	ESTs	1	0.32	upregulate stage
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.15	0.12	upregulate stage
416226	N55342	Hs.34372	ESTs	2.35	0.21	upregulate stage
416239	AL038450	Hs.48948	ESTs	4.05	0.14	upregulate stage
416241	N52639	Hs.32683	ESTs	5	0.09	upregulate stage
416254	H51703	Hs.13640	ESTs	1	0.95	upregulate stage
416269	AA177138	Hs.161671	ESTs	4.07	0.2	upregulate stage
416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	1.84	0.45	upregulate stage
416280	H44180	Hs.181789	ESTs	1	1	upregulate stage
416309	R84694	Hs.79194	cAMP responsive element binding protein	9.35	0.08	upregulate stage
416324	H47983	Hs.1870	phenylalanine hydroxylase	5.15	0.13	upregulate stage
416332	H91284	Hs.244461	ESTs	1	1	upregulate stage
416343	H49213		gb:yq19e04.r1 Soares fetal liver spleen	1	1	upregulate stage
416353	T77127	Hs.191297	ESTs, Moderately similar to ALU6_HUMAN A	1.46	0.59	upregulate stage
416395	R94575		gb:yt73e10.s1 Soares fetal liver spleen	9.2	0.09	upregulate stage
416437	N48990	Hs.37204	ESTs	4.15	0.12	upregulate stage
416476	H58137	Hs.268639	ESTs	1	0.22	upregulate stage
416537	T99086	Hs.144904	nuclear receptor co-repressor 1	5.45	0.12	upregulate stage
416539	Y07909	Hs.79368	epithelial membrane protein 1	9.45	0.09	upregulate stage
416575	W02414	Hs.38383	ESTs	4.95	0.1	upregulate stage
416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	1	0.22	upregulate stage
416644	H70701	Hs.269135	ESTs	5.65	0.12	upregulate stage
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.65	0.05	upregulate stage
416682	R99700	Hs.36152	ESTs	1	0.25	upregulate stage
416690	H84078	Hs.108551	ESTs	5.35	0.13	upregulate stage
416709	R99369	Hs.283108	hemoglobin, gamma G	5.4	0.13	upregulate stage
416712	N68576	Hs.81602	ESTs	1	0.25	upregulate stage
416715	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.32	upregulate stage
416731	T58115	Hs.10336	ESTs	1	0.4	upregulate stage
416734	H81213	Hs.14825	ESTs	3.8	0.16	upregulate stage
416735	R11275	Hs.194485	ESTs	11.5	0.06	upregulate stage
416738	N29218	Hs.40290	ESTs	1	0.42	upregulate stage
416856	N27833	Hs.269028	ESTs	2.6	0.22	upregulate stage
416883	AW140128	Hs.184902	ESTs	11.3	0.07	upregulate stage
416923	N32498	Hs.42829	ESTs	1	0.61	upregulate stage
416936	N21352	Hs.42987	ESTs, Weakly similar to ORF2 [M.musculus	1	1	upregulate stage
417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	11.3	0.05	upregulate stage
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	5.04	0.15	upregulate stage
417134	N51220	Hs.269068	ESTs	1	0.24	upregulate stage
417185	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	1.98	0.32	upregulate stage
417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.95	0.21	upregulate stage
417265	AL121369	Hs.281117	ESTs	1	0.3	upregulate stage
417283	N62840	Hs.48648	ESTs	1.05	0.27	upregulate stage
417308	H60720	Hs.81892	KIAA0101 gene product	9.2	0.09	upregulate stage
417320	AA195667	Hs.287324	ESTs	2.8	0.16	upregulate stage
417396	T98987		gb:ye66f02.r1 Soares fetal liver spleen	1	1	upregulate stage
417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.75	0.09	upregulate stage
417409	BE272506	Hs.82109	syndecan 1	1.92	0.44	upregulate stage
417448	AA203135	Hs.130186	ESTs	6.45	0.1	upregulate stage
417453	H73183	Hs.129885	ESTs, Moderately similar to unnamed prot	4.65	0.13	upregulate stage
417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.59	0.49	upregulate stage
417540	AA203600	Hs.152250	ESTs	1	1	upregulate stage
417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	5.65	0.1	upregulate stage
417581	R26968	Hs.24104	ESTs, Weakly similar to ALU7_HUMAN ALU S	9.15	0.09	upregulate stage
417596	R07343	Hs.226823	ESTs	4.35	0.14	upregulate stage
417599	AA204688	Hs.136201	ESTs, Weakly similar to ALU7_HUMAN ALU S	0.94	0.9	upregulate stage
417620	R02530	Hs.191198	ESTs	9.1	0.07	upregulate stage
417638	R12490	Hs.189779	ESTs	1	0.32	upregulate stage
417650	T05870	Hs.100640	ESTs	1	0.22	upregulate stage
417715	AW969587	Hs.86366	ESTs	6.31	0.09	upregulate stage
417720	AA205625	Hs.208067	ESTs	4.65	0.11	upregulate stage
417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clon	4.15	0.13	upregulate stage
417750	AI267720	Hs.260523	neuroblastoma RAS viral (v-ras) oncogene	9.98	0.08	upregulate stage
417780	Z43482	Hs.82772	collagen, type XI, alpha 1	2.3	0.14	upregulate stage
417789	R50978	Hs.267054	ESTs	1.05	0.19	upregulate stage

417791	AW965339	Hs.111471	ESTs	5.35	0.1	upregulate stage
417850	AA215724	Hs.82741	primase, polypeptide 1 (49kD)	1	1	upregulate stage
417898	AA826198	Hs.291851	ESTs	2.15	0.21	upregulate stage
417975	AA641836	Hs.30085	Homo sapiens cDNA: FLJ23186 fis, clone L	3.7	0.13	upregulate stage
418004	U37519	Hs.87539	aldehyde dehydrogenase 8	1.57	0.5	upregulate stage
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	17.9	0.02	upregulate stage
418027	AB037807	Hs.83293	hypothetical protein	6.6	0.09	upregulate stage
418030	BE207573	Hs.83321	neuromedin B	12.2	0.04	upregulate stage
418068	AW971155	Hs.293902	ESTs, Weakly similar to prolyl 4-hydroxy	4.26	0.14	upregulate stage
418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	5.21	0.15	upregulate stage
418134	AA397769	Hs.86617	ESTs	1	0.3	upregulate stage
418153	R13696	Hs.112830	ESTs	1	0.3	upregulate stage
418180	BE618087	Hs.83724	Human clone 23773 mRNA sequence	8.79	0.09	upregulate stage
418201	AA214345	Hs.98445	Homo sapiens cDNA: FLJ21652 fis, clone C	3.75	0.13	upregulate stage
418203	X54942	Hs.83758	CDC28 protein kinase 2	13.85	0.04	upregulate stage
418216	AA662240	Hs.283099	AF15q14 protein	9.75	0.07	upregulate stage
418236	AW994005	Hs.172572	hypothetical protein FLJ20093	10.75	0.05	upregulate stage
418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	6.25	0.12	upregulate stage
418259	AA215404	Hs.137289	ESTs	11.5	0.07	upregulate stage
418268	AA810599	Hs.86643	ESTs	1	0.43	upregulate stage
418296	C01566	Hs.86671	ESTs	1	0.45	upregulate stage
418372	AA311833	Hs.84318	replication protein A1 (70kD)	9.04	0.08	upregulate stage
418379	AA218940	Hs.137516	fidgetin-like 1	3.25	0.15	upregulate stage
418422	AW440068	Hs.59425	Homo sapiens cDNA: FLJ23323 fis, clone H	8.95	0.1	upregulate stage
418454	AA315308		gb:EST187095 Colon carcinoma (HCC) cell	2.5	0.15	upregulate stage
418462	BE001596	Hs.85266	integrin, beta 4	1.33	0.59	upregulate stage
418469	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	1.21	0.71	upregulate stage
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.69	0.23	upregulate stage
418480	AA223929	Hs.86902	ESTs	1	1	upregulate stage
418498	T78248		gb:yd79f05.r1 Soares fetal liver spleen	1	0.47	upregulate stage
418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	5.4	0.14	upregulate stage
418546	AA224827		gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens	2.72	0.23	upregulate stage
418573	AA225188		gb:nc21h04.r1 NCI_CGAP_Pr1 Homo sapiens	9.95	0.07	upregulate stage
418577	AA225247	Hs.269300	ESTs, Weakly similar to B34087 hypotheti	1	0.77	upregulate stage
418578	U92459	Hs.86204	glutamate receptor, metabotropic 8	1	1	upregulate stage
418590	AI732672	Hs.252507	ESTs	1	0.59	upregulate stage
418592	X99226	Hs.284153	Fanconi anemia, complementation group A	4.75	0.13	upregulate stage
418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	1	0.23	upregulate stage
418624	AI734080	Hs.104211	ESTs	7.95	0.09	upregulate stage
418661	NM_001949	Hs.1189	Human mRNA for KIAA0075 gene, partial cd	3	0.15	upregulate stage
418663	AK001100	Hs.87013	Homo sapiens cDNA FLJ10238 fis, clone HE	17.2	0.04	upregulate stage
418675	AW299723	Hs.87223	bone morphogenetic protein receptor, typ	1	1	upregulate stage
418686	Z36830	Hs.87268	annexin A8	2.11	0.3	upregulate stage
418687	R61650	Hs.22581	ESTs	6.75	0.07	upregulate stage
418693	AI750878	Hs.87409	thrombospondin 1	4.5	0.08	upregulate stage
418704	AA227235	Hs.83286	ESTs	1	0.33	upregulate stage
418712	Z42183		gb:HSC0BF041 normalized infant brain cDN	1	0.91	upregulate stage
418717	AI334430	Hs.86984	ESTs	4.7	0.12	upregulate stage
418723	AA504428	Hs.10487	ESTs, Weakly similar to Weak similarity	5.85	0.1	upregulate stage
418738	AW388633	Hs.6682	ESTs	3.6	0.09	upregulate stage
418752	AL133556	Hs.88144	hypothetical protein FLJ12476	1	1	upregulate stage
418757	AI864193	Hs.169728	Homo sapiens cDNA FLJ13150 fis, clone NT	9.15	0.09	upregulate stage
418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	9.25	0.08	upregulate stage
418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.83	0.43	upregulate stage
418876	AA740616	Hs.293874	ESTs	11.3	0.06	upregulate stage
418903	AW969665	Hs.154848	ESTs	1	1	upregulate stage
418915	AI474778	Hs.118977	ESTs	4.75	0.12	upregulate stage
418939	AW630803	Hs.89497	lamin B1	2.6	0.13	upregulate stage
418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	1.45	0.53	upregulate stage
418976	AA933082	Hs.126883	ESTs	1	0.23	upregulate stage
419059	T86216		gb:yd84a05.r1 Soares fetal liver spleen	1	0.38	upregulate stage
419078	M93119	Hs.89584	insulinoma-associated 1	1.25	0.18	upregulate stage
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1	1	upregulate stage
419169	AW851980	Hs.262346	ESTs, Weakly similar to ORF2: function u	1.59	0.3	upregulate stage
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	3.55	0.05	upregulate stage
419218	AI248073	Hs.188723	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.27	upregulate stage
419226	AI342491	Hs.87413	ESTs	1	0.37	upregulate stage
419235	AW470411	Hs.288433	neurotrimin	11.9	0.07	upregulate stage
419286	AA236005	Hs.221303	ESTs	4.85	0.14	upregulate stage
419327	AA521504	Hs.190179	ESTs	1	1	upregulate stage
419355	AA428520	Hs.90061	progesterone binding protein	10.6	0.06	upregulate stage
419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.84	0.47	upregulate stage
419413	AA237040	Hs.87589	ESTs	1	1	upregulate stage
419436	AA991639	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC0	6.6	0.1	upregulate stage
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.31	0.64	upregulate stage
419472	AW978038		gb:EST390147 MAGE resequences, MAGO Homo	1	1	upregulate stage
419475	AA243420	Hs.87648	ESTs	1.1	0.24	upregulate stage

419477	AA826279		gb:od03g07.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.56	upregulate stage
419484	AA243474	Hs.272128	Homo sapiens cDNA FLJ13901 fis, clone TH	1	0.22	upregulate stage
419506	N20912	Hs.42369	ESTs	1	1	upregulate stage
419554	AI732138	Hs.104318	ESTs	1	0.5	upregulate stage
419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	1	0.91	upregulate stage
419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	8.1	0.08	upregulate stage
419651	NM_007023	Hs.91971	cAMP-regulated guanine nucleotide exchan	1	1	upregulate stage
419666	NM_014810	Hs.92200	KIAA0480 gene product	5.2	0.12	upregulate stage
419737	H24185	Hs.92918	hypothetical protein	11.7	0.07	upregulate stage
419743	AW408762	Hs.127478	ESTs	6.1	0.09	upregulate stage
419752	AA249573	Hs.152618	ESTs	1.8	0.17	upregulate stage
419769	H27374	Hs.103483	ESTs	1	0.36	upregulate stage
419805	AW966945		gb:EST379019 MAGE resequences, MAGJ Homo	1	0.34	upregulate stage
419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo	1	0.67	upregulate stage
419831	AW448930	Hs.5415	ESTs	7.05	0.1	upregulate stage
419833	AA251131	Hs.220697	ESTs	1.25	0.53	upregulate stage
419834	AA251139		gb:zs03g12.s1 NCI_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
419923	AW081455	Hs.120219	ESTs	5.89	0.13	upregulate stage
419945	AW290975	Hs.118923	ESTs	1	0.24	upregulate stage
419962	AA830111	Hs.291917	ESTs	1	1	upregulate stage
419970	AW612022	Hs.263271	ESTs	9.15	0.09	upregulate stage
419986	AI345455	Hs.78915	GA-binding protein transcription factor,	3.05	0.17	upregulate stage
419998	AA252691		gb:zs26d09.r1 NCI_CGAP_GCB1 Homo sapiens	1	0.47	upregulate stage
420016	AW016908	Hs.88025	ESTs	1	0.8	upregulate stage
420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	4.8	0.11	upregulate stage
420076	AA827860	Hs.293717	ESTs	5.35	0.12	upregulate stage
420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	5.3	0.11	upregulate stage
420145	AA809860	Hs.256284	ESTs	1	1	upregulate stage
420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	14.8	0.04	upregulate stage
420161	AI683069	Hs.175319	ESTs	4.7	0.11	upregulate stage
420184	AA188408	Hs.95665	hypothetical protein	4.35	0.15	upregulate stage
420226	AA773709	Hs.152818	ubiquitin specific protease 8	3.1	0.16	upregulate stage
420230	AL034344	Hs.298020	Homo sapiens cDNA FLJ11796 fis, clone HE	10.35	0.06	upregulate stage
420236	AA256763	Hs.291111	ESTs	4.45	0.14	upregulate stage
420270	AA257990		gb:zs35h07.r1 NCI_CGAP_GCB1 Homo sapiens	10.05	0.08	upregulate stage
420297	AI628272	Hs.88323	ESTs	9.45	0.09	upregulate stage
420344	BE463721	Hs.97101	putative G protein-coupled receptor	11.7	0.05	upregulate stage
420392	AI242930	Hs.97393	KIAA0328 protein	1.7	0.22	upregulate stage
420413	AW971624	Hs.120605	ESTs	1	1	upregulate stage
420445	AA262213	Hs.193514	ESTs	1	1	upregulate stage
420471	AA262452	Hs.192268	ESTs	3.95	0.13	upregulate stage
420479	AW183695	Hs.186572	ESTs	4.95	0.12	upregulate stage
420493	AI635113	Hs.270366	Homo sapiens mRNA; cDNA DKFZp564H0616 (f	4.4	0.15	upregulate stage
420552	AK000492	Hs.98806	hypothetical protein	11.55	0.06	upregulate stage
420572	AL035593	Hs.99016	Human DNA sequence from clone 310J6 on c	1.35	0.22	upregulate stage
420643	W87731		gb:zh65g10.r1 Soares_fetal_liver_spleen_	1.25	0.25	upregulate stage
420650	AA455706	Hs.44581	heat shock protein hsp70-related protein	7.3	0.09	upregulate stage
420654	AA279091	Hs.104420	ESTs	1	0.27	upregulate stage
420655	R74405	Hs.300886	ESTs	1	1	upregulate stage
420717	AA284447	Hs.271887	ESTs	9	0.09	upregulate stage
420734	AW972872	Hs.293736	ESTs	5.2	0.13	upregulate stage
420756	AA411800	Hs.189900	ESTs	1	1	upregulate stage
420789	AI670057	Hs.199882	ESTs	8.85	0.06	upregulate stage
420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	4.6	0.12	upregulate stage
420851	AA281062	Hs.250734	ESTs	8.35	0.08	upregulate stage
420880	AI809621	Hs.105620	ESTs	1	1	upregulate stage
420923	AF097021	Hs.273321	differentially expressed in hematopoieti	10.4	0.03	upregulate stage
420928	AA281809		gb:zt10e01.r1 NCI_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
420936	AA456112	Hs.99410	ESTs	8.71	0.07	upregulate stage
420947	AA491044	Hs.47196	ESTs	1	0.38	upregulate stage
421017	AW979181	Hs.293221	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	1	upregulate stage
421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	1.26	0.62	upregulate stage
421070	AA283185	Hs.19327	ESTs	2.2	0.14	upregulate stage
421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.69	0.28	upregulate stage
421102	AI470093	Hs.89217	ESTs	2.65	0.19	upregulate stage
421103	AI625835	Hs.27104	ESTs	6	0.1	upregulate stage
421114	AW975051	Hs.293156	ESTs	4.7	0.12	upregulate stage
421118	AI471925	Hs.89257	ESTs	1	0.39	upregulate stage
421155	H87879	Hs.102267	lysyl oxidase	1.15	0.18	upregulate stage
421159	AW978316	Hs.136649	ESTs	1	0.44	upregulate stage
421187	NM_014721	Hs.102471	KIAA0680 gene product	5.7	0.11	upregulate stage
421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.07	2.55	upregulate stage
421221	AW276914	Hs.300877	ESTs	8.75	0.07	upregulate stage
421229	AI056590	Hs.7086	Homo sapiens cDNA: FLJ23000 fis, clone L	1.64	0.49	upregulate stage
421261	AA600853	Hs.98133	ESTs	10.9	0.07	upregulate stage
421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	2.65	0.16	upregulate stage
421278	AI367919	Hs.99691	ESTs	1	0.56	upregulate stage

421280	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.34	upregulate stage
421282	AA286914	Hs.183299	ESTs	9	0.08	upregulate stage
421306	AA806207	Hs.125889	ESTs	1	0.95	upregulate stage
421308	AA687322	Hs.192843	ESTs	2.85	0.15	upregulate stage
421373	AA808229	Hs.167771	ESTs	2.45	0.14	upregulate stage
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.6	0.26	upregulate stage
421381	AA361752		gb:EST71314 T-cell lymphoma Homo sapiens	5.05	0.09	upregulate stage
421418	AA806639		gb:ob88g05.s1 NCI_CGAP_GCB1 Homo sapiens	6.55	0.1	upregulate stage
421433	AI829192	Hs.134805	ESTs	9.9	0.07	upregulate stage
421451	AA291377	Hs.50831	ESTs	11.9	0.06	upregulate stage
421491	H99999	Hs.42736	ESTs	3	0.2	upregulate stage
421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.51	0.32	upregulate stage
421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	9	0.09	upregulate stage
421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	5.75	0.12	upregulate stage
421673	H54384	Hs.36892	ESTs	1	1	upregulate stage
421685	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	9.45	0.07	upregulate stage
421708	AW754341		gb:CM0-CT0341-181299-130-h12 CT0341 Homo	1	0.47	upregulate stage
421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	1.97	0.33	upregulate stage
421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	7.05	0.1	upregulate stage
421869	AB003592	Hs.109050	contactin 6	1	1	upregulate stage
421925	S80310	Hs.109620	acidic epididymal glycoprotein-like 1	1	1	upregulate stage
421948	L42583	Hs.111758	keratin 6A	51.9	0.01	upregulate stage
421958	AA357185	Hs.109918	ras homolog gene family, member H	10.17	0.07	upregulate stage
421991	NM_014918	Hs.110488	KIAA0990 protein	4.5	0.17	upregulate stage
422026	U80736	Hs.110826	trinucleotide repeat containing 9	6.5	0.08	upregulate stage
422072	AB018255	Hs.111138	KIAA0712 gene product	9.2	0.08	upregulate stage
422094	AF129535	Hs.272027	F-box only protein 5	6.95	0.09	upregulate stage
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.66	0.17	upregulate stage
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.96	0.1	upregulate stage
422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	2.8	0.16	upregulate stage
422204	AA339015		gb:EST44247 Fetal brain I Homo sapiens c	1	1	upregulate stage
422261	AA307595	Hs.119908	nucleolar protein NOP5/NOP58	1	1	upregulate stage
422271	AB038995	Hs.114159	RAB-8b protein	5.04	0.16	upregulate stage
422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	3.46	0.24	upregulate stage
422282	AF019225	Hs.114309	apolipoprotein L	4.54	0.14	upregulate stage
422322	AB022192	Hs.115240	peroxisome biogenesis factor 13	1	0.53	upregulate stage
422330	D30783	Hs.115263	epiregulin	4.45	0.06	upregulate stage
422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.25	0.19	upregulate stage
422406	AF025441	Hs.116206	Opa-interacting protein 5	9.5	0.07	upregulate stage
422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.35	0.04	upregulate stage
422491	AA338548	Hs.117546	neuronatin	0.64	1.24	upregulate stage
422504	AA311407		gb:EST182167 Jurkat T-cells V Homo sapie	3.6	0.11	upregulate stage
422505	AL120862	Hs.124165	ESTs	2.8	0.14	upregulate stage
422508	AJ000327	Hs.117852	ATP-binding cassette, sub-family D (ALD)	5.25	0.14	upregulate stage
422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.57	0.31	upregulate stage
422540	AI050751	Hs.22895	Homo sapiens cDNA: FLJ23548 fis, clone L	1	0.59	upregulate stage
422588	AA312730		gb:EST183651 Monocytes, stimulated II Ho	3	0.14	upregulate stage
422678	AA247778	Hs.119155	Homo sapiens mRNA; cDNA DKFZp434B249 (fr	10.7	0.07	upregulate stage
422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.1	0.13	upregulate stage
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	5.94	0.1	upregulate stage
422823	D89974	Hs.121102	vanin 2	10	0.07	upregulate stage
422892	AA988176	Hs.121553	hypothetical protein FLJ20641	1	0.27	upregulate stage
422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.2	0.08	upregulate stage
422964	AW439476	Hs.256895	ESTs	11.75	0.07	upregulate stage
422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	3.05	0.14	upregulate stage
423001	AA320014	Hs.208603	ESTs	9.1	0.09	upregulate stage
423090	BE387529	Hs.123536	melanoma antigen, family E, 1, cancer/te	1	0.49	upregulate stage
423100	AA323114		gb:EST25873 Cerebellum II Homo sapiens c	1	1	upregulate stage
423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	2.8	0.19	upregulate stage
423156	AA131493	Hs.124752	fibroblast growth factor 12B	1	0.27	upregulate stage
423198	M81933	Hs.1634	cell division cycle 25A	8.95	0.07	upregulate stage
423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.2	0.57	upregulate stage
423262	NM_005479	Hs.126057	frequently rearranged in advanced T-cell	9.75	0.07	upregulate stage
423296	AW957193	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	4.95	0.12	upregulate stage
423309	BE006775	Hs.126782	sushi-repeat protein	1.58	0.34	upregulate stage
423347	AI660412	Hs.234557	ESTs	1	0.45	upregulate stage
423359	NM_014170	Hs.127496	HSPC135 protein	1	0.69	upregulate stage
423368	AA364195		gb:EST75015 Pineal gland II Homo sapiens	1	0.95	upregulate stage
423389	AI471609	Hs.54347	ESTs	3.95	0.14	upregulate stage
423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	1.62	0.43	upregulate stage
423441	R68649	Hs.278359	absent in melanoma 1 like	6.25	0.1	upregulate stage
423453	AW450737	Hs.128791	CGI-09 protein	8.45	0.09	upregulate stage
423500	AF020763	Hs.129705	clone 1900 unknown protein	1	0.8	upregulate stage
423578	AW960454	Hs.222830	ESTs	11.94	0.07	upregulate stage
423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.4	0.17	upregulate stage
423632	AA328824		gb:EST32358 Embryo, 12 week I Homo sapie	1	0.71	upregulate stage
423642	AW452650	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	8.35	0.1	upregulate stage

423644	AA329048		gb:EST32875 Embryo, 12 week I Homo sapie	1	0.43	upregulate stage
423648	AK000456	Hs.130546	hypothetical protein FLJ20449	10.4	0.07	upregulate stage
423651	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	5.75	0.1	upregulate stage
423654	AI674253	Hs.35828	ESTs	3.15	0.18	upregulate stage
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	29.7	0.02	upregulate stage
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.1	0.16	upregulate stage
423745	AI809797	Hs.43222	ESTs	1	0.5	upregulate stage
423748	AI149048	Hs.30211	hypothetical protein FLJ22313	4.25	0.13	upregulate stage
423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	1.18	0.71	upregulate stage
423758	AA338153	Hs.82124	laminin, beta 1	1	1	upregulate stage
423774	L39064	Hs.1702	interleukin 9 receptor	3.08	0.15	upregulate stage
423818	AA332439		gb:EST36554 Embryo, 8 week I Homo sapien	1	0.38	upregulate stage
423827	AI472828	Hs.172625	ESTs	1	0.43	upregulate stage
423837	AW937063		gb:PM3-DT0037-231299-001-g11 DT0037 Homo	1.44	0.55	upregulate stage
423912	BE091233		gb:PM0-BT0726-300300-001-H07 BT0726 Homo	1	1	upregulate stage
423938	AL049328	Hs.135642	Homo sapiens mRNA; cDNA DKFZp564E026 (fr	1	1	upregulate stage
423942	AF209704	Hs.135723	glycolipid transfer protein	11.65	0.05	upregulate stage
423944	T91433	Hs.128291	phosphodiesterase 10A	1	0.45	upregulate stage
423946	AL137344	Hs.135892	Homo sapiens mRNA; cDNA DKFZp761I1311 (f	1	1	upregulate stage
423956	W28203	Hs.136169	Homo sapiens clone 25215 mRNA sequence,	5.35	0.09	upregulate stage
424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	8.8	0.06	upregulate stage
424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	3.14	0.19	upregulate stage
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.6	0.26	upregulate stage
424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	1.8	0.22	upregulate stage
424075	AI807320	Hs.227630	RE1-silencing transcription factor	9.1	0.06	upregulate stage
424087	N69333	Hs.21638	ESTs	1	1	upregulate stage
424193	AK002005	Hs.142868	Homo sapiens cDNA FLJ11143 fis, clone PL	1	0.23	upregulate stage
424353	AA339646		gb:EST44755 Fetal brain I Homo sapiens c	1	1	upregulate stage
424364	AW383226	Hs.201189	ESTs, Weakly similar to DRPLA [H.sapiens	2.18	0.33	upregulate stage
424406	D54120	Hs.146409	wingless-type MMTV integration site fami	2.05	0.17	upregulate stage
424420	BE614743	Hs.146688	prostaglandin E synthase	1.19	0.67	upregulate stage
424425	AB031480	Hs.146824	SPR1 protein	1.42	0.54	upregulate stage
424486	BE002477	Hs.278714	chloride intracellular channel 6	1	0.27	upregulate stage
424490	AJ278016	Hs.55565	ankyrin repeat domain 3	2.02	0.39	upregulate stage
424492	AI133482	Hs.165210	ESTs	3.15	0.14	upregulate stage
424505	AA446131	Hs.124918	Homo sapiens cDNA FLJ13186 fis, clone NT	11.55	0.05	upregulate stage
424513	BE385864	Hs.149894	mitochondrial translational initiation f	2.65	0.23	upregulate stage
424575	AL110217	Hs.150751	DKFZP572C163 protein	1	1	upregulate stage
424583	AF017445	Hs.150926	fucose-1-phosphate guanylyltransferase	1.8	0.26	upregulate stage
424589	AW854298		gb:RC3-CT0254-100500-211-c03 CT0254 Homo	0.85	0.94	upregulate stage
424602	AK002055	Hs.301129	Homo sapiens clone 23859 mRNA sequence	2.85	0.2	upregulate stage
424625	AW904466	Hs.151310	PDZ domain protein (Drosophila inaD-like	1	0.4	upregulate stage
424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.41	0.52	upregulate stage
424643	AF241850	Hs.151428	ret finger protein 2	9.75	0.07	upregulate stage
424649	BE242035	Hs.151461	embryonic ectoderm development	5.85	0.13	upregulate stage
424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	1	0.56	upregulate stage
424670	W61215	Hs.116651	epithelial V-like antigen 1	1.42	0.52	upregulate stage
424690	BE538356	Hs.151777	Human translation initiation factor eIF-	4.3	0.1	upregulate stage
424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	3.85	0.11	upregulate stage
424702	AF250237	Hs.152009	G protein-coupled receptor 85	1	1	upregulate stage
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.05	0.09	upregulate stage
424735	U31875	Hs.152677	Homo sapiens cDNA FLJ20338 fis, clone HE	1.04	0.59	upregulate stage
424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.11	0.65	upregulate stage
424749	NM_002451	Hs.152817	methylthioadenosine phosphorylase	1	1	upregulate stage
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	18.5	0.03	upregulate stage
424841	AI280215	Hs.96885	ESTs	1	1	upregulate stage
424860	W60828	Hs.153529	Homo sapiens clone 24540 mRNA sequence	1	1	upregulate stage
424878	H57111	Hs.221132	ESTs	9.45	0.07	upregulate stage
424879	AA348013	Hs.159354	ESTs	10.7	0.07	upregulate stage
424888	AA348126	Hs.24882	ESTs	2.8	0.21	upregulate stage
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	7.75	0.07	upregulate stage
424930	AA885344	Hs.96910	ESTs	1.45	0.38	upregulate stage
424948	AA348810	Hs.190503	ESTs	3.2	0.12	upregulate stage
424951	AW964082		gb:EST376155 MAGE resequences, MAGH Homo	8.75	0.09	upregulate stage
424993	F07625		gb:HSC2CF021 normalized infant brain cDN	1	1	upregulate stage
425020	U09368	Hs.154205	zinc finger protein 140 (clone pHZ-39)	1	1	upregulate stage
425024	R39235	Hs.12407	ESTs	2.65	0.13	upregulate stage
425057	AA826434	Hs.96944	ESTs	1	0.22	upregulate stage
425068	AL048716	Hs.154387	KIAA0103 gene product	9.5	0.07	upregulate stage
425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	1.66	0.52	upregulate stage
425191	AF052146	Hs.155085	Homo sapiens clone 24653 mRNA sequence	1	0.32	upregulate stage
425216	U81504	Hs.155172	adaptor-related protein complex 3, beta	7.05	0.1	upregulate stage
425234	AW152225	Hs.165909	ESTs	19.7	0.04	upregulate stage
425239	BE567924	Hs.155244	pre-mRNA splicing factor similar to S. c	1	0.69	upregulate stage
425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	10.45	0.05	upregulate stage
425304	AA463844	Hs.31339	fibroblast growth factor 11	1.57	0.51	upregulate stage
425316	AA354977	Hs.191565	ESTs, Moderately similar to NSD1 protein	5.05	0.12	upregulate stage

425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	14.7	0.05	upregulate stage
425362	AA355936		gb:EST64410 Jurkat T-cells VI Homo sapie	1	1	upregulate stage
425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	8.24	0.09	upregulate stage
425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	1	0.22	upregulate stage
425415	M13903	Hs.157091	involucrin	1.19	0.55	upregulate stage
425420	BE536911	Hs.234545	ESTs, Weakly similar to AF155135 1 novel	2.85	0.13	upregulate stage
425463	AK000740	Hs.157986	hypothetical protein FLJ20733	9	0.07	upregulate stage
425465	L18964	Hs.1904	protein kinase C, iota	9.6	0.07	upregulate stage
425467	R16484	Hs.190075	ESTs	1	0.83	upregulate stage
425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.2	0.15	upregulate stage
425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	1	1	upregulate stage
425608	AA360486	Hs.92448	ESTs	4.7	0.14	upregulate stage
425614	AI334963	Hs.156256	ESTs	2.65	0.14	upregulate stage
425641	D79758	Hs.14355	Homo sapiens cDNA FLJ13207 fis, clone NT	4.86	0.1	upregulate stage
425660	AA521184	Hs.105504	ESTs	1	0.31	upregulate stage
425665	AK001050	Hs.159066	hypothetical protein FLJ10188	1.25	0.19	upregulate stage
425672	AA361483		gb:EST70790 T-cell lymphoma Homo sapiens	1	1	upregulate stage
425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	3.96	0.13	upregulate stage
425726	AF085808	Hs.159330	uroplakin 3	0.92	0.79	upregulate stage
425742	AJ001454	Hs.159425	testican 3	1	1	upregulate stage
425785	T27017	Hs.159528	Homo sapiens clone 24400 mRNA sequence	1	0.39	upregulate stage
425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.89	0.44	upregulate stage
425843	BE313280	Hs.159627	death associated protein 3	3.1	0.15	upregulate stage
425852	AK001504	Hs.159651	death receptor 6	1.72	0.47	upregulate stage
425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	0.95	0.68	upregulate stage
426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone C	1	0.34	upregulate stage
426028	NM_001110	Hs.172028	*a disintegrin and metalloproteinase doma*	14.3	0.04	upregulate stage
426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	11.75	0.05	upregulate stage
426108	AA622037	Hs.166468	programmed cell death 5	3.23	0.18	upregulate stage
426115	H08895	Hs.166733	leucyl/cystinyl aminopeptidase	1	0.32	upregulate stage
426168	NM_003152	Hs.167503	signal transducer and activator of trans	1.97	0.4	upregulate stage
426257	AL137201	Hs.168625	KIAA0979 protein	1	0.29	upregulate stage
426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.8	0.16	upregulate stage
426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	14.75	0.04	upregulate stage
426451	AI908165	Hs.169946	GATA-binding protein 3	3.05	0.28	upregulate stage
426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	1	0.36	upregulate stage
426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	14.17	0.05	upregulate stage
426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	1.15	0.47	upregulate stage
426561	AA381437		gb:EST94514 Activated T-cells I Homo sap	5.65	0.11	upregulate stage
426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	11.05	0.05	upregulate stage
426731	AW303411	Hs.130332	ESTs	2.4	0.21	upregulate stage
426759	AI590401	Hs.21213	ESTs	9.5	0.06	upregulate stage
426786	AA319798	Hs.172247	eukaryotic translation elongation factor	9.25	0.09	upregulate stage
426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	5.63	0.14	upregulate stage
426818	AA554827	Hs.124841	ESTs, *Weakly similar to* ALU5_HUMAN ALU S	9	0.08	upregulate stage
426824	D87717	Hs.172652	KIAA0013 gene product	1	0.87	upregulate stage
426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	8.95	0.09	upregulate stage
426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	1	0.19	upregulate stage
426935	NM_000088	Hs.172928	collagen, type I, alpha 1	1.15	0.72	upregulate stage
426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	11.06	0.06	upregulate stage
427071	AA397958	Hs.192719	ESTs	5.75	0.08	upregulate stage
427126	AA620613	Hs.191827	ESTs	2.55	0.18	upregulate stage
427134	AA398409	Hs.173561	EST	3.4	0.18	upregulate stage
427142	AA398510	Hs.133148	ESTs	1	0.25	upregulate stage
427259	AA400096		gb:zu69f07.s1 Soares_testis_NHT Homo sap	1	0.22	upregulate stage
427308	D26067	Hs.174905	KIAA0033 protein	5.9	0.1	upregulate stage
427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	6.12	0.11	upregulate stage
427356	AW023482	Hs.97849	ESTs	2.7	0.13	upregulate stage
427370	AI243615	Hs.97740	ESTs	3.6	0.14	upregulate stage
427376	AA401533	Hs.19440	ESTs	2.1	0.16	upregulate stage
427387	BE244966	Hs.177584	3-oxoacid CoA transferase	1	0.39	upregulate stage
427470	AW999924	Hs.178357	Homo sapiens cDNA FLJ13657 fis, clone PL	3.4	0.16	upregulate stage
427519	AW085233	Hs.180696	ESTs	8.23	0.1	upregulate stage
427521	AW973352	Hs.299056	ESTs	7.75	0.1	upregulate stage
427528	AU077143	Hs.179565	*minichromosome maintenance deficient (S.*	5.7	0.15	upregulate stage
427566	AI743515		gb:wf72b08.x2 Soares_NFL_T_GBC_S1 Homo s	1	1	upregulate stage
427581	NM_014788	Hs.179703	KIAA0129 gene product	11.45	0.06	upregulate stage
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.25	0.16	upregulate stage
427603	AI090838	Hs.98006	ESTs	1	1	upregulate stage
427646	AI678042	Hs.271953	ESTs	5.7	0.11	upregulate stage
427652	AI673025	Hs.43874	ESTs	1	0.34	upregulate stage
427742	AA411880	Hs.190888	ESTs	2.4	0.16	upregulate stage
427814	W28383	Hs.180900	Williams-Beuren syndrome chromosome regi	9.13	0.08	upregulate stage
427839	AA608823	Hs.98244	ESTs	1.9	0.19	upregulate stage
427878	C05766	Hs.181022	CGI-07 protein	4.1	0.14	upregulate stage
427922	AK001934	Hs.181112	HSPC126 protein	2.6	0.19	upregulate stage
427933	AW974643	Hs.190571	ESTs	4.55	0.14	upregulate stage

427934	AA810541	Hs.291866	ESTs	1	1	upregulate stage
427944	AA417878	Hs.48401	ESTs, Weakly similar to ALU8_HUMAN ALU S	6.15	0.1	upregulate stage
427961	AW293165	Hs.143134	ESTs	4.85	0.11	upregulate stage
427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.55	0.13	upregulate stage
428003	AL110200	Hs.181384	Homo sapiens mRNA; cDNA DKFZp586B0922 (f	1.45	0.36	upregulate stage
428004	AA449563	Hs.300270	ESTs	3.95	0.12	upregulate stage
428010	AA806554	Hs.185375	ESTs	1	0.38	upregulate stage
428057	AI343641	Hs.185798	ESTs	10.1	0.06	upregulate stage
428058	AI821625	Hs.191602	ESTs	1	0.5	upregulate stage
428071	AF212848	Hs.182339	ets homologous factor	6.4	0.09	upregulate stage
428182	BE386042	Hs.293317	ESTs, Weakly similar to JM27 [H.sapiens]	1	0.23	upregulate stage
428192	AA424051		gb:zv80d03.s1 Soares_total_fetus_Nb2HF8_	2.45	0.16	upregulate stage
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	9.25	0.04	upregulate stage
428403	AI393048	Hs.239894	leucine rich repeat (in FLII) interactin	9.94	0.06	upregulate stage
428436	BE080180		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	1	1	upregulate stage
428450	NM_014791	Hs.184339	KIAA0175 gene product	4.43	0.16	upregulate stage
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	9.2	0.07	upregulate stage
428529	AW262022	Hs.106278	Homo sapiens cDNA FLJ12839 fis, clone NT	1	1	upregulate stage
428576	AW009330	Hs.167621	ESTs	1	0.3	upregulate stage
428605	AB037862	Hs.186756	KIAA1441 protein	9.25	0.09	upregulate stage
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.8	0.08	upregulate stage
428685	AF131853	Hs.189527	Homo sapiens clone 25016 mRNA sequence	1	1	upregulate stage
428716	AL122118	Hs.190614	Homo sapiens mRNA; cDNA DKFZp434O1221 (f	1	0.65	upregulate stage
428783	AW070204	Hs.178176	ESTs	1.6	0.23	upregulate stage
428788	AF082283	Hs.193516	B-cell CLL/lymphoma 10	9.6	0.08	upregulate stage
428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	5.45	0.11	upregulate stage
428839	AI767756	Hs.82302	ESTs	10	0.06	upregulate stage
428881	AI298368	Hs.98918	ESTs	1.4	0.18	upregulate stage
428954	AF100781	Hs.194678	WNT1 inducible signaling pathway protein	1	1	upregulate stage
428988	AA442900	Hs.27947	ESTs	3.05	0.13	upregulate stage
429042	AW015489	Hs.235920	ESTs	1	0.56	upregulate stage
429057	AF156557	Hs.194816	stomatin-like protein 1	0.95	0.93	upregulate stage
429066	AA868555	Hs.178222	ESTs	6	0.11	upregulate stage
429072	AI376228	Hs.108043	Friend leukemia virus integration 1	1	1	upregulate stage
429083	Y09397	Hs.227817	BCL2-related protein A1	11.12	0.03	upregulate stage
429091	AA935658	Hs.187939	ESTs	8.9	0.08	upregulate stage
429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14098 fis, clone MA	4.1	0.17	upregulate stage
429127	AA749382	Hs.107233	ESTs	1	0.23	upregulate stage
429135	AA446966	Hs.99090	ESTs, Moderately similar to similar to K	1	1	upregulate stage
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	8.6	0.08	upregulate stage
429174	BE559598	Hs.197803	KIAA0160 protein	8.4	0.06	upregulate stage
429236	AA448407		gb:zw68d11.s1 Soares_testis_NHT Homo sap	1	0.36	upregulate stage
429268	AA205386	Hs.198481	RAR-related orphan receptor B	2.9	0.16	upregulate stage
429300	AB011108	Hs.198891	serine/threonine-protein kinase PRP4 hom	4.25	0.15	upregulate stage
429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	2.95	0.11	upregulate stage
429344	R94038	Hs.199538	inhibin, beta C	2.91	0.28	upregulate stage
429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.19	0.68	upregulate stage
429376	AI867889	Hs.43227	ESTs	1	1	upregulate stage
429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	8.15	0.07	upregulate stage
429450	AA824451	Hs.94292	Homo sapiens cDNA: FLJ23311 fis, clone H	3.3	0.17	upregulate stage
429472	AW452421	Hs.15652	ESTs	1	1	upregulate stage
429482	AF076974	Hs.203952	transformation/transcription domain-asso	1.52	0.59	upregulate stage
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	2.9	0.15	upregulate stage
429572	AW295375	Hs.39474	ESTs	1	0.95	upregulate stage
429584	AI817785	Hs.183037	protein kinase, cAMP-dependent, regulato	6.55	0.1	upregulate stage
429590	AI219490	Hs.44445	ESTs, Weakly similar to Kelch motif cont	1	1	upregulate stage
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.6	0.14	upregulate stage
429601	AI804293	Hs.119406	ESTs, Weakly similar to AF143946 1 trans	1.36	0.58	upregulate stage
429602	AA521463	Hs.183424	ESTs	1	0.34	upregulate stage
429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	10.8	0.07	upregulate stage
429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	3.4	0.12	upregulate stage
429631	AA455612	Hs.136710	EST	1	1	upregulate stage
429644	AA455892	Hs.156379	ESTs	3.4	0.15	upregulate stage
429653	NM_005955	Hs.211581	metal-regulatory transcription factor 1	4.45	0.17	upregulate stage
429664	L20433	Hs.211588	POU domain, class 4, transcription facto	1.17	0.74	upregulate stage
429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.19	0.22	upregulate stage
429699	AI383469	Hs.159300	ESTs	4.4	0.1	upregulate stage
429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.25	0.13	upregulate stage
429813	AW139678	Hs.180791	ESTs	1	0.95	upregulate stage
429828	AB019494	Hs.225767	IDN3 protein	4.2	0.14	upregulate stage
429838	AW904907	Hs.108241	ESTs, Weakly similar to The KIAA0191 gen	3.25	0.14	upregulate stage
429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	1	0.36	upregulate stage
429913	AA460608	Hs.99552	ESTs	1.35	0.2	upregulate stage
429917	H80572		gb:yu76c02.r1 Soares fetal liver spleen	4.8	0.13	upregulate stage
429921	AA526911	Hs.102756	ESTs	1	0.63	upregulate stage
429950	AW081608	Hs.105053	ESTs	3.7	0.13	upregulate stage
429971	AF079550	Hs.227098	glial cells missing (Drosophila) homolog	1	0.83	upregulate stage

429979	AA463338		gb:zx97a10.r1 Soares_NhHMPu_S1 Homo sapi	1	0.32	upregulate stage
429982	AW449534	Hs.99607	Homo sapiens cDNA FLJ13841 fis, clone TH	9.45	0,08	upregulate stage
429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.78	0.58	upregulate stage
430020	AI539029	Hs.99607	Homo sapiens cDNA FLJ13841 fis, clone TH	1	0.36	upregulate stage
430021	AA463913	Hs.221160	ESTs	1	0.56	upregulate stage
430049	AW277085	Hs.99619	ESTs	3.55	0.17	upregulate stage
430060	NM_002941	Hs.301198	roundabout (axon guidance receptor, Dros	1	0.59	upregulate stage
430076	AA465115		gb:aa32c11.r1 NCI_CGAP_GCB1 Homo sapiens	5.4	0.12	upregulate stage
430134	BE380149	Hs.105223	ESTs, Weakly similar to contains similar	3.6	0.13	upregulate stage
430184	AB013802	Hs.234790	contactin 5	1	1	upregulate stage
430195	AW969308	Hs.188594	ESTs	9.15	0.1	upregulate stage
430279	R85974	Hs.16279	ESTs	1.2	0.52	upregulate stage
430287	AW182459	Hs.125759	ESTs, Weakly similar to tumor suppressor	4.05	0.15	upregulate stage
430291	AV660345	Hs.238126	CGI-49 protein	7.2	0.08	upregulate stage
430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	11.9	0.06	upregulate stage
430350	BE169639		gb:PM1-HT0527-280200-005-a05 HT0527 Homo	7.1	0.09	upregulate stage
430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9	0.11	upregulate stage
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.56	0.2	upregulate stage
430488	D19589	Hs.4220	ESTs, Moderately similar to tetracycline	10.5	0.08	upregulate stage
430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	11.2	0.06	upregulate stage
430519	AF129534	Hs.49210	F-box only protein 4	5.35	0.11	upregulate stage
430550	AK000062	Hs.243756	hypothetical protein FLJ20055	1	1	upregulate stage
430561	BE065227		gb:RC1-BT0314-310300-015-b06 BT0314 Homo	1	1	upregulate stage
430563	AA481269	Hs.178381	ESTs	1	0.45	upregulate stage
430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.75	0.14	upregulate stage
430630	AW269920	Hs.2621	cystatin A (stefin A)	2.52	0.25	upregulate stage
430634	AI860651	Hs.26685	ESTs	1.24	0.61	upregulate stage
430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	1.79	0.47	upregulate stage
430640	AA482636		gb:zv29c06.r1 Soares ovary tumor NbHOT H	9.15	0.08	upregulate stage
430665	BE350122	Hs.157367	ESTs	9.4	0.08	upregulate stage
430726	AL031224	Hs.247850	Human DNA sequence from clone 336H9 on c	1	0.27	upregulate stage
430733	AW975920	Hs.283361	ESTs	3.5	0.13	upregulate stage
430781	AW088127	Hs.278536	ESTs	1	1	upregulate stage
430791	AA486293	Hs.272068	ESTs, Moderately similar to alternativel	1.61	0.42	upregulate stage
430817	AA487242	Hs.185105	ESTs	1	1	upregulate stage
430888	BE155293	Hs.76064	ribosomal protein L27a	3.05	0.17	upregulate stage
430918	NM_000843	Hs.248131	glutamate receptor, metabotropic 6	9.05	0.09	upregulate stage
430926	L05597	Hs.248136	5-hydroxytryptamine (serotonin) receptor	1	0.91	upregulate stage
430994	AA490346	Hs.40530	ESTs	1.03	0.89	upregulate stage
431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin 3	24.8	0.03	upregulate stage
431023	AI283133	Hs.178925	ESTs	2.55	0.15	upregulate stage
431030	AA830525	Hs.291988	ESTs	1	0.47	upregulate stage
431041	AA490967	Hs.105276	ESTs	1	0.36	upregulate stage
431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.65	0.45	upregulate stage
431082	AA491600	Hs.161942	ESTs	9.85	0.06	upregulate stage
431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	43.15	0.01	upregulate stage
431146	Z83850	Hs.250649	Human DNA sequence from PAC 82J11 and co	1	0.4	upregulate stage
431173	AW971198	Hs.294068	ESTs	6.3	0.12	upregulate stage
431245	AA496933	Hs.191687	ESTs	1	1	upregulate stage
431253	R06428	Hs.226351	ESTs	1	0.8	upregulate stage
431267	AW969661	Hs.124047	ESTs	1	0.31	upregulate stage
431287	BE044989	Hs.274901	ESTs	1	1	upregulate stage
431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	10.8	0.06	upregulate stage
431332	AA503297	Hs.117108	ESTs	6.55	0.1	upregulate stage
431343	AW970603	Hs.300941	Homo sapiens cDNA FLJ11661 fis, clone HE	5.65	0.09	upregulate stage
431346	AA371059	Hs.251636	ubiquitin specific protease 3	1.68	0.52	upregulate stage
431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.12	0.47	upregulate stage
431381	AA577114	Hs.105727	ESTs	1	0.36	upregulate stage
431448	AL137517	Hs.288381	hypothetical protein DKFZp564O1278	3.72	0.13	upregulate stage
431494	AA991355	Hs.129808	ESTs	2.75	0.18	upregulate stage
431510	AA580082	Hs.112264	ESTs	3.75	0.13	upregulate stage
431560	BE244135	Hs.260238	hypothetical protein FLJ10842	9.1	0.08	upregulate stage
431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (	7.5	0.11	upregulate stage
431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	8.2	0.08	upregulate stage
431610	AK000972	Hs.264363	hypothetical protein FLJ10110	6.4	0.1	upregulate stage
431613	AA018515	Hs.264482	Apg12 (autophagy 12, S. cerevisiae)-like	5.8	0.11	upregulate stage
431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.3	0.59	upregulate stage
431663	NM_016569	Hs.267182	TBX3-iso protein	1.6	0.52	upregulate stage
431670	AW971287		gb:EST383376 MAGE resequences, MAGL Homo	1	1	upregulate stage
431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	9.1	0.05	upregulate stage
431691	AI208511	Hs.292510	ESTs	4.15	0.12	upregulate stage
431692	AL021331	Hs.267749	unc93 (C.elegans) homolog A	4.2	0.13	upregulate stage
431694	AW970112	Hs.292697	ESTs	1	0.83	upregulate stage
431726	NM_015361	Hs.268053	KIAA0029 protein	10.1	0.07	upregulate stage
431736	AI912234	Hs.151245	ESTs	9.9	0.08	upregulate stage
431753	X76029	Hs.2841	neuromedin U	1	0.23	upregulate stage
431781	AA515474	Hs.99908	nuclear receptor coactivator 4	1	0.36	upregulate stage

431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like pro	1	0.65	upregulate stage
431814	BE256242	Hs.270847	delta-tubulin	3.35	0.18	upregulate stage
431817	X65233	Hs.271079	zinc finger protein 80 (pT17)	1	1	upregulate stage
431828	AA572994		gb:nm33f12.s1 NCI_CGAP_Lip2 Homo sapiens	4	0.12	upregulate stage
431880	AI700238	Hs.187486	ESTs	1	1	upregulate stage
431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.89	0.27	upregulate stage
431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1	0.18	upregulate stage
431951	AI086335	Hs.136470	ESTs	6.4	0.11	upregulate stage
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.09	0.07	upregulate stage
431989	AW972870	Hs.291069	ESTs	1	0.23	upregulate stage
431992	NM_002742	Hs.2891	protein kinase C, mu	3.9	0.15	upregulate stage
432015	AL157504	Hs.159115	ESTs	6.05	0.09	upregulate stage
432023	AW273128	Hs.214188	ESTs	0.99	0.86	upregulate stage
432028	AJ272208	Hs.272354	interleukin 1 receptor accessory protein	1	0.48	upregulate stage
432039	AF220217	Hs.272374	Homo sapiens rsec15-like protein mRNA, p	1	0.24	upregulate stage
432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	1.38	0.64	upregulate stage
432069	AW975868	Hs.294100	ESTs	4.25	0.15	upregulate stage
432072	N62937	Hs.269109	ESTs	5.9	0.09	upregulate stage
432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	7.9	0.08	upregulate stage
432136	AA157632	Hs.272630	vacuolar proton pump delta polypeptide	1	0.28	upregulate stage
432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.5	0.25	upregulate stage
432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	6.1	0.11	upregulate stage
432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.44	0.29	upregulate stage
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	15	0.02	upregulate stage
432235	AA531129	Hs.190297	ESTs	9.57	0.06	upregulate stage
432237	AK001926	Hs.274132	hypothetical protein FLJ11064	1	0.44	upregulate stage
432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	4.3	0.1	upregulate stage
432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.95	0.15	upregulate stage
432338	AA534197	Hs.272693	ESTs	1	1	upregulate stage
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.97	0.4	upregulate stage
432376	BE536069	Hs.2962	S100 calcium-binding protein P	1.16	0.58	upregulate stage
432407	AA221036	Hs.285026	HERV-H LTR-associating 1	3.75	0.16	upregulate stage
432410	X68561	Hs.2982	Sp4 transcription factor	1	1	upregulate stage
432415	T16971	Hs.289014	ESTs	7.3	0.07	upregulate stage
432432	AA541323	Hs.115831	ESTs	5.35	0.13	upregulate stage
432435	BE218886	Hs.282070	ESTs	5.35	0.1	upregulate stage
432441	AW292425	Hs.163484	ESTs	19.4	0.04	upregulate stage
432518	AI675836	Hs.94319	ESTs	1	0.59	upregulate stage
432580	X82018	Hs.3053	zinc finger protein with interaction dom	9.15	0.08	upregulate stage
432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	10.15	0.05	upregulate stage
432614	AA557153	Hs.185853	ESTs	1	0.33	upregulate stage
432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	10.5	0.07	upregulate stage
432661	AW973823	Hs.283526	ESTs	1	1	upregulate stage
432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein	1	0.16	upregulate stage
432669	AL043482	Hs.267115	ESTs	4.15	0.12	upregulate stage
432673	AB028859	Hs.278605	ER-associated DNAJ; ER-associated Hsp40	10.24	0.06	upregulate stage
432678	AA923424	Hs.135567	ESTs	1	0.69	upregulate stage
432690	AF181490	Hs.278627	prenylcysteine lyase	4.55	0.12	upregulate stage
432724	X98266		gb:H.sapiens mRNA for ligase like protei	1	1	upregulate stage
432758	NM_014091	Hs.278920	PRO1510 protein	1	1	upregulate stage
432773	NM_014124	Hs.278935	PRO0255 protein	1	1	upregulate stage
432789	D26361	Hs.3104	KIAA0042 gene product	3.46	0.22	upregulate stage
432829	W60377	Hs.57772	ESTs	1.33	0.43	upregulate stage
432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.5	0.14	upregulate stage
432900	BE178025	Hs.7942	hypothetical protein FLJ20080	1	0.3	upregulate stage
432917	NM_014125	Hs.279812	PRO0327 protein	6.33	0.12	upregulate stage
432935	AW270239	Hs.213709	ESTs	3.85	0.11	upregulate stage
432963	AA572859	Hs.225791	ESTs	1	0.19	upregulate stage
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	29.9	0.03	upregulate stage
433005	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	1	0.59	upregulate stage
433129	AA577814		gb:nn24d03.s1 NCI_CGAP_Gas1 Homo sapiens	1	1	upregulate stage
433159	AB035898	Hs.150587	kinesin-like protein 2	6	0.1	upregulate stage
433201	AB040896	Hs.21104	KIAA1463 protein	9.2	0.09	upregulate stage
433211	H11850	Hs.12808	MARK	1.6	0.45	upregulate stage
433218	AI040372	Hs.278894	KIAA1482 protein	1	0.44	upregulate stage
433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	5.45	0.12	upregulate stage
433230	AW136134	Hs.220277	ESTs	7.3	0.09	upregulate stage
433237	AB040930	Hs.297021	Homo sapiens cDNA FLJ13211 fis, clone NT	1	1	upregulate stage
433365	AF026944	Hs.293797	ESTs	4.95	0.08	upregulate stage
433371	T25451		gb:PTHI188 HTCDL1 Homo sapiens cDNA 5'/3	4.75	0.12	upregulate stage
433394	AI907753	Hs.93810	cerebral cavernous malformations 1	4.5	0.11	upregulate stage
433424	R68252	Hs.163566	ESTs	1	1	upregulate stage
433440	AF052127		gb:Homo sapiens clone 23850 mRNA sequenc	1	1	upregulate stage
433452	AW296906	Hs.142869	ESTs	9.82	0.08	upregulate stage
433456	AA593447	Hs.124296	ESTs	9.45	0.08	upregulate stage
433467	AI420457	Hs.50955	ESTs	1.11	0.74	upregulate stage
433479	AW511459	Hs.249972	ESTs	3.35	0.13	upregulate stage

433484	BE264397	Hs.148674	ESTs	1	0.27	upregulate stage
433515	AA595800	Hs.190246	ESTs	3.05	0.14	upregulate stage
433602	AI769948	Hs.24906	ESTs	1	1	upregulate stage
433613	AA836126	Hs.5669	ESTs	2.8	0.12	upregulate stage
433625	AW955674	Hs.161762	ESTs	1	0.53	upregulate stage
433658	L03678	Hs.156110	immunoglobulin kappa constant	9.65	0.05	upregulate stage
433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	7.9	0.08	upregulate stage
433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.7	0.11	upregulate stage
433735	AA608955	Hs.109653	ESTs	8.95	0.08	upregulate stage
433895	AI287912	Hs.3628	mitogen-activated protein kinase kinase	4.43	0.16	upregulate stage
433904	AI399956	Hs.208956	ESTs	5.5	0.12	upregulate stage
433929	AI375499	Hs.27379	ESTs	7	0.09	upregulate stage
433966	AF113017	Hs.284301	PRO1268 protein	7.95	0.08	upregulate stage
433967	AF113018	Hs.284302	PRO1621 protein	2.65	0.1	upregulate stage
434006	AF113688		gb:Homo sapiens clone FLB4630	7.85	0.08	upregulate stage
434037	AF116601	Hs.283048	hypothetical protein PRO0128	8.81	0.09	upregulate stage
434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.35	0.09	upregulate stage
434085	AF116673	Hs.250029	hypothetical protein PRO1925	1	1	upregulate stage
434092	AA625155		gb:af70d06.r1 Soares_NhHMPu_S1 Homo sapi	1	1	upregulate stage
434094	AA305599	Hs.238205	hypothetical protein PRO2013	11.5	0.06	upregulate stage
434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	3.55	0.11	upregulate stage
434192	AW387314	Hs.34371	ESTs	1.65	0.22	upregulate stage
434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	7.85	0.09	upregulate stage
434217	AW014795	Hs.23349	ESTs	3.8	0.13	upregulate stage
434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	5.95	0.11	upregulate stage
434271	AA897778	Hs.201677	ESTs	1	0.38	upregulate stage
434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.45	0.07	upregulate stage
434322	AI125686	Hs.152727	ESTs	2.65	0.18	upregulate stage
434351	AW974991	Hs.191852	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.61	upregulate stage
434354	AW974912	Hs.292783	ESTs	1	1	upregulate stage
434398	AA121098	Hs.3838	serum-inducible kinase	10.7	0.08	upregulate stage
434464	BE063921	Hs.295971	ESTs	10.15	0.07	upregulate stage
434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	7.6	0.09	upregulate stage
434484	W79839	Hs.104336	hypothetical protein	5.1	0.15	upregulate stage
434513	AF143888	Hs.18213	Homo sapiens clone IMAGE:121736 mRNA seq	1	1	upregulate stage
434534	H90477	Hs.41407	ESTs	1	0.18	upregulate stage
434540	NM_016045	Hs.5184	TH1 drosophila homolog	12.4	0.06	upregulate stage
434569	AI311295	Hs.58609	ESTs	1.75	0.38	upregulate stage
434575	AI133446	Hs.299964	ESTs	9.7	0.06	upregulate stage
434627	AI221894	Hs.39311	ESTs	1.65	0.17	upregulate stage
434629	AA789081	Hs.4029	glioma-amplified sequence-41	9	0.07	upregulate stage
434663	AA641972	Hs.130058	ESTs	4.55	0.15	upregulate stage
434731	AA648049	Hs.121518	ESTs	8.5	0.1	upregulate stage
434765	AA831115	Hs.190473	ESTs	1	0.71	upregulate stage
434773	AA648962	Hs.152947	ESTs	10.55	0.08	upregulate stage
434792	AA649253	Hs.132458	ESTs	5.45	0.11	upregulate stage
434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1	0.34	upregulate stage
434876	AF160477	Hs.245781	Homo sapiens Ig superfamily receptor LNI	1.4	0.57	upregulate stage
434909	AI479212	Hs.17283	hypothetical protein FLJ10890	1	0.91	upregulate stage
434926	BE543269	Hs.50252	Homo sapiens HSPC283 mRNA, partial cds	4.9	0.13	upregulate stage
434939	AF161422	Hs.21590	Homo sapiens HSPC304 mRNA, partial cds	1	1	upregulate stage
434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	10.75	0.07	upregulate stage
434970	AW272262	Hs.250468	ESTs	9.05	0.08	upregulate stage
434980	AW770553	Hs.293640	ESTs	4.95	0.14	upregulate stage
434997	AW975155	Hs.292163	ESTs	1	0.36	upregulate stage
435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.16	0.71	upregulate stage
435030	AI203316	Hs.148655	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.95	0.14	upregulate stage
435047	AA454985	Hs.54973	cadherin-like protein VR20	3.31	0.2	upregulate stage
435061	AI651474	Hs.163944	ESTs	1.4	0.2	upregulate stage
435080	AI831760	Hs.155111	ESTs	9.05	0.08	upregulate stage
435087	AW975241	Hs.23567	ESTs	1	1	upregulate stage
435108	AW975018	Hs.287440	Homo sapiens cDNA FLJ11692 fis, clone HE	1	0.2	upregulate stage
435136	R27299	Hs.10172	ESTs	8.9	0.07	upregulate stage
435159	AA668879	Hs.116649	ESTs	1.35	0.25	upregulate stage
435162	AI911044	Hs.213893	ESTs	1	1	upregulate stage
435166	AI391470	Hs.158618	ESTs	5.5	0.12	upregulate stage
435212	AW300100	Hs.164185	ESTs	1	1	upregulate stage
435237	AI026836	Hs.114689	ESTs	8.75	0.1	upregulate stage
435255	W87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	3.4	0.14	upregulate stage
435256	AF193766	Hs.13872	cytokine-like protein C17	3.2	0.14	upregulate stage
435257	AA677026	Hs.191217	ESTs	4.5	0.12	upregulate stage
435298	AA677696	Hs.189196	ESTs	1	1	upregulate stage
435307	W90610	Hs.192003	ESTs	1	0.87	upregulate stage
435347	AW014873	Hs.116963	ESTs	2.45	0.14	upregulate stage
435382	N54493		gb:yv40g05.s1 Soares fetal liver spleen	1	0.56	upregulate stage
435408	H07897	Hs.4302	ESTs	0.84	0.97	upregulate stage
435491	T98543	Hs.191900	ESTs	1	0.3	upregulate stage

435525	AI831297	Hs.123310	ESTs	3.25	0.15	upregulate stage
435597	AW305188	Hs.163027	ESTs	1	0.57	upregulate stage
435637	AF220051	Hs.110853	uncharacterized hematopoietic stem/proge	8.76	0.09	upregulate stage
435647	AI653240	Hs.49823	ESTs	3.19	0.25	upregulate stage
435738	AA699633	Hs.269543	ESTs	2.9	0.16	upregulate stage
435762	AW043836	Hs.212460	ESTs	1	1	upregulate stage
435809	H90213	Hs.191330	ESTs	1.25	0.23	upregulate stage
435826	AI554089	Hs.117880	ESTs	6.55	0.08	upregulate stage
435854	AJ278120	Hs.4996	DKFZP564D166 protein	2.76	0.29	upregulate stage
435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.25	upregulate stage
435981	H74319	Hs.188620	ESTs	6.35	0.11	upregulate stage
435990	AI015862	Hs.131793	ESTs	4.25	0.08	upregulate stage
435999	AA703271	Hs.269903	ESTs, Moderately similar to ALU1_HUMAN A	1	1	upregulate stage
436016	AA806465	Hs.121536	ESTs	1.45	0.23	upregulate stage
436023	T81819		gb:yd95f05.s1 Soares fetal liver spleen	9.15	0.07	upregulate stage
436052	AI021983	Hs.271432	ESTs	1	0.23	upregulate stage
436115	AW512033	Hs.102004	ESTs	1.9	0.21	upregulate stage
436118	AI221173	Hs.145080	ESTs	1	1	upregulate stage
436120	AI248193	Hs.119860	ESTs	9.61	0.08	upregulate stage
436149	AI754308	Hs.159452	ESTs	2.4	0.19	upregulate stage
436156	AA705466	Hs.119900	ESTs	1	0.26	upregulate stage
436170	AW450381	Hs.14529	ESTs	1	0.91	upregulate stage
436202	AA706315	Hs.192057	ESTs	1	1	upregulate stage
436246	AW450963	Hs.119991	ESTs	3.85	0.11	upregulate stage
436274	AA732755	Hs.120299	ESTs	2.85	0.13	upregulate stage
436282	R91913	Hs.272104	ESTs	3.95	0.11	upregulate stage
436299	AK000767	Hs.5111	hypothetical protein FLJ20729	6	0.09	upregulate stage
436300	AA831601	Hs.275736	ESTs	1	1	upregulate stage
436326	BE085236	Hs.181244	major histocompatibility complex, class	2.49	0.28	upregulate stage
436360	AI962796	Hs.136754	ESTs	2.4	0.17	upregulate stage
436363	AA843926	Hs.124434	ESTs	3.35	0.1	upregulate stage
436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	1	0.67	upregulate stage
436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	4	0.15	upregulate stage
436408	AW274577	Hs.252954	ESTs	9.1	0.09	upregulate stage
436422	AA716141	Hs.147027	ESTs	1	0.26	upregulate stage
436429	AA357003	Hs.17546	hypothetical protein FLJ23499	1	1	upregulate stage
436463	H06502	Hs.6656	ESTs	5.45	0.12	upregulate stage
436476	AA326108	Hs.53631	ESTs, Weakly similar to enhancer-of-spli	7.75	0.07	upregulate stage
436507	AA721209	Hs.201630	ESTs	2.45	0.18	upregulate stage
436518	AA766433	Hs.122864	ESTs	3.15	0.21	upregulate stage
436522	AA721381	Hs.129876	ESTs	4.75	0.1	upregulate stage
436578	AI091435	Hs.134859	ESTs	3.4	0.12	upregulate stage
436670	AI690021	Hs.201536	ESTs	6.85	0.11	upregulate stage
436740	AW975133		gb:EST387239 MAGE resequences, MAGN Homo	7.4	0.09	upregulate stage
436764	AW976004	Hs.291731	ESTs	1	1	upregulate stage
436785	AA745597	Hs.291400	ESTs	1	1	upregulate stage
436823	AW749865	Hs.293645	ESTs	4.6	0.12	upregulate stage
436831	AA830173	Hs.291918	ESTs	1.6	0.27	upregulate stage
436839	AA767346	Hs.291614	ESTs	1	1	upregulate stage
436844	AA766458	Hs.122812	ESTs	1.5	0.28	upregulate stage
436853	BE328074	Hs.148661	ESTs	5.05	0.14	upregulate stage
436860	H12751	Hs.5327	PRO1914 protein	8.95	0.08	upregulate stage
436925	AA742327	Hs.292687	ESTs	1	1	upregulate stage
437044	AL035864	Hs.69517	ESTs, Highly similar to differentially e	1.61	0.5	upregulate stage
437087	AA745563		gb:ny60e04.s1 NCI_CGAP_Pr18 Homo sapiens	1	1	upregulate stage
437144	AL049466	Hs.7859	ESTs	1	0.31	upregulate stage
437170	R49202	Hs.181694	ESTs	8.7	0.08	upregulate stage
437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	4.4	0.05	upregulate stage
437207	T27503	Hs.15929	Homo sapiens cDNA FLJ12910 fis, clone NT	1.4	0.22	upregulate stage
437214	BE092336		gb:IL2-BT0734-240400-072-A12 BT0734 Homo	5.65	0.09	upregulate stage
437240	AA747537		gb:nx85c05.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.45	upregulate stage
437257	AI283085	Hs.290931	ESTs, Weakly similar to unknown [S.cerev	3.8	0.14	upregulate stage
437258	AL041243	Hs.174104	ESTs	9.72	0.08	upregulate stage
437267	AW511443	Hs.258110	ESTs	4.25	0.12	upregulate stage
437274	AA747965		gb:nx79a10.s1 NCI_CGAP_Ew1 Homo sapiens	1	0.19	upregulate stage
437288	AA748182	Hs.160377	ESTs	1	0.61	upregulate stage
437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	3.1	0.17	upregulate stage
437324	AL162077		gb:Homo sapiens mRNA; cDNA DKFZp761A219	1	0.25	upregulate stage
437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	7.95	0.07	upregulate stage
437356	BE622396	Hs.284252	Homo sapiens mRNA; cDNA DKFZp762O1615 (f	1	1	upregulate stage
437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	9.15	0.09	upregulate stage
437471	AL390169		gb:Homo sapiens mRNA; cDNA DKFZp547D064	1	1	upregulate stage
437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	1.1	0.56	upregulate stage
437567	AW627990	Hs.288954	Homo sapiens cDNA: FLJ21466 fis, clone C	1	1	upregulate stage
437575	AW954355	Hs.36529	ESTs	10.25	0.06	upregulate stage
437717	AA804765	Hs.132853	ESTs	1	0.77	upregulate stage
437722	AW292947	Hs.122872	ESTs	9.75	0.05	upregulate stage

437752	AA767376	Hs.291631	ESTs	6.7	0.08	upregulate stage
437770	AA767881	Hs.122897	ESTs	2.57	0.24	upregulate stage
437798	AW811767		gb:RC2-ST0165-300999-011-g02 ST0165 Homo	1	1	upregulate stage
437799	R51083	Hs.90787	ESTs	1	1	upregulate stage
437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.77	0.3	upregulate stage
437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	8.8	0.08	upregulate stage
437887	AA811524	Hs.29263	Homo sapiens cDNA FLJ11896 fis, clone HE	3.8	0.17	upregulate stage
437889	AA830524	Hs.124357	ESTs	1	0.69	upregulate stage
437937	AI917222	Hs.121655	ESTs	1	0.38	upregulate stage
437938	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	1.37	0.52	upregulate stage
437983	AI303023	Hs.30211	hypothetical protein FLJ22313	8.82	0.08	upregulate stage
438011	BE466173	Hs.145696	splicing factor (CC1.3)	9	0.09	upregulate stage
438032	BE045624	Hs.152992	ESTs	5.65	0.13	upregulate stage
438069	N80701	Hs.33790	ESTs	3.25	0.13	upregulate stage
438077	AA777330	Hs.50429	ESTs	1	1	upregulate stage
438081	H49546	Hs.298964	ESTs	3.75	0.11	upregulate stage
438102	AA777793	Hs.137580	xylulokinase (H. influenzae) homolog	1	1	upregulate stage
438112	W85729	Hs.194279	ESTs	1	0.33	upregulate stage
438113	AI457908	Hs.8882	ESTs	1.21	0.55	upregulate stage
438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	11.75	0.07	upregulate stage
438144	AA778894	Hs.118364	ESTs	1	1	upregulate stage
438153	AI268632	Hs.146159	ESTs	1	1	upregulate stage
438171	AW976507	Hs.293515	ESTs	2.82	0.24	upregulate stage
438271	L21934	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1	1	upregulate stage
438290	AA843719	Hs.122341	ESTs	3.9	0.13	upregulate stage
438321	AA576635	Hs.6153	CGI-48 protein	9.4	0.08	upregulate stage
438325	AA804258	Hs.123229	ESTs	4.65	0.11	upregulate stage
438334	AA806992	Hs.291686	ESTs	1	1	upregulate stage
438366	AA805760		gb:ns43f01.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.34	upregulate stage
438370	AA843242	Hs.48523	ESTs	4	0.14	upregulate stage
438374	AA321866	Hs.6193	Homo sapiens mRNA; cDNA DKFZp434C1717 (f	1	0.84	upregulate stage
438377	AA806070	Hs.291716	ESTs	1	0.24	upregulate stage
438378	AW970529	Hs.86434	Homo sapiens cDNA: FLJ21816 fis, clone H	6.65	0.11	upregulate stage
438401	AL046321	Hs.197484	ESTs	1	1	upregulate stage
438403	AA806607	Hs.292206	ESTs	2.75	0.14	upregulate stage
438412	AA806776	Hs.130814	ESTs	1	1	upregulate stage
438448	AA807344	Hs.172932	Homo sapiens mRNA for partial 3'UTR, seq	1	0.34	upregulate stage
438451	AI081972	Hs.220261	ESTs	5.7	0.09	upregulate stage
438473	H07986	Hs.136901	ESTs	1	1	upregulate stage
438487	AI684733	Hs.88820	HDCMC28P protein	1	0.21	upregulate stage
438529	AW007287	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	1	0.36	upregulate stage
438534	AW204052	Hs.123644	ESTs	1	0.37	upregulate stage
438693	AA814360	Hs.249595	ESTs	3.55	0.15	upregulate stage
438698	AW297855	Hs.125815	ESTs	3.12	0.22	upregulate stage
438728	AA815202	Hs.25657	ESTs	1	0.67	upregulate stage
438746	AI885815	Hs.184727	ESTs	1.5	0.35	upregulate stage
438805	AA826048	Hs.117887	ESTs	9.35	0.07	upregulate stage
438812	AA826199	Hs.44287	ESTs	1	0.57	upregulate stage
438817	AI023799	Hs.163242	ESTs	4.2	0.08	upregulate stage
438886	AA827728	Hs.128705	ESTs, Weakly similar to AF149422 2 unkno	4.05	0.12	upregulate stage
438913	AI380429	Hs.172445	ESTs	5.4	0.11	upregulate stage
438950	H23789	Hs.144530	ESTs	1	1	upregulate stage
438961	H42135	Hs.101848	ESTs	7.85	0.08	upregulate stage
438990	AF085890		gb:Homo sapiens full length insert cDNA	1	0.83	upregulate stage
439026	R98978	Hs.117767	ESTs	1	0.27	upregulate stage
439052	AF085917	Hs.37921	ESTs	1	0.22	upregulate stage
439057	H59623	Hs.271561	ESTs	1	1	upregulate stage
439176	AI446444	Hs.190394	ESTs	5.8	0.12	upregulate stage
439179	AA831250	Hs.292693	ESTs	1	1	upregulate stage
439183	AW970600		gb:EST382681 MAGE resequences, MAGK Homo	4.5	0.13	upregulate stage
439208	AK000299	Hs.180952	dynactin p62 subunit	11.9	0.06	upregulate stage
439212	AF087995	Hs.134877	ESTs	11.4	0.07	upregulate stage
439223	AW238299	Hs.23945	ESTs	2.79	0.26	upregulate stage
439312	AA833902	Hs.270745	ESTs	8.9	0.08	upregulate stage
439330	AF086147		gb:Homo sapiens full length insert cDNA	1	0.19	upregulate stage
439351	W37688	Hs.55158	ESTs, Weakly similar to weak similarity	1	0.31	upregulate stage
439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	3.9	0.15	upregulate stage
439444	AI277652	Hs.54578	ESTs	11	0.07	upregulate stage
439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	12.21	0.05	upregulate stage
439476	AA836340	Hs.165490	ESTs	1	0.65	upregulate stage
439492	AF086310	Hs.103159	ESTs	5.43	0.1	upregulate stage
439527	AW298119	Hs.202536	ESTs	5.25	0.1	upregulate stage
439550	H10438		gb:ym08d10.s1 Soares infant brain 1NIB H	3.2	0.18	upregulate stage
439560	BE555647	Hs.74899	hypothetical protein FLJ12820	1.81	0.32	upregulate stage
439565	AF086386	Hs.145599	ESTs	8.96	0.07	upregulate stage
439592	AF086413	Hs.58399	ESTs	1	1	upregulate stage
439605	AF086431	Hs.134805	ESTs	9.15	0.09	upregulate stage

439606	W79123	Hs.58561	ESTs, Weakly similar to KI01_HUMAN PROBA	8.45	0.06	upregulate stage
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	5.43	0.14	upregulate stage
439780	AL109688		gb:Homo sapiens mRNA full length insert	5	0.09	upregulate stage
439851	AI149520	Hs.144453	ESTs	2.75	0.21	upregulate stage
439862	AI571647	Hs.146170	hypothetical protein FLJ22969	6.3	0.11	upregulate stage
439926	AW014875	Hs.137007	ESTs	33.5	0.02	upregulate stage
439942	AW993791	Hs.94881	ESTs	9.9	0.08	upregulate stage
439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.59	0.15	upregulate stage
439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.95	0.07	upregulate stage
439987	AA860116	Hs.223232	ESTs	2.45	0.17	upregulate stage
439999	AA115811	Hs.6838	ras homolog gene family, member E	8.75	0.07	upregulate stage
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.68	0.41	upregulate stage
440012	AA861072		gb:ak32e05.s1 Soares_testis_NHT Homo sap	1	1	upregulate stage
440126	AA975145	Hs.66194	ESTs	1	1	upregulate stage
440194	R43809	Hs.22688	ESTs	1	1	upregulate stage
440228	AF125392	Hs.7089	insulin induced protein 2	1	1	upregulate stage
440249	AI246590	Hs.125325	ESTs	1.74	0.44	upregulate stage
440284	AA912032	Hs.181059	ESTs	1	1	upregulate stage
440334	BE276112	Hs.7165	zinc finger protein 259	9.45	0.09	upregulate stage
440348	AW015802	Hs.47023	ESTs	1	0.33	upregulate stage
440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.75	0.16	upregulate stage
440366	F08229	Hs.125273	ESTs	3.5	0.12	upregulate stage
440462	T71629	Hs.100554	ESTs	1.54	0.52	upregulate stage
440527	AV657117	Hs.184164	ESTs	3.75	0.14	upregulate stage
440613	AI733034	Hs.137079	ESTs	3.9	0.11	upregulate stage
440705	AA904244	Hs.153205	ESTs	3.9	0.14	upregulate stage
440856	AW993377	Hs.130390	ESTs	8.95	0.09	upregulate stage
440899	AW449445	Hs.172690	diacylglycerol kinase, alpha (80kD)	2.55	0.2	upregulate stage
440917	AA909651	Hs.160025	ESTs	1	0.17	upregulate stage
440980	AL042005	Hs.1117	tripeptidyl peptidase II	8.9	0.09	upregulate stage
440994	AI160011	Hs.193341	ESTs	1.29	0.58	upregulate stage
441092	T99289	Hs.126556	EST	4.9	0.11	upregulate stage
441107	AA917075	Hs.190520	ESTs	5.9	0.09	upregulate stage
441131	AI733222	Hs.126632	ESTs	9.55	0.09	upregulate stage
441143	AI027604	Hs.159650	ESTs	3.8	0.13	upregulate stage
441205	AW137827	Hs.176904	ESTs	4.75	0.12	upregulate stage
441206	BE552314	Hs.131823	ESTs, Weakly similar to TERA HUMAN [H.sa	1	1	upregulate stage
441264	AA927170	Hs.23290	ESTs	4.3	0.14	upregulate stage
441318	AI078234	Hs.176130	ESTs	1.74	0.45	upregulate stage
441334	AI700529	Hs.117964	ESTs	1	1	upregulate stage
441346	AA931077	Hs.186889	Homo sapiens cDNA FLJ12021 fis, clone HE	1	1	upregulate stage
441378	AA931826	Hs.126846	ESTs	4.5	0.1	upregulate stage
441383	AW294408	Hs.222068	ESTs	1	1	upregulate stage
441421	AA356792	Hs.301786	ESTs	1	0.24	upregulate stage
441470	BE503874	Hs.301986	ESTs	0.63	0.93	upregulate stage
441474	AW274946	Hs.144476	ESTs	1	1	upregulate stage
441484	AA935481	Hs.58972	ESTs	1	0.33	upregulate stage
441485	AI792988	Hs.189133	ESTs	4.25	0.1	upregulate stage
441508	AW015203	Hs.232237	ESTs	1	1	upregulate stage
441562	AW578981	Hs.52184	hypothetical protein FLJ20618	4.05	0.12	upregulate stage
441599	AW473362	Hs.127221	ESTs	1	0.29	upregulate stage
441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	8.75	0.08	upregulate stage
441616	BE569122	Hs.74111	RNA-binding protein (autoantigenic)	1.14	0.71	upregulate stage
441643	AI740504	Hs.205128	ESTs	1	0.33	upregulate stage
441677	AW271702	Hs.93739	ESTs	1	0.28	upregulate stage
441693	AA384673	Hs.7943	RPB5-mediating protein	1	0.43	upregulate stage
441703	AW390054	Hs.192843	ESTs	9.85	0.08	upregulate stage
441732	AW298818	Hs.127341	ESTs	4.6	0.14	upregulate stage
441759	C16126	Hs.161377	ESTs	4.55	0.13	upregulate stage
441762	AW592203	Hs.144769	ESTs	1	0.83	upregulate stage
441790	AW294909	Hs.132208	ESTs	9	0.08	upregulate stage
441794	AW197794	Hs.253338	ESTs	4.5	0.12	upregulate stage
441799	AW292276	Hs.127872	ESTs	1	0.22	upregulate stage
441801	AW242799	Hs.211874	ESTs	8	0.06	upregulate stage
441904	AI633206	Hs.128104	ESTs	2	0.19	upregulate stage
441955	AA972327	Hs.142903	ESTs	0.87	0.96	upregulate stage
441989	AA306207	Hs.286241	Homo sapiens cDNA: FLJ22698 fis, clone H	9.17	0.07	upregulate stage
441990	T66139	Hs.113631	ESTs	3.55	0.12	upregulate stage
442029	AW956698	Hs.14456	neural precursor cell expressed, develop	4.65	0.14	upregulate stage
442030	W67167	Hs.109080	ESTs	1	0.35	upregulate stage
442064	AI422867	Hs.88594	ESTs	8.8	0.08	upregulate stage
442071	BE048433	Hs.276043	ESTs	9.15	0.09	upregulate stage
442093	AA976049	Hs.128464	ESTs	1	1	upregulate stage
442194	AA984389	Hs.205088	ESTs	1	0.83	upregulate stage
442202	BE272862	Hs.106534	Homo sapiens cDNA: FLJ22625 fis, clone H	9.9	0.08	upregulate stage
442203	AI921423	Hs.250146	ESTs	1	1	upregulate stage
442214	AI681733	Hs.129003	ESTs	2.2	0.26	upregulate stage

442216	AI733468	Hs.129006	ESTs	1	1	upregulate stage
442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	1.49	0.31	upregulate stage
442319	BE048144	Hs.177677	CGI-102 protein	1	0.29	upregulate stage
442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	22.95	0.03	upregulate stage
442510	AF150179	Hs.249890	ESTs	1	0.63	upregulate stage
442518	AF150226		gb:AF150226 Human mRNA from cd34+ stem c	1	1	upregulate stage
442539	AL119506	Hs.58220	Homo sapiens cDNA: FLJ23005 fis, clone L	1	0.23	upregulate stage
442552	R20624	Hs.83572	son of sevenless (Drosophila) homolog 1	9	0.08	upregulate stage
442562	BE379584	Hs.34789	ESTs	6.55	0.1	upregulate stage
442564	AI590207	Hs.188378	ESTs	1	1	upregulate stage
442577	AA292998	Hs.163900	ESTs	1.41	0.52	upregulate stage
442590	AI002686	Hs.130313	ESTs	1	0.36	upregulate stage
442597	AI499214	Hs.130825	ESTs	1	1	upregulate stage
442611	BE077155	Hs.177537	ESTs	4.35	0.15	upregulate stage
442612	AI005233	Hs.130631	ESTs	1	0.28	upregulate stage
442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	7.85	0.09	upregulate stage
442642	R51853	Hs.226429	ESTs	1	1	upregulate stage
442660	AW138174	Hs.130651	ESTs	4.1	0.09	upregulate stage
442696	BE566962	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	2.65	0.16	upregulate stage
442712	BE465168	Hs.131011	ESTs	2.51	0.23	upregulate stage
442760	BE075297	Hs.10067	ESTs, Weakly similar to KIAA1205 protein	8	0.1	upregulate stage
442769	AW243058	Hs.131155	ESTs	1	0.3	upregulate stage
442785	AW296625	Hs.131188	ESTs	1	0.27	upregulate stage
442806	AW294522	Hs.149991	ESTs	9.6	0.08	upregulate stage
442856	H56735	Hs.282958	Homo sapiens cDNA FLJ13611 fis, clone PL	4.3	0.11	upregulate stage
442861	AA243837	Hs.57787	ESTs	3.9	0.12	upregulate stage
442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	3.85	0.15	upregulate stage
442879	AF032922	Hs.8813	syntaxin binding protein 3	3.95	0.14	upregulate stage
442883	AW195774	Hs.253199	ESTs	1	1	upregulate stage
442961	BE614474	Hs.289074	Homo sapiens cDNA FLJ13986 fis, clone Y7	11.55	0.07	upregulate stage
442966	AI394036	Hs.132237	ESTs, Weakly similar to dual specificity	2.95	0.16	upregulate stage
442980	AA857025	Hs.8878	kinesin-like 1	1	0.24	upregulate stage
442992	AI914699	Hs.13297	ESTs	6.1	0.14	upregulate stage
442994	AI026718	Hs.16954	ESTs	8.9	0.07	upregulate stage
443054	AI745185	Hs.8939	yes-associated protein 65 kDa	5.7	0.11	upregulate stage
443113	AI040686	Hs.132908	ESTs	3.9	0.14	upregulate stage
443119	AA312264	Hs.7980	ESTs, Moderately similar to ALU4_HUMAN A	8.73	0.08	upregulate stage
443171	BE281128	Hs.9030	TONDU	3.18	0.22	upregulate stage
443211	AI128388	Hs.143655	ESTs	6.55	0.08	upregulate stage
443242	BE243910	Hs.9082	nucleoporin p54	11.05	0.06	upregulate stage
443243	AI452496	Hs.132056	ESTs	8.9	0.09	upregulate stage
443247	BE614387	Hs.47378	ESTs, Moderately similar to hypothetical	10.95	0.05	upregulate stage
443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	3.75	0.2	upregulate stage
443299	AI733642	Hs.133042	ESTs	1	0.69	upregulate stage
443362	AI053464	Hs.166505	ESTs	2.9	0.16	upregulate stage
443383	AI792453	Hs.166507	ESTs	5	0.14	upregulate stage
443411	AW134566	Hs.65320	ESTs	1	0.59	upregulate stage
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.68	0.31	upregulate stage
443447	AI094222	Hs.166572	ESTs	1	0.38	upregulate stage
443542	AI927065	Hs.146040	ESTs	5.65	0.13	upregulate stage
443557	AV645987	Hs.145681	ESTs	1	1	upregulate stage
443584	AI807036	Hs.101619	ESTs	1	0.36	upregulate stage
443606	AI078664	Hs.199424	ESTs	1.15	0.33	upregulate stage
443634	H73972	Hs.134460	ESTs	3.05	0.16	upregulate stage
443640	AI872643	Hs.134218	ESTs	3.65	0.12	upregulate stage
443715	AI583187	Hs.9700	cyclin E1	5.65	0.11	upregulate stage
443799	AA150320	Hs.9800	protein kinase Njmu-R1	1.8	0.19	upregulate stage
443899	AW842283	Hs.79933	cyclin I	4.65	0.13	upregulate stage
443917	AW503739	Hs.72325	Human DNA sequence from clone RP1-187J11	1	1	upregulate stage
443919	AI091284	Hs.135224	ESTs	8.05	0.07	upregulate stage
443967	AW294013	Hs.200942	ESTs	5.55	0.13	upregulate stage
443977	AL120986	Hs.150627	ESTs	4	0.14	upregulate stage
443979	AV647366	Hs.282365	ESTs	1	1	upregulate stage
444020	R92962	Hs.35052	ESTs	10.45	0.08	upregulate stage
444105	AW189097	Hs.166597	ESTs	6.29	0.1	upregulate stage
444129	AW294292	Hs.256212	ESTs	1	0.77	upregulate stage
444152	AI125694	Hs.149305	Homo sapiens cDNA FLJ14264 fis, clone PL	1.64	0.48	upregulate stage
444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.12	0.81	upregulate stage
444166	AV648429	Hs.282393	ESTs	1	1	upregulate stage
444270	AI138580	Hs.255220	EST	1	0.47	upregulate stage
444271	AW452569	Hs.149804	ESTs	3.2	0.12	upregulate stage
444282	AI138955		gb:qd79b07.x1 Soares_testis_NHT Homo sap	1	1	upregulate stage
444333	AI262567	Hs.253801	trinucleotide repeat containing 15	1	0.77	upregulate stage
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	6.9	0.06	upregulate stage
444378	R41339	Hs.12569	ESTs	1	0.32	upregulate stage
444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	2.85	0.26	upregulate stage
444431	AW513324	Hs.42280	ESTs	6.27	0.12	upregulate stage

444437	AI377961	Hs.44041	ESTs	9.9	0.07	upregulate stage
444444	AI149332	Hs.14855	ESTs	1.16	0.47	upregulate stage
444525	AW593778	Hs.259699	ESTs	1	0.5	upregulate stage
444584	AI168422		gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.6	0.15	upregulate stage
444599	AI174377	Hs.143796	ESTs	1	0.44	upregulate stage
444646	AI184565		gb:qd60b08.x1 Soares_testis_NHT Homo sap	1	1	upregulate stage
444649	AW207523	Hs.197628	ESTs	9.35	0.06	upregulate stage
444675	AI186380	Hs.244621	ESTs	9.88	0.08	upregulate stage
444698	AI188139	Hs.147050	ESTs	1	0.36	upregulate stage
444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moi	2.1	0.15	upregulate stage
444762	AI733700	Hs.143883	ESTs	3.9	0.14	upregulate stage
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.44	0.53	upregulate stage
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	6.65	0.07	upregulate stage
444838	AV651680	Hs.208558	ESTs	4.84	0.14	upregulate stage
444849	AI199438	Hs.148480	ESTs	3.05	0.17	upregulate stage
444950	AI950256	Hs.224875	ESTs	1	0.51	upregulate stage
445027	AV652692	Hs.282498	ESTs	11.1	0.08	upregulate stage
445091	AI652154	Hs.147294	ESTs	1	1	upregulate stage
445098	AL050272	Hs.12305	DKFZP566B183 protein	9.75	0.07	upregulate stage
445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	10.9	0.07	upregulate stage
445250	AI597838	Hs.175621	ESTs	9.8	0.08	upregulate stage
445258	AI635931	Hs.147613	ESTs	3.05	0.13	upregulate stage
445390	AI222165	Hs.144923	ESTs	10.6	0.06	upregulate stage
445396	BE181792		gb:QV1-HT0639-070500-193-g06 HT0639 Homo	1	0.29	upregulate stage
445413	AA151342	Hs.12677	CGI-147 protein	4.65	0.12	upregulate stage
445436	AI224105	Hs.151408	ESTs	1.35	0.22	upregulate stage
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	10.7	0.07	upregulate stage
445483	AI307150	Hs.148845	ESTs	1	1	upregulate stage
445496	AB007860	Hs.12802	development and differentiation enhancin	12.05	0.06	upregulate stage
445525	BE149866	Hs.14831	ESTs	10.65	0.06	upregulate stage
445527	W39694	Hs.83286	ESTs	4.85	0.1	upregulate stage
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	9.7	0.06	upregulate stage
445546	AW468821	Hs.156054	ESTs	4.2	0.13	upregulate stage
445576	AI793233	Hs.145608	ESTs	1	0.31	upregulate stage
445623	AI245366	Hs.149158	ESTs	1	1	upregulate stage
445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.7	0.13	upregulate stage
445668	AI557114	Hs.181591	EST	1	0.34	upregulate stage
445766	AI623607	Hs.282977	Homo sapiens cDNA FLJ13490 fis, clone PL	1	0.23	upregulate stage
445770	AL119499	Hs.13285	neuronal potassium channel alpha subunit	1	1	upregulate stage
445778	AA196443	Hs.86043	Homo sapiens cDNA FLJ13558 fis, clone PL	9.7	0.07	upregulate stage
445787	AI253167	Hs.145395	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.1	0.13	upregulate stage
445814	H92020	Hs.101624	ESTs	1	1	upregulate stage
445818	BE045321	Hs.136017	ESTs	1	1	upregulate stage
445829	AI452457	Hs.145526	ESTs	1	0.37	upregulate stage
445832	AI261545		gb:qz30a07.x1 NCI_CGAP_Kid11 Homo sapien	3.21	0.22	upregulate stage
445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	5.25	0.12	upregulate stage
445880	AV655474	Hs.131058	ESTs	1.05	0.27	upregulate stage
445883	AF070559	Hs.13413	Homo sapiens clone 24463 mRNA sequence	1	1	upregulate stage
445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	3.25	0.15	upregulate stage
445939	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	8.85	0.08	upregulate stage
446019	AI362520	Hs.94133	ESTs	9.75	0.08	upregulate stage
446054	AB014537	Hs.13604	KIAA0637 gene product	10.25	0.07	upregulate stage
446062	AA211738	Hs.282974	ESTs, Weakly similar to transformation-r	1	1	upregulate stage
446080	AI221741	Hs.117777	ESTs	9.75	0.09	upregulate stage
446082	AI274139	Hs.156452	ESTs	1.37	0.4	upregulate stage
446099	T93096	Hs.17126	ESTs	2.4	0.31	upregulate stage
446119	D29527		gb:HUMNK667 Human epidermal keratinocyte	1	1	upregulate stage
446120	N26080	Hs.43741	ESTs	1	0.31	upregulate stage
446126	AW085909	Hs.47413	ESTs	9.35	0.08	upregulate stage
446127	AA333608	Hs.13980	ubiquitously transcribed tetratricopepti	1	0.25	upregulate stage
446152	AI292036	Hs.150028	ESTs	4.7	0.12	upregulate stage
446196	AI744888	Hs.149470	ESTs	1	0.83	upregulate stage
446229	AI744964	Hs.14449	KIAA1609 protein	2.4	0.36	upregulate stage
446248	AI283014	Hs.149638	ESTs	1	1	upregulate stage
446269	AW263155	Hs.14559	hypothetical protein FLJ10540	10.85	0.07	upregulate stage
446303	X77244	Hs.14732	malic enzyme 1, NADP(+)-dependent, cytos	1	1	upregulate stage
446312	BE087853		gb:QV1-BT0681-290400-181-h05 BT0681 Homo	11.75	0.06	upregulate stage
446332	AK001635	Hs.14838	hypothetical protein FLJ10773	6.45	0.1	upregulate stage
446356	AI816736	Hs.14896	DHHC1 protein	8.9	0.08	upregulate stage
446362	AW612481	Hs.255914	ESTs	7.6	0.1	upregulate stage
446398	AI681317	Hs.150074	ESTs	1	1	upregulate stage
446411	AI298828	Hs.153439	ESTs	1	0.37	upregulate stage
446474	AI301227	Hs.150186	ESTs	3.35	0.13	upregulate stage
446501	AI302616	Hs.150819	ESTs	4.25	0.12	upregulate stage
446507	AA352554	Hs.15164	nuclear DNA-binding protein	11.25	0.06	upregulate stage
446526	H89616	Hs.296290	Homo sapiens cDNA FLJ13357 fis, clone PL	10.25	0.07	upregulate stage
446555	AV659046	Hs.201847	ESTs	1	1	upregulate stage

446577	AB040933	Hs.15420	KIAA1500 protein	1	0.51	upregulate stage
446629	AI436046	Hs.156148	Homo sapiens cDNA: FLJ23082 fis, clone L	1	0.25	upregulate stage
446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	2.54	0.28	upregulate stage
446682	AW205632	Hs.211198	ESTs	4	0.18	upregulate stage
446701	AK001621	Hs.15921	hypothetical protein FLJ10759	1.32	0.69	upregulate stage
446718	AV660019	Hs.282676	ESTs	1	1	upregulate stage
446719	W39500	Hs.47305	ESTs, Weakly similar to LONN_HUMAN MITOC	9.65	0.07	upregulate stage
446720	AI439136	Hs.140546	ESTs	4.55	0.12	upregulate stage
446765	AV660348	Hs.282688	ESTs	1	0.91	upregulate stage
446771	AA128965	Hs.60679	TATA box binding protein (TBP)-associate	11.2	0.06	upregulate stage
446821	W03766	Hs.301482	ESTs	8.9	0.09	upregulate stage
446830	BE179030	Hs.64239	Human DNA sequence from clone RP5-1174N9	10.65	0.07	upregulate stage
446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	14.05	0.05	upregulate stage
446853	AV660630	Hs.87627	disrupter of silencing 10	9.7	0.09	upregulate stage
446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ12534 fis, clone NT	11.05	0.06	upregulate stage
446922	BE175605		gb:RC5-HT0580-100500-022-H07 HT0580 Homo	2.75	0.16	upregulate stage
446950	AA305800	Hs.293454	ESTs, Weakly similar to Similarity to Ye	9.6	0.06	upregulate stage
446988	AW339533	Hs.272108	ESTs	1	0.29	upregulate stage
446989	AK001898	Hs.16740	hypothetical protein FLJ11036	1.75	0.51	upregulate stage
447052	AV661911	Hs.282735	ESTs	1	1	upregulate stage
447065	AI829014	Hs.158678	ESTs	1	0.25	upregulate stage
447069	AI359927	Hs.157722	ESTs	1	0.4	upregulate stage
447078	AW885727	Hs.301570	ESTs	4.4	0.13	upregulate stage
447080	AI418781	Hs.300144	ESTs	1	0.31	upregulate stage
447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	3.55	0.12	upregulate stage
447118	AB014599	Hs.17411	KIAA0699 protein	10.15	0.07	upregulate stage
447153	AA805202	Hs.173912	eukaryotic translation initiation factor	6.2	0.12	upregulate stage
447154	H52284	Hs.293545	ESTs	1	0.24	upregulate stage
447159	AI685286	Hs.280386	EST	1.25	0.25	upregulate stage
447215	BE617056	Hs.283000	ESTs	2.4	0.16	upregulate stage
447228	AW192200	Hs.158188	ESTs	1	0.29	upregulate stage
447258	BE047911		gb:tz44a05.y1 NCI_CGAP_Brn52 Homo sapien	1.15	0.23	upregulate stage
447286	AW197097	Hs.183858	transcriptional intermediary factor 1	1	1	upregulate stage
447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1	1	upregulate stage
447334	AA515032	Hs.91109	ESTs	9.15	0.08	upregulate stage
447342	AI199268	Hs.19322	ESTs	5.95	0.09	upregulate stage
447343	AA256641	Hs.236894	ESTs, Highly similar to LRP1_HUMAN LOW-D	2.11	0.33	upregulate stage
447376	AI376747		gb:tc35h05.x1 Soares_total_fetus_Nb2HF8_	1	0.33	upregulate stage
447397	BE247676	Hs.18442	E-1 enzyme	5.3	0.14	upregulate stage
447430	AI742989	Hs.206112	ESTs	3.65	0.13	upregulate stage
447444	AK000318	Hs.18616	hypothetical protein FLJ20311	9.2	0.08	upregulate stage
447519	U46258	Hs.23448	ESTs	14.4	0.05	upregulate stage
447522	BE143888		gb:MR0-HT0165-081199-001-b04 HT0165 Homo	1.7	0.18	upregulate stage
447578	AA912347	Hs.136585	ESTs	1.5	0.3	upregulate stage
447606	AI588954	Hs.170995	ESTs	2.7	0.16	upregulate stage
447688	N87079	Hs.19236	NADH dehydrogenase (ubiquinone) 1 beta s	4.55	0.12	upregulate stage
447701	BE619526	Hs.255527	ESTs, Weakly similar to unnamed protein	1.63	0.46	upregulate stage
447741	AI421737	Hs.167253	ESTs	1	1	upregulate stage
447748	AI422023	Hs.161338	ESTs	3.9	0.11	upregulate stage
447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	1.44	0.59	upregulate stage
447881	BE620886	Hs.23037	ESTs	12.15	0.06	upregulate stage
447963	AI452973	Hs.165900	ESTs, Weakly similar to ALUC_HUMAN !!!!	8.9	0.08	upregulate stage
447977	AI457097	Hs.255906	ESTs	1	1	upregulate stage
447978	AI457098	Hs.280848	ESTs	1	1	upregulate stage
447982	H22953	Hs.137551	ESTs	4.25	0.13	upregulate stage
448032	AW511770	Hs.246868	ESTs	1	1	upregulate stage
448045	AJ297436	Hs.20166	prostate stem cell antigen	2.22	0.29	upregulate stage
448058	AI458998	Hs.170424	ESTs	1	0.51	upregulate stage
448062	AW295923	Hs.255472	ESTs	5.9	0.08	upregulate stage
448138	AW847925	Hs.170736	ESTs	1	1	upregulate stage
448154	AL120320	Hs.203230	ESTs	9.85	0.07	upregulate stage
448165	NM_005591	Hs.202379	meiotic recombination (S. cerevisiae) 11	7.3	0.09	upregulate stage
448168	AW605999	Hs.22549	hypothetical protein FLJ12799	1	0.77	upregulate stage
448236	AA890449	Hs.20766	oxysterol 7alpha-hydroxylase	1	0.47	upregulate stage
448256	BE614149	Hs.20814	CGI-27 protein	11.95	0.07	upregulate stage
448289	AW390251	Hs.202402	ESTs	1	0.47	upregulate stage
448356	AL120837	Hs.20993	high-glucose-regulated protein 8	11	0.07	upregulate stage
448357	N20169	Hs.108923	ESTs	1.34	0.61	upregulate stage
448408	AA322866	Hs.21107	neuroligin	1.7	0.24	upregulate stage
448455	AI252625	Hs.269860	ESTs	8.8	0.09	upregulate stage
448459	AW069838	Hs.171055	ESTs	1	0.27	upregulate stage
448464	AI522053	Hs.196093	ESTs	10.35	0.06	upregulate stage
448468	BE550361	Hs.171072	ESTs	1	1	upregulate stage
448502	AW805285	Hs.239699	ESTs	9.3	0.08	upregulate stage
448552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.75	0.13	upregulate stage
448556	AW885606	Hs.5064	ESTs	9.8	0.08	upregulate stage
448569	BE382657	Hs.21486	signal transducer and activator of trans	2.14	0.35	upregulate stage

448632	BE614269		gb:601504311T1 NIH_MGC_71 Homo sapiens c	1	1	upregulate stage
448643	AI557531		gb:pt2.1-06.D06.r tumor2 Homo sapiens cD	3.6	0.14	upregulate stage
448649	T94590	Hs.222855	ESTs	1.95	0.21	upregulate stage
448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar t	4.3	0.12	upregulate stage
448680	AW245890	Hs.21753	JM5 protein	0.97	0.93	upregulate stage
448725	AA193251	Hs.40289	ESTs	2.6	0.19	upregulate stage
448729	BE614535	Hs.138580	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.25	0.16	upregulate stage
448743	AB032962	Hs.21896	KIAA1136 protein	1.9	0.19	upregulate stage
448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	1.78	0.44	upregulate stage
448914	AI927656	Hs.196459	ESTs	2.75	0.19	upregulate stage
448946	AI652855	Hs.155796	ESTs	9.7	0.07	upregulate stage
448958	AB020651	Hs.22653	KIAA0844 protein	1	0.18	upregulate stage
448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	5.85	0.11	upregulate stage
448979	AI611378	Hs.192610	ESTs	1	1	upregulate stage
449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	5.2	0.11	upregulate stage
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	1	0.33	upregulate stage
449053	AI625777	Hs.270344	ESTs	5.73	0.12	upregulate stage
449057	AB037784	Hs.22941	KIAA1363 protein	9.25	0.07	upregulate stage
449148	AW836677	Hs.287564	Homo sapiens cDNA FLJ13345 fis, clone OV	7.2	0.09	upregulate stage
449203	AI634578	Hs.282121	ESTs	7	0.1	upregulate stage
449207	AL044222	Hs.23255	nucleoporin 155kD	2.34	0.36	upregulate stage
449219	AI637581	Hs.195012	ESTs	1	1	upregulate stage
449230	BE613348	Hs.23348	S-phase kinase-associated protein 2 (p45	3.08	0.25	upregulate stage
449246	AW411209	Hs.23363	hypothetical protein FLJ10983	4.79	0.16	upregulate stage
449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanog	2.8	0.16	upregulate stage
449328	AI962493	Hs.197647	ESTs	2.55	0.17	upregulate stage
449343	AI151418	Hs.272458	protein phosphatase 3 (formerly 2B), cat	4.75	0.12	upregulate stage
449344	AI640355		gb:wa17c04.x1 NCI_CGAP_Kid11 Homo sapien	2.1	0.22	upregulate stage
449351	AW016537	Hs.200760	ESTs	2.45	0.14	upregulate stage
449370	AK002114	Hs.23495	hypothetical protein FLJ11252	1.55	0.14	upregulate stage
449424	AW448937	Hs.197030	ESTs	4.05	0.12	upregulate stage
449425	AW103433	Hs.195684	ESTs	4.6	0.12	upregulate stage
449434	AW294858	Hs.197641	ESTs	1	0.29	upregulate stage
449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	2.38	0.34	upregulate stage
449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	5.9	0.12	upregulate stage
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.45	0.1	upregulate stage
449528	H63337	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	2.85	0.18	upregulate stage
449565	AI824925	Hs.197066	ESTs	1	1	upregulate stage
449568	AL157479	Hs.23740	KIAA1598 protein	10.15	0.06	upregulate stage
449618	AI076459	Hs.14366	Homo sapiens cDNA FLJ12819 fis, clone NT	11.7	0.06	upregulate stage
449639	AA001968	Hs.59956	ESTs, Highly similar to MGR7_HUMAN METAB	1	1	upregulate stage
449666	AA002047		gb:zh84e05.r1 Soares_fetal_liver_spleen_	1.85	0.33	upregulate stage
449704	AK000733	Hs.23900	GTPase activating protein	2.82	0.3	upregulate stage
449722	BE280074	Hs.23960	cyclin B1	6.44	0.12	upregulate stage
449764	N93104	Hs.54895	ESTs, Weakly similar to ZNF91L [H.sapien	1	1	upregulate stage
449784	AW161319	Hs.12915	ESTs	6.25	0.11	upregulate stage
449829	N51440	Hs.47261	ESTs	1	0.57	upregulate stage
449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	10.2	0.07	upregulate stage
449892	N73608	Hs.50309	ESTs	6.5	0.1	upregulate stage
449894	AK001578	Hs.24129	hypothetical protein FLJ10716	4.55	0.12	upregulate stage
449919	AI674685	Hs.200141	ESTs	5.3	0.11	upregulate stage
450020	AI680684	Hs.282219	ESTs	1	1	upregulate stage
450033	R43010	Hs.269452	ESTs, Weakly similar to JH0148 nucleolin	1	0.65	upregulate stage
450063	AI681509	Hs.277133	ESTs	4.2	0.17	upregulate stage
450083	AA131795	Hs.142001	ESTs	3.9	0.16	upregulate stage
450116	AA005355	Hs.222882	ESTs	1	1	upregulate stage
450121	AL040174	Hs.288927	Homo sapiens cDNA: FLJ22944 fis, clone K	1	1	upregulate stage
450135	AI810816	Hs.201142	ESTs	4.95	0.14	upregulate stage
450144	T63961	Hs.301851	ESTs	2.75	0.13	upregulate stage
450149	AW969781	Hs.293440	ESTs, Moderately similar to ZIC2 protein	3.75	0.14	upregulate stage
450151	AI088196	Hs.295233	ESTs	2.51	0.28	upregulate stage
450152	AI138635	Hs.22968	ESTs	2.45	0.15	upregulate stage
450195	AA007352	Hs.256042	ESTs	4.1	0.14	upregulate stage
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1	0.3	upregulate stage
450238	T89693	Hs.138777	ESTs	12.2	0.07	upregulate stage
450257	AW820313		gb:QV2-ST0296-150200-028-d02 ST0296 Homo	1	1	upregulate stage
450313	AI038989	Hs.24809	hypothetical protein FLJ10826	4.35	0.15	upregulate stage
450314	AA574309	Hs.283402	TCR eta	10.1	0.07	upregulate stage
450350	T97817	Hs.174880	ESTs	3.65	0.1	upregulate stage
450411	D61167	Hs.202156	ESTs	1	0.67	upregulate stage
450447	AF212223	Hs.25010	hypothetical protein P15-2	10.75	0.07	upregulate stage
450448	D54299	Hs.36244	ESTs	1	1	upregulate stage
450449	AI696596	Hs.202068	ESTs	1	1	upregulate stage
450506	NM_004460	Hs.418	fibroblast activation protein, alpha	11.45	0.05	upregulate stage
450573	AW964334		gb:EST376407 MAGE resequences, MAGH Homo	1.2	0.2	upregulate stage
450628	AW382884	Hs.204715	ESTs	4.95	0.13	upregulate stage
450636	AI703076	Hs.201959	ESTs	1	0.69	upregulate stage

450655	AI707846	Hs.279860	hypothetical protein FLJ20030	1	1	upregulate stage
450664	AA808358	Hs.36830	ESTs	1	0.34	upregulate stage
450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.51	0.09	upregulate stage
450722	AI732318	Hs.101120	ESTs	1	0.87	upregulate stage
450751	AI733251	Hs.126853	ESTs, Weakly similar to JU0033 hypotheti	1	1	upregulate stage
450772	BE326391	Hs.280146	ESTs, Weakly similar to JU0033 hypotheti	1	1	upregulate stage
450800	BE395161	Hs.243963	ESTs, Weakly similar to ALU5_HUMAN ALU S	8.7	0.08	upregulate stage
450824	R09055	Hs.269204	ESTs	3.03	0.22	upregulate stage
450832	AW970602	Hs.105421	ESTs	6.15	0.08	upregulate stage
450870	AA011471		gb:zi01h08.r1 Soares_fetal_liver_spleen_	1.15	0.23	upregulate stage
450937	R49131	Hs.26267	ATP-dependant interferon response protei	9.75	0.08	upregulate stage
450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.32	0.26	upregulate stage
451052	AA281504	Hs.24444	ESTs, Moderately similar to ALUE_HUMAN !	9.25	0.08	upregulate stage
451067	BE172186	Hs.180789	S164 protein	2.8	0.21	upregulate stage
451088	AA015600	Hs.82415	ESTs	1	0.32	upregulate stage
451094	AI949825	Hs.260395	ESTs	4.45	0.14	upregulate stage
451096	BE383234	Hs.25925	Homo sapiens clone 23860 mRNA sequence	4.15	0.14	upregulate stage
451126	H30600	Hs.40910	ESTs	1	1	upregulate stage
451161	AA211329	Hs.26006	hypothetical protein FLJ10559	2.15	0.16	upregulate stage
451166	T98171	Hs.185675	ESTs	9.26	0.08	upregulate stage
451222	AA018386	Hs.64341	ESTs	1	0.36	upregulate stage
451225	AI433694	Hs.293608	ESTs	9.19	0.08	upregulate stage
451228	AI767166	Hs.207025	ESTs	1	1	upregulate stage
451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	7.35	0.11	upregulate stage
451266	AA016292	Hs.290849	ESTs	1	0.33	upregulate stage
451276	AW294386	Hs.236533	ESTs, Highly similar to dJ742C19.2 [H.sa	1	1	upregulate stage
451277	AK001123	Hs.26176	hypothetical protein FLJ10261	11.7	0.06	upregulate stage
451291	R39288	Hs.6702	ESTs	1	1	upregulate stage
451326	AW296946	Hs.300967	ESTs	10.55	0.07	upregulate stage
451347	AI288679	Hs.101139	ESTs	1	1	upregulate stage
451359	H85334		gb:ys90e05.r1 Soares retina N2b5HR Homo	2.7	0.15	upregulate stage
451365	AI791783		gb:op20h10.y5 NCI_CGAP_Co12 Homo sapiens	8.9	0.09	upregulate stage
451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	2.45	0.19	upregulate stage
451440	AA017599	Hs.293817	ESTs	1	1	upregulate stage
451487	AA018072		gb:ze51g02.r1 Soares retina N2b4HR Homo	5.7	0.1	upregulate stage
451492	AA018119	Hs.297824	ESTs, Highly similar to CIK1_HUMAN VOLTA	1	1	upregulate stage
451495	H86887		gb:yt07a01.r1 Soares retina N2b5HR Homo	4.25	0.13	upregulate stage
451535	AW970577		gb:EST382658 MAGE resequences, MAGK Homo	6.8	0.12	upregulate stage
451553	AA018454	Hs.269211	ESTs, Weakly similar to B34087 hypotheti	1	1	upregulate stage
451562	H04150	Hs.107708	ESTs	4.65	0.11	upregulate stage
451580	AW138195	Hs.184326	CDC10 (cell division cycle 10, S. cerevi	1	0.42	upregulate stage
451592	AI805416	Hs.213897	ESTs	2.8	0.17	upregulate stage
451651	AI097337	Hs.88977	hypothetical protein dJ511E16.2	1	0.18	upregulate stage
451658	AW195351	Hs.250520	ESTs	9.55	0.07	upregulate stage
451684	AF216751	Hs.26813	CDA14	3.7	0.15	upregulate stage
451690	AW451469	Hs.209990	ESTs	10.86	0.07	upregulate stage
451724	AI903765		gb:UI-BT037-301298-102 BT037 Homo sapien	8.85	0.09	upregulate stage
451743	AW074266	Hs.23071	ESTs	2.17	0.35	upregulate stage
451794	AA019799	Hs.111911	ESTs	1	1	upregulate stage
451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	6.5	0.11	upregulate stage
451903	W19617	Hs.261003	ESTs, Moderately similar to B34087 hypot	2.2	0.21	upregulate stage
451914	AI822115	Hs.270618	ESTs, Weakly similar to KIAA0822 protein	11.67	0.07	upregulate stage
451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	11.65	0.06	upregulate stage
451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	1	0.95	upregulate stage
451971	AA021185	Hs.226306	ESTs	1	1	upregulate stage
451998	AW594129	Hs.213666	ESTs	1	0.26	upregulate stage
452028	AK001859	Hs.27595	hypothetical protein FLJ10997	1	0.21	upregulate stage
452036	NM_003966	Hs.27621	sema domain, seven thrombospondin repeat	1.76	0.41	upregulate stage
452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	8.9	0.07	upregulate stage
452122	AF216833	Hs.1710	ATP-binding cassette, sub-family B (MDR/	1	0.47	upregulate stage
452163	AI863140		gb:tz43h12.x1 NCI_CGAP_Brn52 Homo sapien	1	0.2	upregulate stage
452179	H16725	Hs.27463	ESTs	3	0.13	upregulate stage
452198	AI097560	Hs.61210	ESTs	1	0.28	upregulate stage
452206	AW340281	Hs.33074	ESTs, Moderately similar to ALU1_HUMAN A	12.4	0.07	upregulate stage
452234	AW084176	Hs.223296	ESTs	6.8	0.09	upregulate stage
452240	AI591147	Hs.61232	ESTs	3.75	0.07	upregulate stage
452247	AL137432	Hs.28564	hypothetical protein DKFZp761E1824	3.9	0.15	upregulate stage
452250	BE618654	Hs.28607	hypothetical protein A-211C6.1	8.75	0.09	upregulate stage
452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	5.2	0.09	upregulate stage
452266	AI767250	Hs.165240	ESTs	10.45	0.06	upregulate stage
452277	AL049013	Hs.28783	KIAA1223 protein	8.9	0.05	upregulate stage
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	8.2	0.04	upregulate stage
452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.5	0.13	upregulate stage
452328	AA805679	Hs.61271	ESTs	3.5	0.14	upregulate stage
452331	AA598509	Hs.29117	H.sapiens mRNA for pur alpha extended 3'	11.75	0.07	upregulate stage
452345	AA293279	Hs.29173	hypothetical protein FLJ20515	1.08	0.73	upregulate stage
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.15	0.07	upregulate stage

452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1	0.17	upregulate stage
452404	AW450675	Hs.212709	ESTs	3.63	0.2	upregulate stage
452430	AF118083	Hs.29494	PRO1912 protein	1	0.41	upregulate stage
452436	BE077546	Hs.31447	ESTs	10	0.07	upregulate stage
452457	AW062499		gb:MR0-CT0065-100899-001-d02 CT0065 Homo	1	0.13	upregulate stage
452461	N78223	Hs.108106	transcription factor	8.1	0.06	upregulate stage
452518	AA280722	Hs.24758	ESTs	9.3	0.08	upregulate stage
452519	BE006701		gb:RC0-BN0132-270300-021-a03 BN0132 Homo	1	0.19	upregulate stage
452524	AW136499	Hs.29796	Homo sapiens mRNA; cDNA DKFZp434D1319 (f	1	0.45	upregulate stage
452531	AA429462	Hs.293946	ESTs	2.94	0.22	upregulate stage
452547	AA335295	Hs.74120	adipose specific 2	1.51	0.53	upregulate stage
452560	BE077084		gb:RC5-BT0603-220200-013-C07 BT0603 Homo	5.35	0.11	upregulate stage
452571	W31518	Hs.34665	ESTs	2.55	0.11	upregulate stage
452607	AI160029	Hs.61438	ESTs	4.75	0.11	upregulate stage
452677	BE167202	Hs.212065	ESTs	1	0.32	upregulate stage
452680	AW138410	Hs.45051	ESTs	1	1	upregulate stage
452724	R84810	Hs.30464	cyclin E2	1	0.27	upregulate stage
452738	AL133800		gb:DKFZp761A0614_r1 761 (synonym: hamy2)	3.45	0.15	upregulate stage
452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	3.05	0.16	upregulate stage
452747	BE153855	Hs.61460	ESTs	2.54	0.28	upregulate stage
452761	BE244742	Hs.30532	CGI-77 protein	3.85	0.14	upregulate stage
452825	AI921523		gb:wo26d09.x1 NCI_CGAP_Gas4 Homo sapiens	1	1	upregulate stage
452831	AW864089	Hs.135145	ESTs	2.4	0.19	upregulate stage
452846	AA082160	Hs.204295	ESTs	8.9	0.08	upregulate stage
452850	H23230	Hs.22481	ESTs	4.75	0.14	upregulate stage
452859	AI300555	Hs.288158	Homo sapiens cDNA: FLJ23591 fis, clone L	9.15	0.08	upregulate stage
452862	AW378065	Hs.8687	ESTs	5.95	0.07	upregulate stage
452899	M96739	Hs.30956	Human NSCL-1 mRNA sequence	1.04	0.9	upregulate stage
452902	AI926501	Hs.249729	ESTs	6.8	0.1	upregulate stage
452909	NM_015368	Hs.30985	pannexin 1	5.6	0.1	upregulate stage
452931	AW190011	Hs.158006	hypothetical protein	1	0.53	upregulate stage
452934	AA581322	Hs.4213	ESTs	1.44	0.55	upregulate stage
452956	AW003578	Hs.231872	ESTs	1	0.22	upregulate stage
452974	BE090803	Hs.61506	ESTs	1.75	0.18	upregulate stage
453011	N62952	Hs.46473	ESTs	1	1	upregulate stage
453050	AW136479	Hs.224046	ESTs	1	0.39	upregulate stage
453074	AA031813	Hs.271880	ESTs	1	1	upregulate stage
453076	AI978583	Hs.232161	ESTs	3.75	0.14	upregulate stage
453123	AI953718	Hs.221849	ESTs	6.6	0.11	upregulate stage
453134	AA032211	Hs.118493	ESTs	1.68	0.42	upregulate stage
453135	T07866	Hs.31834	Homo sapiens clone 25129 mRNA sequence	1	1	upregulate stage
453137	AI954733	Hs.223640	ESTs	1	0.51	upregulate stage
453144	AW268807	Hs.61646	ESTs	1	0.26	upregulate stage
453153	N53893	Hs.24360	ESTs	5	0.13	upregulate stage
453156	BE463762	Hs.223784	ESTs	2.8	0.15	upregulate stage
453204	R10799	Hs.191990	ESTs	9.5	0.05	upregulate stage
453228	AW628325	Hs.232327	ESTs	1	1	upregulate stage
453274	AA018511	Hs.32769	Homo sapiens mRNA full length insert cDN	1	1	upregulate stage
453293	AA382267	Hs.10653	ESTs	8.4	0.09	upregulate stage
453321	AI984381	Hs.232521	ESTs	6.7	0.1	upregulate stage
453329	T97205	Hs.17998	ESTs	8.9	0.08	upregulate stage
453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal ki	1	0.18	upregulate stage
453437	H10751	Hs.79981	Human clone 23560 mRNA sequence	1	0.83	upregulate stage
453450	AW797627	Hs.89474	ADP-ribosylation factor 6	7.09	0.08	upregulate stage
453459	BE047032	Hs.257789	ESTs	2.35	0.3	upregulate stage
453476	AI640500	Hs.24633	SAM domain, SH3 domain and nuclear local	2.75	0.16	upregulate stage
453651	AA971698	Hs.159397	x 010 protein	8.95	0.08	upregulate stage
453653	AW505554	Hs.300284	ESTs	4.6	0.1	upregulate stage
453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.4	0.1	upregulate stage
453776	R15749	Hs.31677	ESTs	1	1	upregulate stage
453846	AL157586		gb:DKFZp761H0216_r1 761 (synonym: hamy2)	1	0.95	upregulate stage
453884	AA355925	Hs.36232	KIAA0186 gene product	10.25	0.06	upregulate stage
453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.75	0.12	upregulate stage
453913	AW004683	Hs.233502	ESTs	3.65	0.14	upregulate stage
453925	AW021088	Hs.181614	ESTs	3.7	0.13	upregulate stage
453931	AL121278	Hs.25144	ESTs	3.45	0.18	upregulate stage
453945	NM_005171	Hs.36908	activating transcription factor 1	6.35	0.12	upregulate stage
454032	W31790	Hs.194293	ESTs	6.15	0.07	upregulate stage
454049	AW022885		gb:df45e05.y1 Morton Fetal Cochlea Homo	2.8	0.15	upregulate stage
454069	AW025160	Hs.34161	ESTs, Moderately similar to ALU1_HUMAN A	1	0.32	upregulate stage
454099	AW062974		gb:IL1-ST0041-020899-001-H08 ST0041 Homo	1	1	upregulate stage
454111	AW081681	Hs.269064	ESTs	2.8	0.18	upregulate stage
454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	9.4	0.05	upregulate stage
454259	AL110136	Hs.47679	Homo sapiens mRNA; cDNA DKFZp564I112 (fr	6.2	0.11	upregulate stage
454327	BE064097		gb:QV3-BT0297-231199-020-h08 BT0297 Homo	1	1	upregulate stage
454331	AW372937		gb:QV3-BT0381-161299-042-a09 BT0381 Homo	1	0.43	upregulate stage
454380	AW858722		gb:RC3-CT0347-281199-011-c04 CT0347 Homo	1	0.29	upregulate stage

454524	AW857191		gb:RC2-CT0304-080100-011-b12 CT0304 Homo	10.55	0.08	upregulate stage
454592	AW810112		gb:MR4-ST0124-100400-006-e07 ST0124 Homo	1	0.37	upregulate stage
454648	AW811960		gb:RC2-ST0168-240300-017-f09 ST0168 Homo	1	0.4	upregulate stage
454687	AW814473		gb:MR3-ST0203-010200-109-c11 ST0203 Homo	1	1	upregulate stage
454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192 Homo	4.45	0.14	upregulate stage
454702	BE145915		gb:MR0-HT0208-221299-204-h08 HT0208 Homo	9.65	0.08	upregulate stage
454729	AW817003		gb:QV0-ST0247-040100-081-f03 ST0247 Homo	1	0.8	upregulate stage
454789	BE156314		gb:QV0-HT0367-150200-114-d02 HT0367 Homo	1	0.31	upregulate stage
454797	BE161168		gb:PM0-HT0425-170100-002-a10 HT0425 Homo	4.1	0.14	upregulate stage
454863	AW835610		gb:QV4-LT0016-090200-100-c02 LT0016 Homo	1	1	upregulate stage
454893	AW837753		gb:CM1-LT0042-310100-112-g03 LT0042 Homo	4.45	0.18	upregulate stage
454898	AW838125		gb:QV2-LT0051-240300-097-e12 LT0051 Homo	1	1	upregulate stage
454951	AW847464		gb:RC3-CT0208-270999-021-h12 CT0208 Homo	7.4	0.1	upregulate stage
454956	AW847725		gb:IL3-CT0213-180200-041-H10 CT0213 Homo	1	0.23	upregulate stage
455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	4.25	0.13	upregulate stage
455128	AW861555		gb:RC2-CT0321-110100-013-b05 CT0321 Homo	2.9	0.13	upregulate stage
455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	3.15	0.16	upregulate stage
455207	AW994394		gb:RC3-BN0036-060400-014-h12 BN0036 Homo	1	0.18	upregulate stage
455331	AW897292		gb:CM0-NN0057-150400-338-b02 NN0057 Homo	1	0.87	upregulate stage
455351	AW901942		gb:QV0-NN1022-100400-190-b04 NN1022 Homo	1	0.39	upregulate stage
455380	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	1.96	0.33	upregulate stage
455414	AW936969		gb:RC1-DT0029-160200-013-f10 DT0029 Homo	1	1	upregulate stage
455428	AW938204		gb:QV0-DT0048-170200-124-f01 DT0048 Homo	1	0.67	upregulate stage
455573	BE004988		gb:MR2-BN0114-100500-020-b04 BN0114 Homo	1	1	upregulate stage
455586	BE070794		gb:RC3-BT0501-130100-011-h02 BT0501 Homo	1	1	upregulate stage
455595	BE008343		gb:CM0-BN0154-080400-325-g10 BN0154 Homo	1	1	upregulate stage
455610	BE011703		gb:CM3-BN0223-100500-177-h09 BN0223 Homo	6.05	0.12	upregulate stage
455647	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	1	1	upregulate stage
455650	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	1	0.67	upregulate stage
455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.87	0.4	upregulate stage
455669	BE065803		gb:RC2-BT0318-241199-011-g02 BT0318 Homo	2.85	0.2	upregulate stage
455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.8	0.18	upregulate stage
455761	BE080895		gb:QV1-BT0631-280200-084-e01 BT0631 Homo	1	0.48	upregulate stage
455799	BE169911	Hs.14570	Homo sapiens cDNA: FLJ22530 fis, clone H	5.7	0.11	upregulate stage
455831	BE144966		gb:RC6-HT0187-201099-031-c04 HT0187 Homo	1	1	upregulate stage
455874	BE152283		gb:QV4-HT0316-191199-039-b01 HT0316 Homo	1	0.67	upregulate stage
455903	BE155185		gb:PM1-HT0350-231299-005-g05 HT0350 Homo	1	0.31	upregulate stage
455938	BE159432		gb:MR0-HT0407-140200-009-e06 HT0407 Homo	2.4	0.15	upregulate stage
455950	BE161004		gb:PM0-HT0425-170100-002-h03 HT0425 Homo	1	0.44	upregulate stage
455951	BE161001		gb:PM0-HT0425-170100-002-f10 HT0425 Homo	1	0.38	upregulate stage
455965	BE167014		gb:CM2-HT0502-140200-088-d08 HT0502 Homo	1	1	upregulate stage
455981	BE177000		gb:RC4-HT0587-070400-015-b07 HT0587 Homo	1	0.57	upregulate stage
456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	8.29	0.05	upregulate stage
456046	R51494	Hs.71818	ESTs	3.15	0.17	upregulate stage
456122	R11813		gb:yf53a04.r1 Soares infant brain 1NIB H	1.3	0.31	upregulate stage
456212	N51636		gb:yy87b01.s1 Soares_multiple_sclerosis_	4.45	0.14	upregulate stage
456265	AI968210	Hs.173623	ESTs	1	0.34	upregulate stage
456285	R67585	Hs.268748	ESTs	1	0.83	upregulate stage
456320	AI734064	Hs.136212	ESTs	1	1	upregulate stage
456353	AI042330	Hs.87128	ESTs, Weakly similar to similar to YBS4	5.15	0.11	upregulate stage
456486	AA676544	Hs.171545	HIV-1 Rev binding protein	1	0.27	upregulate stage
456493	AA261830		gb:zs17g09.r1 NCI_CGAP_GCB1 Homo sapiens	1	0.8	upregulate stage
456504	AK000532	Hs.98491	Homo sapiens cDNA FLJ20525 fis, clone KA	1	0.29	upregulate stage
456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	17.7	0.05	upregulate stage
456519	AA279917	Hs.88678	ESTs, Weakly similar to Unknown [H.sapie	2.3	0.18	upregulate stage
456536	AW135986	Hs.257859	ESTs	9.45	0.06	upregulate stage
456592	R91600		gb:yq10c02.r1 Soares fetal liver spleen	4.5	0.14	upregulate stage
456621	T35958	Hs.107614	DKFZP564I1171 protein	1	0.2	upregulate stage
456682	AW500321	Hs.246766	Homo sapiens cDNA FLJ12360 fis, clone MA	1	0.24	upregulate stage
456726	H43102	Hs.144183	ESTs	1	0.69	upregulate stage
456736	AW248217	Hs.1619	achaete-scute complex (Drosophila) homol	0.89	0.91	upregulate stage
456786	AK002084	Hs.132851	hypothetical protein FLJ11222	3.2	0.13	upregulate stage
456800	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	1	0.69	upregulate stage
456823	AL161979	Hs.146128	Homo sapiens mRNA; cDNA DKFZp761G1823 (f	8.95	0.07	upregulate stage
456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	5.55	0.1	upregulate stage
456999	AA319798	Hs.172247	eukaryotic translation elongation factor	11.3	0.07	upregulate stage
457015	AA688058	Hs.261544	ESTs	9.25	0.08	upregulate stage
457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	2.65	0.17	upregulate stage
457158	AA135370	Hs.188536	Homo sapiens cDNA: FLJ21635 fis, clone C	1	1	upregulate stage
457190	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1	0.87	upregulate stage
457309	AF131843	Hs.239340	Homo sapiens clone 24987 mRNA sequence	2.6	0.15	upregulate stage
457376	AI026984	Hs.293662	ESTs	1	1	upregulate stage
457402	AW452648	Hs.149342	activation-induced cytidine deaminase	2.9	0.16	upregulate stage
457435	AW972024	Hs.154645	ESTs, Weakly similar to tyrosine kinase	1	0.36	upregulate stage
457437	AW969732		gb:EST381810 MAGE resequences, MAGK Homo	2.5	0.14	upregulate stage
457465	AW301344	Hs.195969	ESTs	6.3	0.1	upregulate stage
457467	AW974815	Hs.292786	ESTs	1	1	upregulate stage

457474	AW972935		gb:EST385031 MAGE resequences, MAGM Homo	1	0.29	upregulate stage
457530	AW973713	Hs.293596	ESTs	1	0.39	upregulate stage
457637	AI288373	Hs.149875	ESTs	1	1	upregulate stage
457643	AI375499	Hs.27379	ESTs	3.25	0.19	upregulate stage
457650	AA649162	Hs.236456	ESTs	8.9	0.08	upregulate stage
457661	AA917801	Hs.128596	ESTs	0.96	0.9	upregulate stage
457692	AA744046	Hs.133350	ESTs	1	1	upregulate stage
457857	AW814892	Hs.273104	ESTs	1	1	upregulate stage
457892	AA744389		gb:ny51e10.s1 NCI_CGAP_Pr18 Homo sapiens	8.7	0.06	upregulate stage
457902	AI624876	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.2	0.21	upregulate stage
457943	AA765625	Hs.155690	ESTs	3.55	0.1	upregulate stage
457948	AI498640	Hs.159354	ESTs	2.65	0.19	upregulate stage
457964	NM_016353	Hs.5943	rec	1.5	0.17	upregulate stage
458004	AW976942	Hs.153057	ESTs	1	0.87	upregulate stage
458027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34	3.45	0.12	upregulate stage
458079	AI796870	Hs.54277	ESTs	11.5	0.05	upregulate stage
458158	AW296778	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.sa	1	1	upregulate stage
458171	AI420016	Hs.192090	ESTs	0.69	1.09	upregulate stage
458172	BE007237		gb:PM0-BN0139-050500-003-g09 BN0139 Homo	3	0.16	upregulate stage
458186	AA904244	Hs.153205	ESTs	4.6	0.15	upregulate stage
458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	3.1	0.16	upregulate stage
458270	T66139	Hs.113631	ESTs	1	0.67	upregulate stage
458282	AA984075	Hs.22580	alkylglycerone phosphate synthase	1	1	upregulate stage
458287	AA987556	Hs.12867	ESTs	5.05	0.13	upregulate stage
458580	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	1	0.28	upregulate stage
458586	AI683479	Hs.65390	ESTs	8.2	0.07	upregulate stage
458608	AW444662	Hs.202247	ESTs	1	0.27	upregulate stage
458632	AI744445	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT	1.05	0.23	upregulate stage
458663	AV658444	Hs.280776	Homo sapiens cDNA FLJ13684 fis, clone PL	5.05	0.13	upregulate stage
458670	AI301987	Hs.233398	ESTs	8.9	0.08	upregulate stage
458680	N73773	Hs.282950	ESTs	1	0.23	upregulate stage
458720	AV662037	Hs.124740	ESTs	1	0.3	upregulate stage
458722	AA741545	Hs.282832	ESTs	3.2	0.11	upregulate stage
458747	BE618395	Hs.257391	ESTs, Weakly similar to GTPase-activatin	3.3	0.14	upregulate stage
458760	AI498631	Hs.111334	ferritin, light polypeptide	11	0.07	upregulate stage
458781	AI444821		gb:RET4B7 subtracted retina cDNA library	6.05	0.12	upregulate stage
458801	N98648	Hs.276860	ESTs	4.45	0.13	upregulate stage
458880	AA046742		gb:zf48c09.r1 Soares retina N2b4HR Homo	9	0.08	upregulate stage
458886	AI247487	Hs.103277	ESTs	1	0.3	upregulate stage
458946	AA009716	Hs.42311	ESTs	8.7	0.08	upregulate stage
459023	AW968226	Hs.60798	ESTs	2.95	0.15	upregulate stage
459028	AI940577		gb:IL5-HT0009-120799-001-G07 HT0009 Homo	2.6	0.17	upregulate stage
459030	H86658	Hs.107699	ESTs, Weakly similar to hypothetical pro	1	1	upregulate stage
459058	H85939	Hs.209605	ESTs	1	1	upregulate stage
459128	AI902169		gb:IL-BT002-221198-051 BT002 Homo sapien	1	0.26	upregulate stage
459182	BE178517		gb:PM1-HT0603-090300-001-e09 HT0603 Homo	1	1	upregulate stage
459204	AW194601	Hs.13219	ESTs	2.85	0.16	upregulate stage
459256	AW967468	Hs.99821	Homo sapiens mRNA; cDNA DKFZp564C046 (fr	10.65	0.07	upregulate stage
459319	NM_000059		gb:Homo sapiens breast cancer 2, early o	1	1	upregulate stage
459395	Z30300	Hs.281935	ESTs	4.05	0.14	upregulate stage
459459	AA460445		gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	4.8	0.13	upregulate stage
459464	AA854847		gb:aj77h02.s1 Soares_parathyroid_tumor_N	1	0.38	upregulate stage
459492	AL118619		gb:DKFZp761E2410_r1 761 (synonym: hamy2)	1	1	upregulate stage
459530	AW770811		gb:hn49d07.x1 NCI_CGAP_Co17 Homo sapiens	1	1	upregulate stage
401519				12.65	0.06	upregulate stage
402474				25.55	0.03	upregulate stage
402727				16.25	0.05	upregulate stage
405411				12.95	0.05	upregulate stage
406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	14.42	0.03	upregulate stage
406685	M18728		gb:Human nonspecific crossreacting antig	15.75	0.03	upregulate stage
407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	16.3	0.04	upregulate stage
407242	M18728		gb:Human nonspecific crossreacting antig	12.56	0.03	upregulate stage
407347	AA829847	Hs.167347	ESTs, Weakly similar to ALU8_HUMAN ALU S	12.91	0.06	upregulate stage
407796	AA195509	Hs.272239	lymphocyte activation-associated protein	14.2	0.06	upregulate stage
408243	Y00787	Hs.624	interleukin 8	18.52	0.02	upregulate stage
408380	AF123050	Hs.44532	diubiquitin	16	0.03	upregulate stage
408618	AK000637	Hs.46624	HSPC043 protein	12.6	0.06	upregulate stage
408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	15.5	0.03	upregulate stage
409417	AA156247	Hs.295908	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.55	0.04	upregulate stage
410315	AI638871	Hs.17625	ESTs	14	0.05	upregulate stage
410324	AW292539	Hs.30177	ESTs	15.65	0.05	upregulate stage
412420	AL035668	Hs.73853	bone morphogenetic protein 2	12.6	0.05	upregulate stage
412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	16.45	0.03	upregulate stage
413281	AA861271	Hs.34396	ESTs	12.95	0.04	upregulate stage
414004	AA737033	Hs.7155	ESTs, Weakly similar to 2115357A TYKI pr	15.25	0.04	upregulate stage
414161	AA136106	Hs.184852	KIAA1553 protein	13.25	0.06	upregulate stage
414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	12.5	0.05	upregulate stage

414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	12.71	0.05	upregulate stage
414493	AL133921	Hs.76272	retinoblastoma-binding protein 2	13.05	0.05	upregulate stage
414522	AW518944	Hs.76325	Homo sapiens cDNA: FLJ23125 fis, clone L	30.45	0.02	upregulate stage
414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	29	0.02	upregulate stage
414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	13.2	0.05	upregulate stage
416114	AI695549	Hs.183868	glucuronidase, beta	14.7	0.04	upregulate stage
416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	13	0.06	upregulate stage
416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	13.3	0.04	upregulate stage
416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	15.55	0.04	upregulate stage
416980	AA381133	Hs.80684	high-mobility group (nonhistone chromoso	23.85	0.03	upregulate stage
417258	N58885	Hs.294040	ESTs	15.05	0.06	upregulate stage
417274	N92036	Hs.81848	RAD21 (S. pombe) homolog	23.05	0.04	upregulate stage
417353	AA375752	Hs.76362	general transcription factor IIA, 2 (12k	13	0.06	upregulate stage
417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	19.45	0.04	upregulate stage
417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	12.45	0.03	upregulate stage
417777	AI823763	Hs.7055	ESTs	12.6	0.06	upregulate stage
417821	BE245149	Hs.82643	protein tyrosine kinase 9	20.8	0.04	upregulate stage
417928	AA209344	Hs.282973	ESTs	14.65	0.05	upregulate stage
418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	13	0.05	upregulate stage
418791	AA935633	Hs.194628	ESTs	12.95	0.06	upregulate stage
419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	13.2	0.05	upregulate stage
421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	12.6	0.05	upregulate stage
422150	AI867118	Hs.2953	ribosomal protein S15a	13.55	0.05	upregulate stage
422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	15.7	0.05	upregulate stage
424673	AA345051	Hs.294092	ESTs	16.9	0.04	upregulate stage
424848	AI263231	Hs.145607	ESTs	15.2	0.05	upregulate stage
424865	AF011333	Hs.153563	lymphocyte antigen 75	12.85	0.04	upregulate stage
425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	13.25	0.06	upregulate stage
425787	AA363867	Hs.155029	ESTs	17.55	0.05	upregulate stage
426252	BE176980	Hs.28917	ESTs	12.95	0.05	upregulate stage
426329	AL389951	Hs.271623	nucleoporin 50kD	13.8	0.05	upregulate stage
427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	13.85	0.05	upregulate stage
427351	AW402593	Hs.123253	Homo sapiens cDNA: FLJ22009 fis, clone H	12.8	0.06	upregulate stage
427979	BE379776	Hs.181309	proteasome (prosome, macropain) subunit,	16.95	0.05	upregulate stage
428044	AA093322	Hs.182225	RNA binding motif protein 3	14.65	0.05	upregulate stage
428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	17.15	0.05	upregulate stage
428840	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene	16.8	0.05	upregulate stage
430191	AI149880	Hs.188809	ESTs	14.5	0.05	upregulate stage
430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	14.9	0.05	upregulate stage
430853	AI734179	Hs.105676	ESTs	13.55	0.06	upregulate stage
431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	16.2	0.04	upregulate stage
431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (conn	27	0.01	upregulate stage
431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	13.45	0.06	upregulate stage
431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	21.2	0.03	upregulate stage
431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	13.05	0.06	upregulate stage
431863	AA188185	Hs.271871	spindlin	15.6	0.05	upregulate stage
434263	N34895	Hs.44648	ESTs	14.25	0.05	upregulate stage
434651	BE616902	Hs.285313	core promoter element binding protein	17.95	0.05	upregulate stage
436286	AA804442	Hs.3459	Homo sapiens cDNA: FLJ22003 fis, clone H	14.95	0.05	upregulate stage
436385	BE551618	Hs.144097	ESTs	13.85	0.06	upregulate stage
437192	AW975786	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	12.75	0.06	upregulate stage
438000	AI825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	15.3	0.04	upregulate stage
439941	AI392640	Hs.18272	ESTs	17.42	0.05	upregulate stage
440086	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom	12.59	0.05	upregulate stage
440116	AI798851	Hs.9403	ESTs	14.5	0.05	upregulate stage
441020	W79283	Hs.35962	ESTs	12.4	0.04	upregulate stage
441633	AW958544	Hs.112242	ESTs	15.85	0.03	upregulate stage
441980	AK001441	Hs.8055	hypothetical protein FLJ10579	13.6	0.05	upregulate stage
442043	BE567620	Hs.99210	ESTs	12.5	0.06	upregulate stage
442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	12.65	0.06	upregulate stage
442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	15.15	0.05	upregulate stage
443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	13.4	0.05	upregulate stage
445033	AV652402	Hs.155145	ESTs	13.3	0.05	upregulate stage
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	30.5	0.02	upregulate stage
446847	T51454	Hs.82845	Human clone 23815 mRNA sequence	13.8	0.04	upregulate stage
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	15.15	0.04	upregulate stage
448712	W01046	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L	13.2	0.05	upregulate stage
448772	AW390822	Hs.24639	ESTs	12.75	0.06	upregulate stage
448926	AI798164	Hs.140903	ESTs, Moderately similar to neuronal thr	13.35	0.06	upregulate stage
449962	AA004879	Hs.187820	ESTs	12.79	0.05	upregulate stage
450139	AK001838	Hs.296323	Homo sapiens cDNA FLJ10976 fis, clone PL	14.76	0.06	upregulate stage
451035	AU076785	Hs.430	plastin 1 (I isoform)	17.65	0.04	upregulate stage
451334	AI122691	Hs.13268	ESTs	14.7	0.05	upregulate stage
452567	D87120	Hs.29882	predicted osteoblast protein	12.45	0.06	upregulate stage
453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	13.4	0.05	upregulate stage
453331	AI240665	Hs.8895	ESTs	12.6	0.05	upregulate stage
400365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.2	0.17	upregulate stage

401256				2	0.16	upregulate stage
402075				1	0.1	upregulate stage
403029				1.75	0.16	upregulate stage
403047				3.3	0.1	upregulate stage
403426				1.7	0.18	upregulate stage
403754				2.8	0.12	upregulate stage
403822				1.2	0.14	upregulate stage
407835	AK002081	Hs.40337	hypothetical protein	1.9	0.15	upregulate stage
407980	AA046309		gb:zf12f01.s1 Soares_fetal_heart_NbHH19W	1.35	0.1	upregulate stage
408081	AW451597	Hs.167409	ESTs	2.3	0.18	upregulate stage
408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	1.65	0.12	upregulate stage
408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	1	0.2	upregulate stage
409810	AW500895		gb:UI-HF-BP0p-air-a-02-0-UI.r1 NIH_MGC_5	2.25	0.2	upregulate stage
410094	BE147897	Hs.58593	general transcription factor IIF, polype	4.05	0.12	upregulate stage
410603	AA086219	Hs.68714	ESTs	1.9	0.18	upregulate stage
410763	AF279145	Hs.8966	tumor endothelial marker 8	4.15	0.13	upregulate stage
411418	BE241870		gb:TCAAP2E0047 Pediatric acute myelogeno	1.6	0.22	upregulate stage
411691	AW857199		gb:RC2-CT0304-080100-011-f06 CT0304 Homo	1.45	0.24	upregulate stage
411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	2.2	0.2	upregulate stage
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	1.75	0.06	upregulate stage
412102	H56435	Hs.75935	KIAA0077 protein	1.7	0.2	upregulate stage
412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	1	0.17	upregulate stage
412312	AW936686		gb:PM2-DT0023-080300-004-g01 DT0023 Homo	3.4	0.16	upregulate stage
412598	AI681997	Hs.107057	ESTs	2.25	0.2	upregulate stage
413383	AA128978	Hs.154706	Homo sapiens cDNA FLJ13594 fis, clone PL	2.3	0.17	upregulate stage
413406	AW452823	Hs.135268	ESTs	3.52	0.14	upregulate stage
413618	BE154078		gb:PM0-HT0339-200400-010-F04 HT0339 Homo	1	0.18	upregulate stage
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	1.05	0.12	upregulate stage
417708	N74392	Hs.50495	ESTs	2	0.16	upregulate stage
417974	AA210765		gb:zr90c06.r1 NCI_CGAP_GCB1 Homo sapiens	1.7	0.18	upregulate stage
418604	AA225632	Hs.190016	ESTs	3.75	0.13	upregulate stage
418631	AA225921	Hs.115105	ESTs	1.75	0.2	upregulate stage
418830	BE513731	Hs.88959	Human DNA sequence from clone 967N21 on	3.8	0.09	upregulate stage
418893	N32264	Hs.44330	ESTs	2.35	0.14	upregulate stage
418950	T78517	Hs.13941	ESTs	2.15	0.19	upregulate stage
419044	AI799135	Hs.87164	Homo sapiens cDNA FLJ14001 fis, clone Y7	1.85	0.15	upregulate stage
420082	N43741	Hs.203148	ESTs	3.8	0.14	upregulate stage
420653	AI224532	Hs.88550	ESTs	2.05	0.16	upregulate stage
421112	AW243875	Hs.265427	ESTs	3.3	0.13	upregulate stage
421683	AI147535	Hs.143769	ESTs	2	0.14	upregulate stage
421799	AW972292	Hs.292998	ESTs	2.35	0.15	upregulate stage
422177	AA720878	Hs.201375	ESTs	3.3	0.14	upregulate stage
422429	AA310527		gb:EST181333 Jurkat T-cells V Homo saple	3.45	0.12	upregulate stage
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	2.15	0.11	upregulate stage
424026	AI798295	Hs.123218	ESTs	3.8	0.14	upregulate stage
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	1	0.09	upregulate stage
425761	AW664214	Hs.196729	ESTs	2	0.19	upregulate stage
426427	M86699	Hs.169840	TTK protein kinase	2.1	0.16	upregulate stage
427558	D49493	Hs.2171	growth differentiation factor 10	2.15	0.14	upregulate stage
427635	BE397988	Hs.179982	tumor protein p53-binding protein	3.9	0.11	upregulate stage
428766	AA477989	Hs.98800	ESTs	3.8	0.12	upregulate stage
429761	AI276780	Hs.135173	ESTs	1.9	0.17	upregulate stage
430132	AA204686	Hs.234149	hypothetical protein FLJ20647	5.05	0.11	upregulate stage
430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.55	0.15	upregulate stage
430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.5	0.14	upregulate stage
431187	AW971146	Hs.293187	ESTs	3.95	0.13	upregulate stage
431364	AW971382	Hs.294016	ESTs, Weakly similar to alpha-1(XVIII) c	1.8	0.15	upregulate stage
431401	AA504626	Hs.105735	ESTs	1.65	0.22	upregulate stage
431419	AL041844	Hs.277522	ESTs, Weakly similar to FYVE finger-cont	1.45	0.16	upregulate stage
432361	AI378562	Hs.159585	ESTs	2.15	0.14	upregulate stage
432810	AA863400	Hs.23054	ESTs	3.7	0.08	upregulate stage
432926	AA570416	Hs.32271	hypothetical protein FLJ10846	2	0.2	upregulate stage
433108	AB002446		gb:Homo sapiens mRNA from chromosome 5q2	2.35	0.14	upregulate stage
434153	AF118072	Hs.283916	Homo sapiens PRO1716 mRNA, complete cds	1	0.14	upregulate stage
435202	AI971313	Hs.170204	KIAA0551 protein	1.25	0.16	upregulate stage
435313	AI769400	Hs.189729	ESTs	2	0.18	upregulate stage
435359	T60843	Hs.189679	ESTs	3.6	0.11	upregulate stage
435488	H57954	Hs.34394	ESTs	2.2	0.22	upregulate stage
436583	AW293909	Hs.156935	ESTs	1.4	0.19	upregulate stage
436862	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	3.2	0.12	upregulate stage
437485	AI149570	Hs.127363	ESTs	2.05	0.22	upregulate stage
437854	AL119723		gb:DKFZp761A2124_r1 761 (synonym: hamy2)	2.75	0.15	upregulate stage
438316	AA789249		gb:aj27g08.s1 Soares_testis_NHT Homo sap	2.45	0.13	upregulate stage
438390	AI422017		gb:tf45f12.x1 NCI_CGAP_Brn23 Homo sapien	3.1	0.13	upregulate stage
438915	AA280174	Hs.23282	ESTs	1.35	0.12	upregulate stage
439983	AA858394	Hs.117955	ESTs	4	0.13	upregulate stage
442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	5.55	0.09	upregulate stage

442369	AI565071	Hs.159983	ESTs	3.85	0.14	upregulate stage
442748	AI016713	Hs.135787	ESTs	2.35	0.23	upregulate stage
443717	BE163884	Hs.282331	ESTs	2.5	0.18	upregulate stage
445935	AA287537	Hs.167585	ESTs	1	0.2	upregulate stage
446078	AI339982	Hs.156061	ESTs	2.25	0.24	upregulate stage
446139	H77395	Hs.39749	ESTs	2.15	0.18	upregulate stage
446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	3.45	0.14	upregulate stage
448253	H25899	Hs.201591	ESTs	1.65	0.18	upregulate stage
448956	AK001674	Hs.22630	cofactor required for Sp1 transcriptiona	2.2	0.14	upregulate stage
449199	AI990122	Hs.196988	ESTs	1.25	0.23	upregulate stage
449558	AA001765	Hs.157079	KIAA1227 protein	1	0.16	upregulate stage
449576	AW014631	Hs.225068	ESTs	2.3	0.19	upregulate stage
449859	T98077	Hs.18214	ESTs	6.3	0.07	upregulate stage
450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.e	1.65	0.22	upregulate stage
450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	1.35	0.19	upregulate stage
451337	AI400209	Hs.60787	ESTs	1.6	0.16	upregulate stage
451686	AA059246	Hs.110293	ESTs	3.4	0.14	upregulate stage
452079	AA830908	Hs.15825	ESTs	1.9	0.23	upregulate stage
452220	BE158006	Hs.212296	ESTs	3.1	0.17	upregulate stage
453918	AW005123	Hs.231975	ESTs	1	0.21	upregulate stage
455350	AW901809		gb:QV0-NN1020-170400-195-h02 NN1020 Homo	2	0.2	upregulate stage
456511	AA282330	Hs.145668	ESTs	1.15	0.12	upregulate stage
456986	D38299	Hs.170917	prostaglandin E receptor 3 (subtype EP3)	1.65	0.18	upregulate stage
457427	AW971287		gb:EST383376 MAGE resequences, MAGL Homo	2.35	0.16	upregulate stage
400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1	0.27	upregulate stage
400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	2.33	0.2	upregulate stage
400471				7.45	0.09	upregulate stage
400641				0.71	0.31	upregulate stage
400749				7.25	0.1	upregulate stage
400751				5.35	0.09	upregulate stage
400761				5.9	0.1	upregulate stage
400843				5.85	0.07	upregulate stage
401045				2.42	0.17	upregulate stage
401049				1.2	0.19	upregulate stage
401192				2.47	0.3	upregulate stage
401203				6.73	0.08	upregulate stage
401205				6.63	0.1	upregulate stage
401276				6.95	0.1	upregulate stage
401561				2.2	0.13	upregulate stage
401604				1	0.19	upregulate stage
402245				7.65	0.09	upregulate stage
402296				1	0.33	upregulate stage
402530				5.1	0.13	upregulate stage
402812				1.65	0.17	upregulate stage
402820				1	0.34	upregulate stage
402892				1	1	upregulate stage
403344				6.5	0.08	upregulate stage
404156				3.7	0.11	upregulate stage
404290				4.45	0.09	upregulate stage
404538				8.38	0.09	upregulate stage
404676				8.3	0.09	upregulate stage
404977				0.9	0.35	upregulate stage
405033				1.52	0.31	upregulate stage
405109	N47812	Hs.81360	CGI-35 protein	6.2	0.1	upregulate stage
405654				1.95	0.06	upregulate stage
406081				3	0.07	upregulate stage
406270				6.09	0.13	upregulate stage
406399				1.55	0.41	upregulate stage
406475				6.2	0.12	upregulate stage
406485				1	0.48	upregulate stage
406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	5.4	0.07	upregulate stage
406867	AA157857	Hs.182265	keratin 19	2.26	0.37	upregulate stage
407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	3.35	0.11	upregulate stage
407230	AA157857	Hs.182265	keratin 19	2.15	0.38	upregulate stage
407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	2.1	0.09	upregulate stage
407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.25	0.11	upregulate stage
407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	6.25	0.08	upregulate stage
407870	AB032990	Hs.40719	hypothetical protein KIAA1164	4.5	0.12	upregulate stage
407877	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	3.3	0.15	upregulate stage
407968	NM_004863	Hs.59403	serine palmitoyltransferase, long chain	7.35	0.1	upregulate stage
408162	AA993833	Hs.118527	ESTs	6.2	0.09	upregulate stage
408363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	5.36	0.14	upregulate stage
408576	NM_003542	Hs.46423	H4 histone family, member G	7.28	0.1	upregulate stage
408673	BE208517	Hs.184109	ribosomal protein L37a	2.53	0.24	upregulate stage
408684	R61377	Hs.12727	hypothetical protein FLJ21610	1	0.3	upregulate stage
409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	7.7	0.06	upregulate stage
409592	BE280951	Hs.55058	EH-domain containing 4	3.95	0.1	upregulate stage

409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	1.55	0.16	upregulate stage
410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	4.1	0.18	upregulate stage
410232	AW372451	Hs.61184	CGI-79 protein	3.65	0.14	upregulate stage
410269	AW613597		gb:hh79g12.x1 NCI_CGAP_GU1 Homo sapiens	7.55	0.09	upregulate stage
410297	AA148710	Hs.159441	ESTs	3.8	0.1	upregulate stage
410337	M83822	Hs.62354	cell division cycle 4-like	4.35	0.19	upregulate stage
410418	D31382	Hs.63325	transmembrane protease, serine 4	1.42	0.4	upregulate stage
410541	AA065003	Hs.64179	hypothetical protein	1.61	0.48	upregulate stage
410724	AW799269		gb:RC0-UM0051-210300-012-f01 UM0051 Homo	6.65	0.12	upregulate stage
410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	1.4	0.16	upregulate stage
410968	AA199907	Hs.67397	homeo box A1	3.05	0.1	upregulate stage
411162	AW819944		gb:QV0-ST0294-240300-172-e03 ST0294 Homo	2	0.23	upregulate stage
411173	R81571		gb:yj02h10.r1 Soares placenta Nb2HP Homo	7.2	0.1	upregulate stage
411243	AB039886	Hs.69319	CA11	0.36	0.93	upregulate stage
411407	R00903		gb:ye87a07.r1 Soares fetal liver spleen	8	0.09	upregulate stage
411704	AI499220	Hs.71573	hypothetical protein FLJ10074	1.75	0.22	upregulate stage
412121	AB033061	Hs.73287	KIAA1235 protein	5.3	0.11	upregulate stage
412123	BE251328	Hs.73291	hypothetical protein FLJ10881	6.9	0.1	upregulate stage
412129	M21984	Hs.73454	troponin T3, skeletal, fast	0.27	1.06	upregulate stage
412354	AW939148		gb:QV1-DT0069-110200-067-d06 DT0069 Homo	6.9	0.11	upregulate stage
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.88	0.21	upregulate stage
412700	BE222433	Hs.201262	ESTs	2.85	0.15	upregulate stage
412706	R97106	Hs.167546	ESTs	3.75	0.16	upregulate stage
412935	BE267045	Hs.75064	tubulin-specific chaperone c	7	0.09	upregulate stage
413402	T24065		gb:seq2245 HMSWMYK Homo sapiens cDNA clo	6.3	0.12	upregulate stage
413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.45	0.11	upregulate stage
413445	BE141022		gb:MR0-HT0067-201099-002-d10 HT0067 Homo	3.9	0.13	upregulate stage
413587	AA156164	Hs.271833	Homo sapiens cDNA FLJ13473 fis, clone PL	7.63	0.09	upregulate stage
413800	AI129238	Hs.192235	ESTs	3.2	0.18	upregulate stage
413859	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme	2.54	0.33	upregulate stage
413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	1.75	0.21	upregulate stage
413991	H44725	Hs.71300	ESTs	1.3	0.21	upregulate stage
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	8.1	0.07	upregulate stage
414203	BE262170		gb:601150419F1 NIH_MGC_19 Homo sapiens c	1.45	0.14	upregulate stage
414343	AL036166	Hs.75914	coated vesicle membrane protein	1	0.23	upregulate stage
414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cds	1	0.36	upregulate stage
414987	AA524394	Hs.165544	ESTs	1.51	0.51	upregulate stage
414993	AW819403	Hs.77724	KIAA0586 gene product	2.72	0.23	upregulate stage
415276	U88666	Hs.78353	SFRS protein kinase 2	6.95	0.1	upregulate stage
415303	R11813		gb:yf53a04.r1 Soares infant brain 1NIB H	8.1	0.09	upregulate stage
415392	Z44067		gb:HSC1RF051 normalized infant brain cDN	5.56	0.11	upregulate stage
415572	F12294		gb:HSC38B051 normalized infant brain cDN	5.7	0.11	upregulate stage
415773	R21651		gb:yh19g02.r1 Soares placenta Nb2HP Homo	5.3	0.11	upregulate stage
416012	AF061959	Hs.78961	protein phosphatase 1, regulatory (inhib	2.19	0.28	upregulate stage
416074	R40174	Hs.21209	ESTs	7.61	0.11	upregulate stage
416182	NM_004354	Hs.79069	cyclin G2	1	0.39	upregulate stage
416518	H60730	Hs.18917	ESTs	6.6	0.1	upregulate stage
416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	3.9	0.17	upregulate stage
416987	D86957	Hs.80712	KIAA0202 protein	2.54	0.31	upregulate stage
417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.26	0.12	upregulate stage
417275	X63578	Hs.81849	parvalbumin	1	0.12	upregulate stage
417395	BE564245	Hs.82084	integrin beta 3 binding protein (beta3-e	8.4	0.08	upregulate stage
417683	AW566008	Hs.239154	Homo sapiens cDNA FLJ12814 fis, clone NT	2.2	0.17	upregulate stage
417759	R13567	Hs.12548	ESTs	8.18	0.09	upregulate stage
417848	AA206581	Hs.39457	ESTs	8.6	0.08	upregulate stage
417985	AA187545	Hs.83114	crystallin, zeta (quinone reductase)	7	0.11	upregulate stage
418073	R39789	Hs.119714	EST	6.3	0.11	upregulate stage
418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	1.63	0.46	upregulate stage
418406	X73501	Hs.84905	cytokeratin 20	3.5	0.02	upregulate stage
418555	AI417215	Hs.87159	Homo sapiens cDNA FLJ12577 fis, clone NT	6.75	0.06	upregulate stage
418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	4.1	0.11	upregulate stage
418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	7.5	0.08	upregulate stage
418827	BE327311	Hs.47166	HT021	5.6	0.13	upregulate stage
418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	1.5	0.22	upregulate stage
419551	AW582256	Hs.91011	anterior gradient 2 (Xenepus laevis) hom	2.44	0.29	upregulate stage
419590	AF005043	Hs.91390	poly (ADP-ribose) glycohydrolase	8.08	0.1	upregulate stage
419693	AA133749	Hs.92323	FXYD domain-containing ion transport reg	1.64	0.48	upregulate stage
419712	AA360838	Hs.179909	Homo sapiens cDNA: FLJ22995 fis, clone K	5.4	0.11	upregulate stage
419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	7.9	0.06	upregulate stage
419720	AA249131	Hs.143607	hypothetical protein FLJ11068	2.95	0.15	upregulate stage
419791	AI579909	Hs.105104	ESTs	2.45	0.2	upregulate stage
419872	AI422951	Hs.146162	ESTs	4.25	0.17	upregulate stage
419903	T16938	Hs.87902	ESTs	2.5	0.22	upregulate stage
419932	AA281594		gb:zt03a01.r1 NCI_CGAP_GCB1 Homo sapiens	6.1	0.12	upregulate stage
420026	AI831190	Hs.166676	ESTs	3.4	0.14	upregulate stage
420187	AK001714	Hs.95744	hypothetical protein similar to ankyrin	4.03	0.18	upregulate stage
420193	AI460080	Hs.202869	ESTs	1	0.28	upregulate stage

420281	AI623693	Hs.191533	ESTs	6.6	0.11	upregulate stage
420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	6	0.09	upregulate stage
420370	Y13645	Hs.97234	uroplakin 2	1.2	0.45	upregulate stage
420383	T55154	Hs.144880	ESTs	3.8	0.12	upregulate stage
420450	AW968969	Hs.177726	ESTs	2.75	0.14	upregulate stage
420588	AF000982	Hs.147916	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	8.1	0.09	upregulate stage
420763	AA419392	Hs.178354	ESTs	8	0.09	upregulate stage
420838	AW118210	Hs.5244	ESTs	8.65	0.07	upregulate stage
420981	L40904	Hs.100724	peroxisome proliferative activated recep	1.98	0.32	upregulate stage
421013	M62397	Hs.1345	mutated in colorectal cancers	1	0.29	upregulate stage
421072	AI215069	Hs.89113	ESTs	5.8	0.12	upregulate stage
421110	AJ250717	Hs.1355	cathepsin E	5.45	0.03	upregulate stage
421141	AW117261	Hs.125914	ESTs	2.75	0.16	upregulate stage
421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	7.45	0.09	upregulate stage
421508	NM_004833	Hs.105115	absent in melanoma 2	4.21	0.19	upregulate stage
421634	AA437414	Hs.106283	hypothetical protein FLJ10262	7.79	0.08	upregulate stage
421674	T10707	Hs.296355	neuronal PAS domain protein 2	7.5	0.1	upregulate stage
421810	AK001718	Hs.108530	hypothetical protein FLJ10856	8.45	0.08	upregulate stage
421855	F06504	Hs.27384	ESTs	2.9	0.16	upregulate stage
421898	AA259011	Hs.109268	hypothetical protein FLJ12552	7.06	0.11	upregulate stage
422156	N34524	Hs.300893	ESTs, Weakly similar to envelope protein	3.75	0.16	upregulate stage
422225	BE245652	Hs.118281	zinc finger protein 266	2.95	0.17	upregulate stage
422243	AW803733	Hs.250655	*prothymosin, alpha (gene sequence 28)*	8.15	0.08	upregulate stage
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.21	0.17	upregulate stage
422634	NM_016010	Hs.118821	CGI-62 protein	1.3	0.29	upregulate stage
422988	AW673847	Hs.97321	ESTs	4.15	0.11	upregulate stage
423081	AF262992	Hs.123159	sperm associated antigen 4	2.82	0.3	upregulate stage
423596	AA328195	Hs.234101	ESTs, Weakly similar to CTL1 protein [H.	2.75	0.19	upregulate stage
423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	1.95	0.13	upregulate stage
423979	AF229181	Hs.136644	CS box-containing WD protein	7.12	0.11	upregulate stage
424005	AB033041	Hs.137507	KIAA1215 protein	1.71	0.37	upregulate stage
424014	AA333653	Hs.24790	KIAA1573 protein	4.85	0.12	upregulate stage
424028	AF055084	Hs.153692	KIAA0686 protein	8.5	0.07	upregulate stage
424194	BE245833	Hs.169854	hypothetical protein SP192	6.1	0.1	upregulate stage
424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.59	0.11	upregulate stage
424550	AI650541	Hs.115298	ESTs	3.25	0.12	upregulate stage
424631	AA688021	Hs.179808	ESTs	5.45	0.11	upregulate stage
424659	AW891298	Hs.301877	ESTs, Weakly similar to hSIAH2 [H.sapien	3.55	0.15	upregulate stage
424704	AI263293	Hs.152096	cytochrome P450, subfamily IIJ (arachido	8.45	0.06	upregulate stage
424775	AB014540	Hs.153026	SWAP-70 protein	6.65	0.11	upregulate stage
424800	AL035588	Hs.153203	MyoD family inhibitor	1.94	0.3	upregulate stage
425086	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	2.85	0.19	upregulate stage
425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.2	0.1	upregulate stage
425277	NM_001241	Hs.155478	cyclin T2	6	0.13	upregulate stage
425508	AA991551	Hs.97013	ESTs	5.67	0.1	upregulate stage
425689	W16480	Hs.24283	ESTs	4.55	0.13	upregulate stage
425721	AC002115	Hs.159309	uroplakin 1A	0.71	0.8	upregulate stage
426069	H10807	Hs.30998	ESTs	3.4	0.17	upregulate stage
426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	6.84	0.09	upregulate stage
426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	6.7	0.1	upregulate stage
426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	3.05	0.14	upregulate stage
426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	1.8	0.26	upregulate stage
426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.96	0.36	upregulate stage
426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	1.32	0.49	upregulate stage
426902	AI125334	Hs.97408	ESTs	5.05	0.07	upregulate stage
426931	NM_003416	Hs.2076	*zinc finger protein 7 (KOX 4, clone HF.1*	2.95	0.12	upregulate stage
427001	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	4.9	0.13	upregulate stage
427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	0.57	0.86	upregulate stage
427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	1.86	0.31	upregulate stage
427399	NM_014883	Hs.177664	KIAA0914 gene product	5	0.13	upregulate stage
427450	AB014526	Hs.178121	KIAA0626 gene product	5.3	0.09	upregulate stage
427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	6.37	0.13	upregulate stage
427737	AA435988	Hs.178066	ESTs, Weakly similar to AF068289 5 HDCME	5.7	0.11	upregulate stage
428042	AA419529		gb:zv03d12.r1 Soares_NhHMPu_S1 Homo sapi	1.65	0.14	upregulate stage
428336	AA503115	Hs.183752	microseminoprotein, beta-	5.37	0.05	upregulate stage
428337	AA644508		gb:af73c01.r1 Soares_NhHMPu_S1 Homo sapi	3.4	0.13	upregulate stage
428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	1	0.17	upregulate stage
428471	X57348	Hs.184510	stratifin	1.81	0.39	upregulate stage
428583	AA430589	Hs.301374	ESTs, Moderately similar to ALU5_HUMAN A	7.55	0.11	upregulate stage
428670	AA431682	Hs.134832	ESTs	8.05	0.1	upregulate stage
428785	AI015953	Hs.125265	ESTs	1.65	0.15	upregulate stage
429332	AF030403	Hs.199263	Ste-20 related kinase	2.64	0.26	upregulate stage
429343	AK000785	Hs.199480	epsin 3	3.15	0.27	upregulate stage
429556	AW139399	Hs.98988	ESTs	1.87	0.31	upregulate stage
429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	0.61	1.02	upregulate stage
429824	AA296363	Hs.121520	Human BAC clone GS1-99H8	2.03	0.39	upregulate stage
429966	BE081342	Hs.226799	HSPC039 protein	7.85	0.08	upregulate stage

429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1	0.61	upregulate stage
430042	AB023170	Hs.227850	KIAA0953 protein	2.5	0.17	upregulate stage
430168	AW968343	Hs.300896	ESTs, Highly similar to AF128113 1 promi	1.98	0.4	upregulate stage
430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	6.7	0.09	upregulate stage
430399	AI916284	Hs.199671	ESTs	8.09	0.08	upregulate stage
430763	AA485468	Hs.105658	ESTs	3.18	0.24	upregulate stage
431474	AL133990	Hs.190642	ESTs	0.37	0.51	upregulate stage
431567	N51357	Hs.260855	Homo sapiens mRNA; cDNA DKFZp761G2311 (f	1.74	0.39	upregulate stage
431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.55	0.15	upregulate stage
431683	AK001749	Hs.267604	hypothetical protein FLJ10450	8.55	0.08	upregulate stage
431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	7.95	0.1	upregulate stage
431846	BE019924	Hs.271580	uroplakin 1B	1.33	0.5	upregulate stage
431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	4.15	0.12	upregulate stage
432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	3.7	0.13	upregulate stage
432520	AI075978	Hs.188007	ESTs	2.05	0.22	upregulate stage
432524	AI458020	Hs.293287	ESTs	5.15	0.14	upregulate stage
432540	AI821517	Hs.105866	ESTs	5.5	0.11	upregulate stage
432623	AA557351	Hs.152448	ESTs, Moderately similar to PUR6_HUMAN M	8.43	0.09	upregulate stage
432632	AW973801	Hs.134656	ESTs	2.45	0.16	upregulate stage
432820	AI554057	Hs.152477	ESTs	8.29	0.09	upregulate stage
432945	AL043683	Hs.271357	ESTs, Weakly similar to unnamed protein	3.22	0.23	upregulate stage
433027	AF191018	Hs.279923	putative nucleotide binding protein, est	2.15	0.39	upregulate stage
433037	NM_014158	Hs.279938	HSPC067 protein	5.1	0.11	upregulate stage
433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	7.9	0.1	upregulate stage
433171	AA579425		gb:nf37c08.s1 NCI_CGAP_Pr2 Homo sapiens	3.54	0.14	upregulate stage
433311	AA688149		gb:nv16h12.s1 NCI_CGAP_Pr22 Homo sapiens	6.6	0.08	upregulate stage
433383	AF034837	Hs.192731	double-stranded RNA specific adenosine d	2.45	0.21	upregulate stage
433409	AI278802	Hs.25661	ESTs	4.75	0.1	upregulate stage
433650	AA603472	Hs.28456	ESTs	1.6	0.18	upregulate stage
433675	AW977653	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H	3.88	0.17	upregulate stage
434328	BE564937	Hs.15984	pp21 homolog	3	0.15	upregulate stage
434476	AW858520	Hs.271825	ESTs	4.6	0.1	upregulate stage
434683	AW298724	Hs.202639	ESTs	2.1	0.19	upregulate stage
434726	AF062719	Hs.139053	ESTs	1.76	0.34	upregulate stage
435124	AA725362	Hs.120456	ESTs	7.7	0.09	upregulate stage
435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	5.8	0.09	upregulate stage
435899	W89093	Hs.189914	ESTs	1.32	0.42	upregulate stage
436026	AI349764	Hs.217081	ESTs	1	0.22	upregulate stage
436154	AA764950	Hs.119898	ESTs	8.4	0.05	upregulate stage
436293	AI601188	Hs.120910	ESTs	2.42	0.2	upregulate stage
436361	AA825814	Hs.149065	ESTs	6.95	0.09	upregulate stage
436455	AI027959	Hs.132300	ESTs	3.25	0.15	upregulate stage
436577	W84774	Hs.17643	ESTs	6.3	0.06	upregulate stage
436684	AW976319	Hs.94806	KIAA1062 protein	4.75	0.12	upregulate stage
437036	AI571514	Hs.133022	ESTs	1.4	0.13	upregulate stage
437146	AA730977		gb:nw55f05.s1 NCI_CGAP_Ew1 Homo sapiens	1	0.37	upregulate stage
437262	BE250537	Hs.174838	Homo sapiens cDNA FLJ14192 fis, clone NT	3.25	0.17	upregulate stage
437277	AA748016	Hs.123370	ESTs	6.75	0.09	upregulate stage
437882	AI243203	Hs.131572	ESTs	8.12	0.09	upregulate stage
438392	AA806395	Hs.123205	ESTs	1	0.34	upregulate stage
438416	N76398	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	8.1	0.1	upregulate stage
438739	AA815391		gb:ai61c02.s1 Soares_testis_NHT Homo sap	4.69	0.12	upregulate stage
439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	6.65	0.11	upregulate stage
439394	AA149250	Hs.56105	ESTs, Weakly similar to WDNM RAT WDNM1 P	3.19	0.11	upregulate stage
439544	W26354	Hs.28891	hypothetical protein FLJ11360	2.3	0.34	upregulate stage
439569	AW602166	Hs.222399	CEGP1 protein	0.73	0.51	upregulate stage
439586	AA922936	Hs.110039	ESTs	4.3	0.1	upregulate stage
439706	AW872527	Hs.59761	ESTs	1	0.14	upregulate stage
439897	NM_015310	Hs.6763	KIAA0942 protein	8.4	0.08	upregulate stage
439898	AW505514	Hs.209561	ESTs, Weakly similar to C05E11.1 gene pr	7.35	0.1	upregulate stage
439949	AW979197	Hs.292073	ESTs	8.55	0.08	upregulate stage
440035	BE561589	Hs.285122	hypothetical protein FLJ21839	6	0.11	upregulate stage
440619	AW408586	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	7.95	0.07	upregulate stage
440635	AW610331		gb:RC4-ST0316-190100-011-c08 ST0316 Homo	5.95	0.11	upregulate stage
440787	AW292043	Hs.209433	ESTs	5.05	0.12	upregulate stage
441233	AA972965	Hs.135568	ESTs	1.7	0.12	upregulate stage
441528	AI003797	Hs.130815	hypothetical protein FLJ21870	7.2	0.09	upregulate stage
441670	AW874090	Hs.127392	ESTs, Moderately similar to p33ING1 [H.s	2.45	0.19	upregulate stage
441683	BE564214	Hs.102946	ESTs	5.9	0.13	upregulate stage
441847	AI215564	Hs.220972	ESTs	6.95	0.11	upregulate stage
442145	AI022650	Hs.8117	erbb2-interacting protein ERBIN	3	0.19	upregulate stage
442299	AW467791	Hs.155561	ESTs	5.05	0.13	upregulate stage
442315	AA173992	Hs.7956	ESTs	3.97	0.17	upregulate stage
442528	AF150317	Hs.134217	ESTs	1.4	0.34	upregulate stage
442571	C06338	Hs.165464	ESTs	8	0.08	upregulate stage
442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	6.7	0.1	upregulate stage
442652	AI005163	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	7.15	0.11	upregulate stage

442947	R40800	Hs.21303	ESTs	8.5	0.08	upregulate stage
442993	BE018682	Hs.44343	ESTs	1.91	0.34	upregulate stage
443015	R33261	Hs.6614	ESTs	8.5	0.09	upregulate stage
443085	AI032660	Hs.164711	ESTs	4	0.13	upregulate stage
443228	W24781	Hs.293798	ESTs	1.61	0.47	upregulate stage
443367	AW071349	Hs.215937	ESTs	1.75	0.29	upregulate stage
443371	AI792888	Hs.145489	ESTs	5.85	0.11	upregulate stage
443564	AI921685	Hs.199713	ESTs	1.4	0.18	upregulate stage
443638	AW028696	Hs.145679	ESTs	3.25	0.15	upregulate stage
443677	AV646096	Hs.293776	ESTs, Weakly similar to 1207289A reverse	6.45	0.11	upregulate stage
443861	AW449462	Hs.134743	ESTs	6.72	0.09	upregulate stage
444097	AW517412	Hs.150757	ESTs	4.25	0.11	upregulate stage
444171	AB018249	Hs.10458	small inducible cytokine subfamily A (Cy	8.45	0.09	upregulate stage
444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	8.1	0.1	upregulate stage
444385	BE278964	Hs.11085	CGI-111 protein	8.6	0.09	upregulate stage
444624	AV650476	Hs.282936	ESTs	7.52	0.1	upregulate stage
444631	AW995395	Hs.84520	ESTs	1.25	0.21	upregulate stage
444707	AI188613	Hs.143866	ESTs	2.1	0.21	upregulate stage
444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	6.8	0.1	upregulate stage
444779	AI192105	Hs.147170	ESTs	0.94	0.6	upregulate stage
444823	BE262989	Hs.12045	putative protein	8.09	0.1	upregulate stage
444858	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein	4.6	0.09	upregulate stage
444875	AI200759	Hs.44737	ESTs	6.85	0.11	upregulate stage
444888	AI651039	Hs.148559	ESTs	3.15	0.18	upregulate stage
445076	AI206888	Hs.154131	ESTs	7.81	0.09	upregulate stage
445182	AW189787	Hs.147474	ESTs	2	0.07	upregulate stage
445189	AI936450	Hs.147482	ESTs	2.65	0.12	upregulate stage
445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 fis, clone C	1.47	0.46	upregulate stage
445594	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	6.2	0.07	upregulate stage
445674	BE410347	Hs.13063	transcription factor CA150	3.8	0.15	upregulate stage
445817	NM_003642	Hs.13340	histone acetyltransferase 1	5.6	0.1	upregulate stage
445871	AI702901	Hs.145582	ESTs	2.3	0.33	upregulate stage
446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone H	2.15	0.18	upregulate stage
446553	AB021179	Hs.15299	HMBA-inducible	2.55	0.18	upregulate stage
446651	AA393907	Hs.97179	ESTs	8.05	0.07	upregulate stage
447086	AI421397	Hs.161321	ESTs	6.9	0.1	upregulate stage
447290	AI476732	Hs.263912	ESTs	2.35	0.18	upregulate stage
447379	AI554946	Hs.158794	ESTs	6.3	0.09	upregulate stage
447390	X95384	Hs.18426	translational inhibitor protein p14.5	7.25	0.08	upregulate stage
447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	1	0.24	upregulate stage
447548	N53388	Hs.7222	ESTs	8.6	0.07	upregulate stage
447731	AA373527	Hs.19385	CGI-58 protein	7.3	0.08	upregulate stage
447853	AI434204	Hs.164285	ESTs, Weakly similar to Afg1p [S.cerevis	6.75	0.11	upregulate stage
447857	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	2.2	0.24	upregulate stage
447965	AW292577	Hs.94445	ESTs	3.6	0.13	upregulate stage
448072	AI459306	Hs.24908	ESTs	5.8	0.11	upregulate stage
448474	AI792014	Hs.13809	ESTs	2.72	0.28	upregulate stage
448513	AA344741	Hs.61773	Homo sapiens cDNA FLJ11648 fis, clone HE	4.8	0.12	upregulate stage
448601	R61666	Hs.293690	ESTs	2.65	0.2	upregulate stage
448625	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22662 fis, clone H	1.68	0.44	upregulate stage
448735	AW473830	Hs.171442	ESTs	2.95	0.19	upregulate stage
448807	AI571940	Hs.7549	ESTs	2.3	0.14	upregulate stage
448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	8.6	0.08	upregulate stage
449448	D60730	Hs.57471	ESTs	1	0.13	upregulate stage
449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	6.4	0.11	upregulate stage
449585	AI655321	Hs.197693	ESTs	1	0.16	upregulate stage
449619	AI655992	Hs.300647	ESTs	8.35	0.09	upregulate stage
449659	R60031	Hs.198899	eukaryotic translation initiation factor	6.65	0.11	upregulate stage
449689	AF228421	Hs.301039	Human DNA sequence from clone RP1-132F21	8.35	0.06	upregulate stage
449901	AI674072		gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	5.8	0.1	upregulate stage
449964	AW001741	Hs.273193	hypothetical protein FLJ10706	8.7	0.09	upregulate stage
450170	AI685366	Hs.32775	ESTs	6.77	0.12	upregulate stage
450193	AI916071	Hs.224623	ESTs	5.73	0.1	upregulate stage
450336	AA046814	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone H	8.2	0.08	upregulate stage
450341	N90956	Hs.17230	hypothetical protein FLJ22087	4.2	0.19	upregulate stage
450353	AI244661	Hs.103296	ESTs	4.71	0.15	upregulate stage
450737	AW007152	Hs.203330	ESTs	2.14	0.25	upregulate stage
450795	AW173371	Hs.60435	ESTs	6	0.1	upregulate stage
450928	AI744417		gb:tr10h12.x1 NCI_CGAP_Ov23 Homo sapiens	1.75	0.18	upregulate stage
451134	AA318315	Hs.25999	hypothetical protein FLJ22195	4.3	0.1	upregulate stage
451230	BE546208	Hs.26090	hypothetical protein FLJ20272	4.75	0.16	upregulate stage
451593	AF151879	Hs.26706	CGI-121 protein	5.8	0.11	upregulate stage
451618	AA115639	Hs.26764	KIAA0546 protein	5.8	0.13	upregulate stage
451668	Z43948	Hs.26789	hypothetical protein FLJ10320	0.73	0.26	upregulate stage
451790	AA927403	Hs.43897	ESTs, Weakly similar to P2CA_HUMAN PROTE	3.2	0.25	upregulate stage
452001	AI827675	Hs.297735	Homo sapiens cDNA: FLJ22094 fis, clone H	3.7	0.13	upregulate stage
452039	AI922988	Hs.172510	ESTs	1	0.65	upregulate stage

452046	AB018345	Hs.27657	KIAA0802 protein	1.13	0.39	upregulate stage
452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.2	0.15	upregulate stage
452278	AL037715	Hs.28785	Homo sapiens mRNA; cDNA DKFZp586F0219 (f	8.25	0.07	upregulate stage
452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.34	upregulate stage
452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	4.97	0.13	upregulate stage
452714	AW770994	Hs.30340	hypothetical protein KIAA1165	7.6	0.09	upregulate stage
453078	AF053551	Hs.31584	metaxin 2	5.3	0.09	upregulate stage
453370	AI470523	Hs.182356	ESTs, Moderately similar to translation	3.78	0.13	upregulate stage
453765	BE279901	Hs.35091	hypothetical protein FLJ10775	3.95	0.11	upregulate stage
453972	AW137224	Hs.245869	ESTs	6	0.09	upregulate stage
454044	AW022393		gb:df37h12.y1 Morton Fetal Cochlea Homo	1.15	0.18	upregulate stage
454289	AL137554	Hs.49927	Homo sapiens mRNA; cDNA DKFZp434H1720 (f	7.05	0.1	upregulate stage
454314	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	1	0.37	upregulate stage
454315	AW373564	Hs.251928	nuclear pore complex interacting protein	2.7	0.13	upregulate stage
454775	BE160229		gb:QV1-HT0413-090200-062-a12 HT0413 Homo	8.5	0.09	upregulate stage
454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	1.15	0.14	upregulate stage
454792	AW820794	Hs.252406	hypothetical protein FLJ12296 similar to	3.65	0.12	upregulate stage
455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	5.7	0.07	upregulate stage
455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	1	0.25	upregulate stage
456141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	8.35	0.09	upregulate stage
456258	AW976410	Hs.289069	Homo sapiens cDNA: FLJ21016 fis, clone C	4.85	0.14	upregulate stage
456279	AW006783	Hs.6686	ESTs	7.25	0.1	upregulate stage
457518	AA825350	Hs.143805	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.84	0.11	upregulate stage
457570	AA579426	Hs.190226	ESTs	2.6	0.2	upregulate stage
457982	AW856093	Hs.183617	ESTs	1	0.25	upregulate stage
458080	BE142728		gb:MR0-HT0157-021299-004-d08 HT0157 Homo	2.05	0.27	upregulate stage
458340	AI457102	Hs.121583	Human glucose transporter pseudogene	2.25	0.18	upregulate stage
458440	AI095468	Hs.135254	ESTs, Weakly similar to thrombospondin t	2.35	0.13	upregulate stage
458771	AW295151	Hs.163612	ESTs	1	0.19	upregulate stage
459092	AA722012	Hs.255757	ESTs, Weakly similar to KIAA0611 protein	6.95	0.1	upregulate stage

TABLE 1B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT	Accessions
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408268	104987_1	AL138247 AA053529 BE173313
408277	1050131_1	AW177959 AW177960 AW178066 AW178022
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437251	435242_1	AW976082 AW976085 AA747803 AA747680
437274	435465_1	AA747965 AI248281 AI752458
437324	43609_1	AL162077 AW023677
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437798	443128_1	AW811767 AA831890 AW977539 AA768655
437854	44418_1	AL119723 AL119874 AI909018 U50537
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438316	454745_1	AA789249 AA904217 AA904142
438366	456119_1	AA805760 BE000856
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439183	46956_1	AW970600 AA503323 H89218 AF086031 H89112
439330	47119_1	AF086147 W20068 N91464

439550	473671_1	H10438 AA837479 H16299 AW978825
439780	47673_1	AL109688 R23665 R26578
440012	483290_1	AA861072 H02819 R25946
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442048	531432_1	AA974603 AI984319 AW340495
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447522	724922_1	BE143888 AI382949 T06429
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454554	1223842_1	AW847505 AW811792 BE061442 BE061433 AW847506 AW806999 AW806996 BE061436 BE061430 BE142460 BE146499 AW806994 AW809156 AW806991 AW814082 AW806992 BE061669 AW807002 BE146659 AW806995 AW807000 AW845743 AW845747 AW847504 BE142458 BE061431 BE061435 AW847507 BE146650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142465 BE142459 BE142462 AW854330 AW854331 BE061434 BE061731 BE142464 AW847501 AW807001 BE142463 AW811800 BE061437 AW811802 BE061440 AW806997 AW806998 BE061745 BE061753
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454637	1227707_1	AW811613 AW811611 AW811610
454648	1227976_1	AW811960 AW811957 AW811959
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454702	1229722_1	BE145915 BE145893 AW892892 BE145806 BE145901 AW814144
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455331	1280616_1	AW897292 AW897251 AW897298 AW897248 AW897259 AW897250 AW897246 AW897242
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455351	1284023_1	AW901942 AW901937 AW902016 AW901947
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455573	1332529_1	BE004988 BE004574
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455595	1335422_1	BE008343 BE008321 BE008326 BE008314 BE008345 BE008330 BE008344 BE008327
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455903	1381603_1	BE155185 BE155264 BE155186
455938	1384537_1	BE159432 BE159313 BE159295 BE159242
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455951	1385886_1	BE161001 BE162494 BE162470 BE161172
455965	1389984_1	BE167014 BE167058 BE167062
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456122	153360_1	R11813 AA164376 T56632
456212	1655565_1	N51636 T51874 T51829
456235	168686_1	AA203637 AA832266 H67452
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456592	202684_1	R91600 T87079 AA291455
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457340	322100_1	AA492071 AA484229 AW969850
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457437	337879_1	AW969732 AW970974 AA515741
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458080	471050_1	BE142728 AA834047 AW937124
458172	497769_1	BE007237 BE007496 BE007263 W19919 BE546311 AA984819
458781	743159_1	AI444821 W26012
458841	784186_1	W28965 W28971
458880	80785_1	AA046742 AA551269 AA001505
459028	868710_1	AI940577 AI940580 AI940568 AI940578 AI940569 AI795858 AI795867 AI940572
459128	918011_1	AI902169 AI902173 AI902323 AI902174 AI902347
459182	922744_1	BE178517 AI908132 BE142437

TABLE 1C

Pkey: Unique number corresponding to an Eos probeset

Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400471	9931670	Minus	105629-105760
400495	9714773	Minus	61902-62137
400528	6981824	Plus	472381-472528,474170-474277,475328-475542,475878-476000
400577	7960401	Plus	101535-101881
400608	9887666	Minus	96756-97558
400641	8117693	Plus	4786-4992
400644	8117693	Plus	27682-27840
400666	8118496	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
400750	8119067	Plus	198991-199168,199316-199548
400751	7331445	Minus	35395-35533
400761	8131609	Minus	114220-115164
400762	8131616	Plus	7235-7605
400773	8131629	Minus	44116-44238,48208-48321
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
400845	9188605	Plus	34428-34612
400846	9188605	Plus	39310-39474
400860	9757499	Minus	151830-152104,152649-152744
400880	9931121	Plus	29235-29336,36363-36580
400887	9958187	Plus	119239-121542
400888	9958187	Minus	199600-199875
400937	7652890	Minus	89519-89905
400977	8072510	Plus	73950-74364
401002	8117251	Minus	77898-78050
401024	8117489	Plus	60551-60802
401045	8117619	Plus	90044-90184,91111-91345
401048	7232177	Plus	132430-132761
401049	7232177	Plus	149157-150692
401086	9957912	Plus	84561-84884
401093	8516137	Minus	22335-23166
401101	8568122	Plus	77081-77226
401192	9719502	Minus	69559-70101
401197	9719705	Plus	176341-176452
401203	9743387	Minus	172961-173056,173868-173928
401205	9743388	Plus	167373-167433,167936-168031
401256	9796573	Minus	45482-45620
401262	9796963	Plus	35662-35799
401271	9797373	Minus	61292-61911
401276	8954274	Minus	15919-16096
401279	9800062	Minus	13535-13669
401342	9908882	Plus	3096-3242
401365	9796180	Minus	119572-119672
401395	7327842	Minus	11502-11771,46357-46489,58720-58916
401420	7452889	Minus	141362-141502
401439	8246737	Plus	92993-94026
401451	6634068	Minus	119926-121272
401508	7534110	Minus	110779-110983
401519	6649315	Plus	157315-157950
401537	7960358	Minus	186786-187029,190607-190779,198218-198348
401561	8224660	Minus	10652-10838,19815-20018
401566	8469090	Minus	96277-96420,96979-97160
401604	7689963	Minus	119835-120185
401619	8516761	Minus	141309-143576
401669	9801805	Plus	25414-26310
401691	3582311	Plus	162333-162715
401694	3540172	Minus	64056-64168
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401759	9929699	Plus	59811-60665
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401866	8018106	Plus	73126-73623
401905	8671966	Plus	153965-154441,156599-156819
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402001	9501818	Plus	68052-68223
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126078
402076	8117410	Plus	128316-128627
402089	7249154	Plus	101610-101819
402110	8131678	Minus	173889-174062

402176	7543687	Minus	10-750
402230	9966312	Minus	29782-29932
402245	7690231	Minus	88253-88417
402296	6598824	Plus	22587-23723
402325	7636348	Minus	60658-60738,61677-61803
402407	3962498	Minus	115812-116187
402408	9796239	Minus	110326-110491
402430	9796372	Minus	62382-62552
402435	9796462	Plus	114593-115588
402472	9797116	Plus	53716-54470
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402480	9797375	Plus	59708-59999
402490	9797648	Plus	149982-150929
402522	9798493	Plus	20605-20731
402530	7630937	Minus	1524-2003
402546	7637348	Plus	24673-25170
402553	9863566	Plus	48292-48398,49564-49944
402604	9909420	Plus	20393-20767
402716	8969253	Minus	84065-84242
402727	9211324	Plus	54596-54777
402812	6010110	Plus	25026-25091,25844-25920
402820	6456853	Minus	82274-82443
402846	9408716	Minus	5726-5850
402889	9931133	Plus	89392-89498,90358-90571
402892	8086844	Minus	194384-194645
402901	8894222	Minus	175426-175667
402922	8216969	Minus	19036-19401,19589-19849,19951-20102
402938	8953442	Plus	22365-22473
402995	2996643	Minus	5962-6216
403005	5791501	Minus	16945-17053,20018-20403
403020	6984114	Minus	96644-97021,97462-97868
403029	7768593	Minus	44558-44766
403047	3540153	Minus	59793-59968
403073	8954241	Plus	142964-143260
403085	8954241	Plus	165035-165334,165420-165713
403092	8954241	Plus	174720-175016,175104-175406,175508-175813
403106	7331404	Plus	77162-77350,81338-81511
403172	7464784	Minus	64007-64275
403212	7630897	Minus	156037-156210
403214	7630945	Minus	76723-77027,79317-79484
403277	8072597	Minus	27494-27642
403331	8567936	Plus	169793-169966
403344	8569726	Plus	70823-70990
403362	8571772	Plus	64099-64260
403381	9438267	Minus	26009-26178
403426	9719529	Minus	157156-158183
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
403567	8101141	Plus	35349-35614
403588	8101227	Minus	197672-197944
403590	8101229	Plus	405-1296
403615	8567964	Plus	107671-107866
403687	7387384	Plus	9009-9534
403754	7229815	Minus	163899-164726
403776	7770611	Minus	1414-1513,1624-1756
403822	9369510	Minus	142803-142922
403851	7708872	Plus	22733-23007
403860	7708960	Minus	95755-96045
403894	7381715	Minus	1442-2224
403903	7710671	Minus	101165-102597
403959	8224399	Minus	175363-177474
404015	8655948	Minus	587821-588222
404059	3548785	Plus	104326-106788
404113	9588571	Minus	13446-13646
404148	9863703	Plus	78218-78418,79571-79709
404152	9884757	Plus	41111-41281,45495-45716,47801-47910
404156	9886577	Plus	127319-127754
404229	7159766	Plus	16607-16841
404232	8218045	Minus	71800-71956
404268	9711362	Plus	33238-33463
404274	9885189	Plus	104127-104318
404288	2769644	Plus	3512-3691
404290	2769644	Plus	36651-36813
404336	9838028	Plus	157951-158129
404403	7272157	Minus	72053-72238
404440	7528051	Plus	80430-81581
404488	8113286	Minus	64835-64994
404498	8151654	Plus	13292-13497

404507	8151803	Plus	146359-146739
404516	8151967	Plus	114153-114322
404538	8247909	Minus	192748-192945
404594	9958262	Minus	15310-15510
404639	9796778	Plus	5779-14387
404653	9796999	Plus	164997-165230
404676	9797204	Minus	56167-56342,58066-58189,58891-59048,60452-60628
404684	9797403	Minus	110881-111020
404685	9797437	Minus	153217-153315,154043-154124,159185-159353,161290-161420,163544-163669,166127-166207,167654-167734
404704	9800728	Minus	88841-89018
404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
404829	6624702	Minus	4913-5093,7310-7469,9472-9621,9951-10082
404860	8979555	Plus	65852-66081
404874	9650523	Minus	96066-96192
404881	5931510	Minus	36360-36608
404894	6850447	Plus	102822-103127
404939	6862697	Plus	175318-175476
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
405059	7656683	Plus	349-822
405064	7658416	Plus	81207-81416
405071	7708797	Minus	11115-11552
405102	8076881	Minus	120922-121296
405167	9966316	Plus	43796-43981,48245-48427,54141-54317
405170	9966524	Plus	37047-37198
405177	7139696	Minus	118466-118663
405186	7229793	Plus	161475-161581,162930-163067
405258	7329310	Plus	129930-130076
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405308	3638954	Plus	40778-41034,41383-41573
405349	2914717	Minus	85552-85806
405379	6513908	Minus	22332-22473,24333-24439
405390	6606064	Minus	94007-94177
405411	3451356	Minus	17503-17778,18021-18290
405463	7715630	Minus	123097-123260
405494	8050952	Minus	70284-70518
405520	9454643	Plus	60849-60981
405526	9558556	Minus	132704-133277
405580	4512267	Plus	169232-169647
405600	5923640	Plus	26662-27225
405654	4895155	Minus	53624-53759
405720	9797144	Plus	13409-13861
405725	9838299	Minus	106417-106521
405735	9931101	Minus	29854-29976
405738	9943998	Plus	44370-45410
405809	5304920	Minus	6655-6883,8687-8859
405838	5686575	Plus	3460-3717
405863	7657810	Plus	49410-49620
405867	6758731	Minus	74553-75173
405906	7705124	Minus	10835-11059
405920	6758795	Plus	120621-120971
405968	8247789	Plus	14893-15148
406017	8272661	Minus	46271-46874
406036	6758919	Plus	17942-18163
406081	9123861	Minus	38115-38691
406137	9166422	Minus	30487-31058
406187	7289992	Plus	8044-8877
406243	7417725	Plus	38899-39369
406270	7534217	Plus	13136-13591
406320	9211754	Minus	20170-20511
406322	9212102	Minus	130230-130418
406360	9256107	Minus	7513-7673
406367	9256126	Minus	58313-58489
406397	9256243	Minus	127317-127454
406399	9256288	Minus	63448-63554
406434	9256651	Minus	17803-17931
406467	9795551	Plus	182212-182958
406471	9795566	Plus	87383-87589
406475	9797684	Plus	125417-125563,128052-128180
406485	7711305	Plus	125036-125422
406511	7711412	Plus	177277-177384
406588	8189273	Minus	135629-135848

TABLE 2A: 485 GENES UP-REGULATED IN BLADDER CANCER

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of mRNA expression in bladder tumors compared to normal bladder

Pkey	ExAccn	UnigeneID	Unigene Title	R1
418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	3.473
412841	AI751157	Hs.101395	hypothetical protein MGC11352	2.279
421066	AU076725	Hs.101408	branched chain aminotransferase 2, mitoc	3.052
435136	R27299	Hs.10172	ESTs	4.717
444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	0.003
421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	188.231
421318	U63973	Hs.103501	rhodopsin kinase	1.381
421359	AK001589	Hs.103816	hypothetical protein FLJ10727	1.000
459462	AA481396	Hs.105167	ESTs	1.000
430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.000
433227	AB040923	Hs.106808	kelch (Drosophila)-like 1	1.000
421742	AW970004	Hs.107528	androgen induced protein	1.514
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	2.782
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	20.064
451686	AA059246	Hs.110293	ESTs	0.033
454417	AI244459	Hs.110826	trinucleotide repeat containing 9	56.751
458760	AI498631	Hs.111334	ferritin, light polypeptide	2.512
422119	AI277829	Hs.111862	KIAA0590 gene product	2.634
422170	AI791949	Hs.112432	anti-Mullerian hormone	0.055
441877	AW273802	Hs.11340	hypothetical protein FLJ23047	0.008
445958	BE326257	Hs.114536	ESTs	0.002
434288	AW189075	Hs.116265	fibrillin3	11.401
435347	AW014873	Hs.116963	ESTs	0.003
453134	AA032211	Hs.118493	ESTs	262.962
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	5.336
436154	AA764950	Hs.119898	ESTs	103.154
436246	AW450963	Hs.119991	ESTs	0.071
436293	AI601188	Hs.120910	ESTs	29.129
433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	274.769
438181	AW978608	Hs.122121	ESTs, Weakly similar to I38022 hypotheti	0.024
449399	AA760881	Hs.122408	ESTs	1.000
437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheti	4.314
457465	AW301344	Hs.122908	DNA replication factor	0.264
409757	NM_001898	Hs.123114	cystatin SN	1.390
439907	AA853978	Hs.124577	ESTs	0.010
437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.344
440304	BE159984	Hs.125395	ESTs	0.025
423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	0.014
441495	AW294603	Hs.127039	ESTs	0.198
435376	AW770956	Hs.127280	ESTs	0.008
427685	AI751124	Hs.127311	ESTs	3.244
423349	AF010258	Hs.127428	homeo box A9	0.134
445457	AF168793	Hs.12743	carnitine O-octanoyltransferase	7.255
420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.000
441875	AI435973	Hs.128056	ESTs	0.013
441940	AW298115	Hs.128152	ESTs	6.075
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	0.137
429983	W92620	Hs.128656	ESTs	162.590
445600	AF034803	Hs.12953	PTPRF interacting protein, binding prote	0.969
437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	9.163
459204	AW194601	Hs.13219	ESTs	1.000
439842	AI910896	Hs.132413	ESTs	1.000
443113	AI040686	Hs.132908	ESTs	0.069
423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	0.100
420792	AA280321	Hs.13392	tethering factor SEC34	16.103
427719	AI393122	Hs.134726	ESTs	0.667
443861	AW449462	Hs.134743	ESTs	5.100
447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28/cdc	1.691
445550	AI242754	Hs.137306	ESTs	0.006
454284	AW297935	Hs.138493	ESTs, *Moderately similar to* ALU7_HUMAN A	0.003
418937	T71508	Hs.13861	ESTs, Weakly similar to T42383 probable	0.042
424098	AF077374	Hs.139322	small proline-rich protein 3	1.347
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	0.186
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	47.949
426900	AW163564	Hs.142375	ESTs	0.404
439337	AA448718	Hs.142505	ESTs	0.012

427961	AW293165	Hs.143134	ESTs	0.073
419888	AI243493	Hs.144049	ESTs	11.958
413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	77.269
445871	AI702901	Hs.145582	ESTs, Weakly similar to FOR4 MOUSE FORMI	183.782
445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.362
424395	AA165082	Hs.146388	microtubule-associated protein 7	203.038
424411	NM_005209	Hs.146549	crystallin, beta A2	1.808
444517	AI939339	Hs.146883	ESTs	0.004
445020	AI205655	Hs.147221	ESTs	0.307
422109	S73265	Hs.1473	gastrin-releasing peptide	1.000
445352	AI221087	Hs.147761	ESTs	0.015
444444	AI149332	Hs.14855	ESTs	140.859
444152	AI125694	Hs.149305	hypothetical protein MGC2603	2.037
446248	AI283014	Hs.149638	ESTs	0.018
433159	AB035898	Hs.150587	kinesin-like protein 2	0.110
428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.179
456840	H03754	Hs.152213	wingless-type MMTV integration site fami	0.005
456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	1.111
425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	257.949
446082	AI274139	Hs.156452	ESTs	0.779
444946	AW139205	Hs.156457	hypothetical protein FLJ22408	1.919
446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	0.417
447073	AW204821	Hs.157726	ESTs	10.349
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	1.839
446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	1.691
447475	AI380797	Hs.158992	ESTs	44.641
425776	U25128	Hs.159499	parathyroid hormone receptor 2	0.340
418343	AA216372	Hs.159501	ESTs	0.023
441143	AI027604	Hs.159650	ESTs	0.280
440917	AA909651	Hs.160025	ESTs	1.000
418365	AW014345	Hs.161690	ESTs	0.066
431839	AW020280	Hs.162025	ESTs	0.005
446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	0.606
438817	AI023799	Hs.163242	ESTs	2.202
432441	AW292425	Hs.163484	ESTs	2.305
442577	AA292998	Hs.163900	ESTs	688.038
435212	AW300100	Hs.164185	ESTs	0.002
425048	H05468	Hs.164502	ESTs	0.083
442083	R50192	Hs.165062	ESTs	3.844
423536	L22075	Hs.1666	guanine nucleotide binding protein (G pr	0.157
418678	NM_001327	Hs.167379	cancer/testis antigen	269.487
446989	AK001898	Hs.16740	hypothetical protein FLJ11036	0.208
456967	AW004056	Hs.168357	T-box 2	160.397
447979	AI457197	Hs.170348	ESTs	0.016
458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	1.036
446312	BE087853	Hs.171802	ESTs, Weakly similar to T08729 RING zinc	1.334
426783	Z19084	Hs.172210	MUF1 protein	1.654
423916	AW993496	Hs.17235	Homo sapiens clone TCCCIA00176 mRNA sequ	154.064
409092	AI735283	Hs.172608	ESTs	0.007
426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	0.009
426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	0.002
407581	R48402	Hs.173508	P3ECSL	0.866
427239	BE270447	Hs.174070	ubiquitin carrier protein	15.708
427268	X78520	Hs.174139	chloride channel 3	207.936
436577	W84774	Hs.17643	ESTs	62.333
420876	AA918425	Hs.177744	ESTs	32.959
427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	1.171
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.000
427747	AW411425	Hs.180655	serine/threonine kinase 12	12.446
429813	AW139678	Hs.180791	ESTs	0.013
439808	AA846824	Hs.180908	ESTs	0.561
427878	C05766	Hs.181022	CGI-07 protein	0.002
440284	AA912032	Hs.181059	ESTs, Weakly similar to 2108276A ssDNA-b	0.030
427922	AK001934	Hs.181112	HSPC126 protein	0.039
427972	AA864870	Hs.181304	putative gene product	0.004
428071	AF212848	Hs.182339	ets homologous factor	4.321
428336	AA503115	Hs.183752	microseminoprotein, beta-	145.128
428450	NM_014791	Hs.184339	KIAA0175 gene product	0.370
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	0.632
438746	AI885815	Hs.184727	ESTs	0.339
420557	AA960844	Hs.186579	Homo sapiens, clone IMAGE:4081483, mRNA	0.006
431014	W67730	Hs.187573	ESTs	0.344
428651	AF196478	Hs.188401	annexin A10	1.459
416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	0.502
432497	AA551104	Hs.189048	ESTs, Moderately similar to ALUC_HUMAN !	2.499
431474	AL133990	Hs.190642	ESTs	0.044
427742	AA411880	Hs.190888	ESTs	0.158

428058	AI821625	Hs.191602	ESTs	0.006
431245	AA496933	Hs.191687	ESTs	0.006
453204	R10799	Hs.191990	ESTs	1.734
436608	AA628980	Hs.192371	down syndrome critical region protein DS	115.500
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	0.152
454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	60.103
449121	AI915858	Hs.194980	ESTs	0.003
447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	305.974
438401	AL046321	Hs.197484	ESTs, Weakly similar to JC4296 ring fing	0.002
457200	U33749	Hs.197764	thyroid transcription factor 1	0.011
429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	9.390
429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	178.436
429276	AF056085	Hs.198612	G protein-coupled receptor 51	0.729
449818	AW594365	Hs.199365	ESTs	1.000
429345	R11141	Hs.199695	hypothetical protein	7.339
443564	AI921685	Hs.199713	ESTs	0.001
449847	AW204447	Hs.199750	organic anion transporter polypeptide-re	1.000
449351	AW016537	Hs.200760	ESTs	0.005
426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	381.474
434411	AA632649	Hs.201372	ESTs	0.039
448045	AJ297436	Hs.20166	prostate stem cell antigen	2.337
446555	AV659046	Hs.201847	ESTs	0.024
450411	D61167	Hs.202156	ESTs	0.004
442282	AW451086	Hs.202390	ESTs	1.000
427587	BE348244	Hs.202628	ESTs, Weakly similar to I78885 serine/th	228.705
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	0.133
426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.070
426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	0.528
448275	BE514434	Hs.20830	kinesin-like 2	19.718
459058	H85939	Hs.209605	EST	0.005
441795	N58115	Hs.21137	AD024 protein	1.000
451592	AI805416	Hs.213897	ESTs	0.012
443367	AW071349	Hs.215937	ESTs	0.003
415949	H10562	Hs.21691	ESTs	0.072
444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLIC	213.962
432548	AW973399	Hs.22133	hypothetical protein FLJ20121	0.250
427867	NM_005073	Hs.2217	solute carrier family 15 (oligopeptide t	0.010
453123	AI953718	Hs.221849	ESTs	0.566
439569	AW602166	Hs.222399	CEGP1 protein	10.625
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	27.603
435956	AF269255	Hs.22604	lysosomal apyrase-like protein 1	127.564
453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptiona	2.216
431253	R06428	Hs.226351	ESTs	0.023
453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.103
430034	X60155	Hs.227767	zinc finger protein 41	1.000
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	0.024
417997	AA418189	Hs.23017	Homo sapiens cDNA: FLJ22747 fis, clone K	1.635
441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	120.167
452956	AW003578	Hs.231872	ESTs	1.000
446009	AI989885	Hs.231926	ESTs	4.000
430499	AW969408	Hs.231991	ESTs	0.014
448560	BE613183	Hs.23213	ESTs	285.090
441508	AW015203	Hs.232237	ESTs	0.261
453228	AW628325	Hs.232327	ESTs	1.000
442167	H18740	Hs.23248	hypothetical protein from EUROIMAGE 2005	0.240
453321	AI984381	Hs.232521	ESTs	0.609
449207	AL044222	Hs.23255	nucleoporin 155kD	0.551
430152	AB001325	Hs.234642	aquaporin 3	1.040
439239	AI031540	Hs.235331	ESTs	0.598
435087	AW975241	Hs.23567	ESTs	0.007
451276	AW294386	Hs.236533	ESTs, Highly similar to dJ742C19.2 [H.sa	0.012
447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	1.280
431011	AA490631	Hs.23783	ESTs	0.016
430307	BE513442	Hs.238944	hypothetical protein FLJ10631	284.526
444371	BE540274	Hs.239	forkhead box M1	3.691
424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	0.255
449722	BE280074	Hs.23960	cyclin B1	0.467
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	13.419
430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.192
452292	AW139588	Hs.244369	ESTs	1.000
412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	2.500
456682	AW500321	Hs.246766	Homo sapiens cDNA FLJ12360 fis, clone MA	0.014
457343	NM_013936	Hs.247862	olfactory receptor, family 12, subfamily	0.233
430978	U53583	Hs.248182	olfactory receptor, family 1, subfamily	1.000
431020	AF097874	Hs.248226	caspase 14, apoptosis-related cysteine p	5.866
431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.838
431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoisoadenylate	0.004

454170	AW177225	Hs.250158	ESTs	0.243
439223	AW238299	Hs.250618	UL16 binding protein 2	0.516
438081	H49546	Hs.251391	claudin 16	0.080
431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	843.974
450663	H43540	Hs.25292	ribonuclease HI, large subunit	5.928
450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.000
413094	H24184	Hs.25413	TOLLIP protein	268.885
450796	NM_001988	Hs.25482	envoplakin	1.643
408827	AW275730	Hs.254825	ESTs	0.008
444129	AW294292	Hs.256212	ESTs	0.002
430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	3.240
436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	0.679
450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	260.231
453459	BE047032	Hs.257789	ESTs	2.133
456536	AW135986	Hs.257859	ESTs	98.795
438424	AI912498	Hs.25895	hypothetical protein FLJ14996	1.882
451161	AA211329	Hs.26006	hypothetical protein FLJ10559	0.012
430634	AI860651	Hs.26685	calcyphosine	9.561
435562	AL046988	Hs.268677	ESTs, Moderately similar to ALU7_HUMAN A	0.957
417964	R71449	Hs.268760	ESTs	0.004
445703	AV654845	Hs.27	glycine dehydrogenase (decarboxylating;	1.324
431846	BE019924	Hs.271580	uroplakin 1B	303.679
453074	AA031813	Hs.271880	ESTs	0.004
431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.828
435182	AA669386	Hs.272035	ESTs, Weakly similar to gonadotropin ind	0.013
430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU S	8.978
432136	AA157632	Hs.272630	*vacuolar proton pump delta polypeptide*	0.316
451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	0.014
451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	26.348
423031	AI278995	Hs.27457	ESTs	53.288
455612	BE042896	Hs.274848	ESTs	21.013
452046	AB018345	Hs.27657	KIAA0802 protein	129.013
436567	AI492860	Hs.276904	ESTs	0.007
459006	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	0.031
430157	BE348706	Hs.278543	ESTs	99.244
452012	AA307703	Hs.279766	kinesin family member 4A	0.408
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.721
458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	38.231
450020	AI680684	Hs.282219	ESTs	0.003
435858	AF254260	Hs.283009	tuftelin 1	1.516
430733	AW975920	Hs.283361	ESTs	1.000
446024	AB040946	Hs.284227	KIAA1513 protein	9.424
433967	AF113018	Hs.284302	PRO1621 protein	0.008
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	0.030
431958	X63629	Hs.2877	*cadherin 3, type 1, P-cadherin (placenta*	1.058
414595	AA641726	Hs.289015	hypothetical protein MGC4171	273.013
432097	X51730	Hs.2905	progesterone receptor	0.002
452345	AA293279	Hs.29173	hypothetical protein FLJ20515	4.010
457733	AW974812	Hs.291971	ESTs	1.000
441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	1.000
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	0.006
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	0.003
433365	AF026944	Hs.293797	ESTs	0.049
417151	AA194055	Hs.293858	ESTs	6.593
424242	AA337476	Hs.293984	hypothetical protein MGC13102	1.656
432375	BE536069	Hs.2962	S100 calcium-binding protein P	17.094
422424	AI186431	Hs.296638	prostate differentiation factor	2.646
432410	X68561	Hs.2982	Sp4 transcription factor	0.007
426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.005
454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT	0.488
452142	AB028947	Hs.301654	KIAA1024 protein	0.009
449773	R76294	Hs.302383	ESTs	0.001
438366	AA805760	Hs.303567	ESTs	1.000
452724	R84810	Hs.30464	cyclin E2	1.000
429343	AK000785	Hs.307036	*Homo sapiens, Similar to epsin 3, clone*	0.494
446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	0.022
430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	16.744
432789	D26361	Hs.3104	KIAA0042 gene product	0.302
432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	0.001
453028	AB006532	Hs.31442	RecQ protein-like 4	13.392
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.766
427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	553.782
453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	84.115
443247	BE614387	Hs.333893	c-Myc target JPO1	79.385
439632	AW410714	Hs.334437	hypothetical protein MGC4248	337.474
431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	0.842
411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	402.500

433958	AW043909	Hs.334707	aminoacylase 1	191.179
432842	AW674093	Hs.334822	hypothetical protein MGC4485	313.462
457292	AI921270	Hs.334882	hypothetical protein FLJ14251	21.744
451359	H85334	Hs.336623	ESTs	0.038
440249	AI246590	Hs.337275	ESTs	0.432
434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	1.102
447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	0.483
447519	U46258	Hs.339665	ESTs	1.032
434192	AW387314	Hs.34371	ESTs	0.003
453765	BE279901	Hs.35091	hypothetical protein FLJ10775	0.056
441020	W79283	Hs.35962	ESTs	75.141
453884	AA355925	Hs.36232	KIAA0186 *gene product*	0.138
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	0.008
453945	NM_005171	Hs.36908	activating transcription factor 1	0.044
447289	AW247017	Hs.36978	melanoma antigen, family A, 3	0.002
407626	U39196	Hs.37169	potassium inwardly-rectifying channel, s	0.009
423620	N71320	Hs.39938	ESTs	1.000
436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	0.042
407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	1.810
443133	AI033878	Hs.41379	ESTs	0.534
434534	H90477	Hs.41407	ESTs	0.013
452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.679
434952	T10269	Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	2.885
432237	AK001926	Hs.44143	polybromo 1	0.010
420900	AL045633	Hs.44269	ESTs	10.436
408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	3.393
435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	386.256
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	0.922
408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	0.003
435647	AI653240	Hs.49823	ESTs	175.910
435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.584
436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	0.610
455506	AA703584	Hs.5105	hypothetical protein FLJ10569	0.008
436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.089
409287	AL080213	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	16.910
435047	AA454985	Hs.54973	cadherin-like protein VR20	0.612
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	5.938
439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	1.000
439482	W70045	Hs.58089	ESTs	0.118
439606	W79123	Hs.58561	G protein-coupled receptor 87	0.095
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	0.055
452240	AI591147	Hs.61232	ESTs	0.221
452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	2.595
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.677
434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	7.587
444783	AK001468	Hs.62180	*anillin (Drosophila Scraps homolog), act*	0.046
438779	NM_003787	Hs.6414	nucleolar protein 4	0.030
439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	12.016
440126	AA975145	Hs.66194	ESTs	0.008
451291	R39288	Hs.6702	ESTs	0.012
439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	1.653
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	8.628
437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	140.908
418107	R41726	Hs.7284	ESTs	0.146
436326	BE085236	Hs.75313	aldo-keto reductase family 1, member B1	0.649
433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	0.237
414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.242
414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	0.202
414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	2.318
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.622
414907	X90725	Hs.77597	*polo (Drosophia)-like kinase*	246.564
451575	AA767622	Hs.78893	KIAA0244 protein	1.000
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	4.552
416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	5.128
458921	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	0.246
409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypotheti	7.249
440371	BE268550	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.792
452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	360.782
417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	60.590
407584	W25945	Hs.8173	hypothetical protein FLJ10803	9.988
417312	AW888411	Hs.81915	leukemia-associated phosphoprotein p18 (	402.705
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	10.806
428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	1.051
438315	R56795	Hs.82419	ESTs	0.226
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	26.260
417933	X02308	Hs.82962	thymidylate synthetase	221.090
418067	AI127958	Hs.83393	cystatin E/M	2.396

438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	1.000
418205	L21715	Hs.83760	troponin I, skeletal, fast	0.159
413385	M34455	Hs.840	Indoleamine-pyrrole 2,3 dioxygenase	0.490
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.527
413529	U11874	Hs.846	interleukin 8 receptor, beta	0.077
458027	L49054	Hs.85195	myeloid leukemia factor 1	0.008
418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.813
418583	AA604379	Hs.86211	hypothetical protein	125.769
441801	AW242799	Hs.86366	ESTs	55.026
414792	BE314949	Hs.87128	hypothetical protein FLJ23309	8.139
407246	S70348	Hs.87149	Integrin, beta 3 (platelet glycoprotein	0.020
433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	313.141
445060	AA830811	Hs.88808	ESTs	1.000
453450	AW797627	Hs.89474	ADP-ribosylation factor 6	137.718
419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	0.006
401464	AF039241	Hs.9028	histone deacetylase 5	6.846
443162	T49951	Hs.9029	DKFZP434G032 protein	14.057
431024	AA713666	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.507
419559	Y07828	Hs.91096	ring finger protein	0.025
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	684.577
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	0.363
424457	AI249036	Hs.94292	hypothetical protein FLJ23311	175.667
410348	AW182663	Hs.95469	ESTs	0.011
439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	428.231
421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	0.005
443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	1.168
426902	AI125334	Hs.97408	ESTs	37.467
444874	AI218496	Hs.97515	BRCA1-Interacting protein 1; BRCA1-assoc	0.067
427356	AW023482	Hs.97849	ESTs	1.000
430000	AW205931	Hs.99598	hypothetical protein MGC5338	0.812
419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	0.342
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	19.785
421934	AA300625		gb:EST13476 Testis tumor Homo sapiens cD	103.769
431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.258
424040	AA334400		gb:EST38610 Embryo, 9 week Homo sapiens	0.011
433108	AB002446		gb:Homo sapiens mRNA from chromosome 5q2	0.023
458829	AI557388		gb:PT2.1_6_G03.r tumor2 Homo sapiens cDN	1.000
459169	AI905517		gb:RC-BT091-210199-105 BT091 Homo sapien	0.773
400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	468.462
440012	AA861072		gb:ak32e05.s1 Soares_testis_NHT Homo sap	0.002
412799	AI267606		gb:aq91h03.x1 Stanley Frontal SB pool 1	0.010
412964	BE019688		gb:bb28g08.x1 NIH_MGC_5 Homo sapiens cDN	0.003
406992	S82472		gb:beta -pol=DNA polymerase beta (exon a	0.005
414969	C16195		gb:C16195 Clontech human aorta polyA mRN	0.023
413158	BE068098		gb:CM1-BT0368-061299-060-c09 BT0368 Homo	0.007
453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	0.994
453846	AL157586		gb:DKFZp761H0216_r1 761 (synonym: hamy2)	0.004
407055	X89211		gb:H.sapiens DNA for endogenous retrovir	0.037
415204	T27434		gb:hbc2294 Human pancreatic Islet Homo s	76.500
434572	AF147340		gb:Homo sapiens full length insert cDNA	0.030
438990	AF085890		gb:Homo sapiens full length insert cDNA	1.000
439780	AL109688		gb:Homo sapiens mRNA full length insert	0.256
413671	Z43712		gb:HSC1JA121 normalized infant brain cDN	0.009
406974	M57293		gb:Human parathyroid hormone-related pep	0.004
455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.616
455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	0.413
432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	0.015
443309	AI821874		gb:nl58f10.x5 NCI_CGAP_Pr3 Homo sapiens	0.007
437240	AA747537		gb:nx85c05.s1 NCI_CGAP_GCB1 Homo sapiens	0.006
455189	AW864176		gb:PM0-SN0014-260400-002-b08 SN0014 Homo	0.069
444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	394.282
455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	0.757
454789	BE156314		gb:QV0-HT0367-150200-114-d02 HT0367 Homo	1.000
433005	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	0.013
455380	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	0.249
455650	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	1.000
436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	1.000
413100	BE065208		gb:RC1-BT0314-310300-015-b09 BT0314 Homo	271.372
428436	BE080180		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	0.002
455831	BE144966		gb:RC6-HT0187-201099-031-c04 HT0187 Homo	0.011
434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	293.654
414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	0.807
409488	AW402825		gb:UI-HF-BK0-aaq-d-08-0-UI.r1 NIH_MGC_36	0.965
437938	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	2.952
451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	7.341
449325	AA001162		gb:ze48b06.r1 Soares retina N2b4HR Homo	0.004
413316	W91931		gb:zh47c01.r1 Soares_fetal_liver_spleen_	0.004

401016		0.342
401335		0.256
401555		1.000
401760		301.372
401781		247.141
401961		1.722
402239		5.180
402305		0.917
402424		551.141
402777		153.231
402778		0.008
402837		0.367
402948		154.103
402952		17.038
403142		0.196
403297		12.744
403637		0.304
403657		0.032
404136		0.008
404249		0.065
404875		1.105
404917		69.590
404983		1.000
405238		1.000
405364		294.141
405531		1.747
405601		145.551
405621		0.224
405932		1.968
406117		0.333
406354		1.000
406548		0.002
406599		0.010
459702	AI204995	0.449

TABLE 2B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409488	1134791_1	AW402825 BE544338
412799	132817_1	AI267606 AA121045 AA126521
412964	1339278_1	BE019688 BE144460
413100	1349119_1	BE065208 BE065224 BE065168 BE065313
413158	1351251_1	BE068098 BE068119 BE068083 BE068088 BE068120 BE068155 BE068111
413316	1360169_1	W91931 W94979 BE081744
413671	1382504_1	Z43712 BE156729 BE156538 BE156731 BE156673 BE156539 BE156674 BE156430 BE156672 BE156675 BE156432 BE156541
414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
414969	1510393_1	C16195 C16230 C16211 C16164 C16251
415204	1529407_1	T27434 Z25288 F00323 D82802 R85077
421934	209339_1	AA300625 R16859 R16860 AW898335 W24337
424040	234659_1	AA334400 AA334257 AW966124
428436	291472_1	BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311 AA429538
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
432189	342819_1	AA527941 AI810608 AI620190 AA635266
433005	357346_1	AW939074 AW939073 BE160476 AW939938 AW939206 AW940012 AW939076 AA573577 AW750479 AA574383 AW970057
433108	35896_1	AB002446 T03146
434414	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570
434572	38911_1	AF147340 T51948 T52029
436383	41888_1	BE065178 AJ227879
437240	435139_1	AA747537 BE089068 BE089070
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996

		AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438990	46760_1	AF085890 H29949 H29856
439780	47673_1	AL109688 R23665 R26578
440012	483290_1	AA861072 H02819 R25946
443309	56604_1	AI821874 AI821868 AA630932 AA653897 AA650103 AI821131 AI821124
444163	593658_1	AI126098 AI184746 AI148521
449325	80480_1	AA001162 AA018950 AA017505 R84446
451385	86787_1	AA017656 AA017374 AA019761
453823	982526_1	AL137967 BE064160 BE064186
453846	983043_1	AL157586 AL157590
454789	1234742_1	BE156314 BE156316 AW820750
455170	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
455189	1259271_1	AW864176 AW864133 AW864185 AW864137
455380	1287679_1	BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
455650	1348720_1	BE064655 BE153953
455797	1366826_1	BE091833 BE091874 BE091871
455807	1370914_1	BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
455831	1373969_1	BE144966 BE144957 BE144958
458829	773443_1	AI557388 BE158936
459169	920641_1	AI905517 AI905455 AI905452

TABLE 2C

Pkey: *Unique number corresponding to an Eos probeset*
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401016	8117441	Plus	126234-126359,128050-128236
401335	9884881	Plus	15736-16352
401555	8099284	Minus	162520-162657
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401961	4581193	Minus	124054-124209
402239	7690131	Plus	38175-38304,42133-42266
402305	7328724	Plus	40832-41362
402424	9796344	Minus	64925-65073
402777	9588235	Plus	126786-126948
402778	9588235	Plus	128560-128702
402837	9369121	Minus	2013-2186,9570-9758,11136-11309,19429-19677,21210-21455,23368-23562,24342-24527,29132-29320
402948	9368458	Minus	143456-143626,143808-143935
402952	9408724	Minus	119452-119619
403142	9444521	Plus	89286-90131
403297	8096824	Minus	16584-17264
403637	8671936	Minus	142647-142771,145531-145762
403657	8843996	Minus	156223-156370
404136	6981900	Minus	42538-46428
404249	8655533	Plus	64270-64633
404875	9801324	Plus	96588-96732,97722-97831
404917	7341851	Plus	49330-49498
404983	4432779	Minus	51178-51374,52000-52173
405238	7249119	Minus	51728-51836
405364	2281075	Minus	48325-48491,49136-49252
405531	9665194	Plus	35602-35803
405601	5815493	Minus	147835-147935,149220-149299
405621	5523811	Plus	59362-59607
405932	7767812	Minus	123525-123713
406117	9142932	Plus	54304-54584
406354	9256049	Minus	2095-2377
406548	7711514	Minus	25138-26762
406599	8248616	Plus	10933-11086

Table 3A: Preferred therapeutic targets for bladder cancer

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of bladder tumor AIs divided by the 90th percentile of normal bladder sample AIs
R2: 90th percentile of bladder tumor AIs divided by the 90th percentile of normal body sample AIs

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
421948	L42583	Hs.334309	keratin 6A	14.20	1.20
439926	AW014875	Hs.137007	ESTs	11.31	21.34
413324	V00571	Hs.75294	corticotropin releasing hormone	9.15	45.75
421110	AJ250717	Hs.1355	cathepsin E	9.07	45.35
417308	H60720	Hs.81892	KIAA0101 gene product	8.50	1.99
431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	8.39	1.28
418406	X73501	Hs.84905	cytokeratin 20	8.10	40.50
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.98	1.38
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	7.67	2.12
408243	Y00787	Hs.624	interleukin 8	7.56	4.85
417715	AW969587	Hs.86366	ESTs	7.45	4.70
417720	AA205625	Hs.208067	ESTs	7.34	9.18
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	7.30	26.07
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.12	35.60
413753	U17760	Hs.75517	*laminin, beta 3 (nicein (125kD), kalinin*	6.95	4.96
441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.42	0.89
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	6.08	3.49
407242	M18728		gb:Human nonspecific crossreacting antig	5.96	0.96
405033			C1002652*:gi|544327|sp|Q04799|FMO5_RABIT	5.84	16.22
449230	BE613348	Hs.211579	melanoma cell adhesion molecule	5.82	2.28
406685	M18728		gb:Human nonspecific crossreacting antig	5.80	0.89
420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	5.77	28.85
415511	AI732617	Hs.182362	ESTs	5.65	28.25
426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	5.60	6.51
424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.59	2.33
428651	AF196478	Hs.188401	annexin A10	5.55	27.75
400843			NM_003105*:Homo sapiens sortilin-related	5.51	4.92
402230			Target Exon	5.36	21.44
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	5.33	2.80
416065	BE267931	Hs.78996	proliferating cell nuclear antigen	5.17	1.98
428450	NM_014791	Hs.184339	KIAA0175 gene product	4.90	2.63
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.77	2.35
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	4.77	3.71
418663	AK001100	Hs.41690	desmocollin 3	4.74	1.48
414683	S78296	Hs.76888	hypothetical protein MGC12702	4.74	2.92
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.68	1.61
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	4.65	11.63
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.63	2.06
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.55	3.35
401780			NM_005557*:Homo sapiens keratin 16 (foca	4.49	1.62
424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	4.43	2.39
401093			C12000586*:gi|6330167|dbj|BAA86477.1| (A	4.40	12.94
417933	X02308	Hs.82962	thymidylate synthetase	4.35	2.29
418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.32	2.82
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	4.24	8.15
401781			Target Exon	4.15	1.31
425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.14	7.39
432842	AW674093	Hs.334822	hypothetical protein MGC4485	4.12	2.51
408380	AF123050	Hs.44532	diubiquitin	4.11	3.26
449722	BE280074	Hs.23960	cyclin B1	4.09	3.72
420344	BE463721	Hs.97101	putative G protein-coupled receptor	4.07	2.50
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.00	7.14
404977			Insulin-like growth factor 2 (somatomedi	3.89	5.17
400409	AF153341		Homo sapiens winged helix/forkhead trans	3.88	7.29
429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	3.87	1.61
444371	BE540274	Hs.239	forkhead box M1	3.87	2.75
443171	BE281128	Hs.9030	TONDU	3.83	9.48
441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.82	2.98
439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.77	3.83
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.73	4.91
426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	3.68	7.08
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.68	2.29
414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.67	3.06
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.67	1.18
421508	NM_004833	Hs.105115	absent in melanoma 2	3.67	3.65
443162	T49951	Hs.9029	DKFZP434G032 protein	3.66	3.21

418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.66	3.57
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.62	2.73
441495	AW294603	Hs.127039	ESTs	3.60	2.71
422282	AF019225	Hs.114309	apolipoprotein L	3.57	3.92
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.55	0.80
417275	X63578	Hs.295449	parvalbumin	3.54	4.60
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	3.52	2.59
418203	X54942	Hs.83758	CDC28 protein kinase 2	3.50	3.61
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.50	17.50
404875			NM_022819*:Homo sapiens phospholipase A2	3.46	3.24
420005	AW271106	Hs.133294	ESTs	3.40	2.22
409757	NM_001898	Hs.123114	cystatin SN	3.39	2.93
427719	AI393122	Hs.134726	ESTs	3.31	2.51
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	3.28	0.42
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	3.28	2.62
406081			Target Exon	3.25	13.54
426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.25	2.46
431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	3.23	2.88
429983	W92620	Hs.260855	ESTs	3.20	2.84
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.18	1.54
426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	3.17	5.44
411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	3.13	15.65
415752	BE314524	Hs.78776	putative transmembrane protein	3.11	2.46
408633	AW963372	Hs.46677	PRO2000 protein	3.11	3.30
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	3.09	1.52
412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.08	2.22
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	3.05	12.49
437931	AI249468	Hs.124434	ESTs	3.01	3.70
421451	AA291377	Hs.50831	ESTs	2.99	14.95
426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.97	2.10
402239			Target Exon	2.97	3.37
429345	R11141	Hs.199695	hypothetical protein	2.96	2.61
435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.93	2.13
423961	D13666	Hs.136348	periostin (OSF-2os)	2.93	1.44
420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.92	0.95
436608	AA628980		down syndrome critical region protein DS	2.92	4.86
447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.88	2.93
439223	AW238299	Hs.250618	UL16 binding protein 2	2.88	2.15
401747			Homo sapiens keratin 17 (KRT17)	2.88	3.44
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	2.86	14.30
444444	AI149332	Hs.14855	ESTs	2.85	2.68
421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	2.84	2.46
431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.78	2.26
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.77	2.34
442994	AI026718	Hs.16954	ESTs	2.75	2.82
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.74	2.44
434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	2.72	3.37
417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.69	2.70
404440			NM_021048:Homo sapiens melanoma antigen,	2.69	13.45
400844			NM_003105*:Homo sapiens sortilin-related	2.69	13.45
426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.69	1.36
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	2.69	12.08
403381			ENSP00000231844*:Ecotropic virus integra	2.68	13.40
411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	2.68	2.43
425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	2.67	2.68
435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.67	1.79
409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	2.65	0.73
413281	AA861271	Hs.222024	transcription factor BMAL2	2.65	2.23
446082	AI274139	Hs.156452	ESTs	2.65	2.65
422424	AI186431	Hs.296638	prostate differentiation factor	2.64	2.68
407839	AA045144	Hs.161566	ESTs	2.64	1.08
432441	AW292425	Hs.163484	ESTs	2.64	6.14
417312	AW888411	Hs.250811	leukemia-associated phosphoprotein p18 (	2.64	1.31
430157	BE348706	Hs.278543	ESTs	2.63	2.58
436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.61	1.93
418686	Z36830	Hs.87268	annexin A8	2.60	1.62
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.59	2.87
429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.57	3.89
439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	2.57	2.49
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	2.56	1.43
414812	X72755	Hs.77367	monokine induced by gamma interferon	2.54	3.10
451668	Z43948	Hs.326444	cartilage acidic protein 1	2.51	3.60
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.50	2.91
414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.49	1.78
429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.49	1.80
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	2.49	3.46
437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	2.48	2.36

418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.46	2.33
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	2.44	2.49
450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.43	1.42
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.41	2.05
449019	AI949095	Hs.67776	ESTs, Weakly similar to T22341 hypothetl	2.40	1.90
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	2.40	0.49
420370	Y13645	Hs.97234	uroplakin 2	2.39	3.81
408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	2.38	1.45
406399			NM_003122*:Homo sapiens serine protease	2.36	4.20
435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.31	4.05
442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	2.31	1.17
436246	AW450963	Hs.119991	ESTs	2.30	11.50
433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	2.30	2.40
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.29	1.89
411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.28	2.14
432829	W60377	Hs.57772	ESTs	2.28	4.85
415025	AW207091	Hs.72307	ESTs	2.28	11.40
436293	AI601188	Hs.120910	ESTs	2.27	3.80
415989	AI267700		ESTs	2.27	11.35
418067	AI127958	Hs.83393	cystatin E/M	2.25	1.54
436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.25	2.45
422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.25	1.55
428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	2.22	11.10
443247	BE614387	Hs.333893	c-Myc target JPO1	2.21	1.32
424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	2.21	1.52
405932			C15000305:gi|3806122|gb|AAC69198.1| (AF0	2.20	1.55
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.19	1.99
423271	W47225	Hs.126256	interleukin 1, beta	2.19	2.01
402305			C19000735*:gi|4508027|ref|NP_003414.1| z	2.19	2.54
421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	2.19	2.16
427747	AW411425	Hs.180655	serine/threonine kinase 12	2.18	1.80
437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	2.17	10.85
431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunl	2.17	2.14
433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	2.16	1.37
407581	R48402	Hs.173508	P3ECSL	2.15	1.95
400845			NM_003105*:Homo sapiens sortilin-related	2.15	2.23
419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.14	1.70
418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.13	1.83
448045	AJ297436	Hs.20166	prostate stem cell antigen	2.13	3.49
453459	BE047032	Hs.257789	ESTs	2.13	2.30
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	2.12	10.60
436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.11	1.89
445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	2.11	2.57
420876	AA918425	Hs.177744	ESTs	2.09	2.30
438817	AI023799	Hs.163242	ESTs	2.09	10.45
434293	NM_004445	Hs.3796	EphB6	2.08	2.42
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.08	2.10
418216	AA662240	Hs.283099	AF15q14 protein	2.08	4.62
437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	2.08	10.40
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalinl	2.05	5.39
431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.05	1.20
400773			NM_003105*:Homo sapiens sortilin-related	2.05	1.78
414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.04	2.06
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.04	1.70
444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	2.03	2.26
447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	2.02	1.73
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	2.02	2.93
407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	2.02	1.55
441801	AW242799	Hs.86366	ESTs	2.01	10.05
439780	AL109688		gb:Homo sapiens mRNA full length insert	2.00	10.00
452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.00	1.53
434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	2.00	1.91
430152	AB001325	Hs.234642	aquaporin 3	1.99	1.74
453134	AA032211	Hs.118493	ESTs	1.99	3.16
412719	AW016610	Hs.816	ESTs	1.99	0.34
442577	AA292998	Hs.163900	ESTs	1.99	3.09
409402	AF208234	Hs.695	cystatin B (stefin B)	1.98	1.50
414774	X02419	Hs.77274	plasminogen activator, urokinase	1.97	1.84
439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.95	1.42
447334	AA515032	Hs.91109	ESTs	1.95	2.53
432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	1.94	9.70
429002	AW248439	Hs.2340	junction plakoglobin	1.94	1.57
410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.94	2.02
420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	1.93	0.56
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	1.92	1.01
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.92	1.47
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.92	1.59

414918	AI219207	Hs.72222	hypothetical protein FLJ13459	1.92	2.77
424522	AL134847	Hs.149957	ribosomal protein S6 kinase, 90kD, polyp	1.92	1.21
413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.92	1.72
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.91	1.41
414595	AA641726	Hs.289015	hypothetical protein MGC4171	1.90	1.61
400846			sortilin-related receptor, L(DLR class)	1.90	1.93
417409	BE272506	Hs.82109	syndecan 1	1.89	1.75
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.88	1.16
418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.88	3.09
419092	J05581	Hs.89603	mucin 1, transmembrane	1.88	1.18
446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	1.87	2.01
431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.86	1.87
430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.86	2.11
412115	AK001763	Hs.73239	hypothetical protein FLJ10901	1.86	1.77
402901			NM_025206*:Homo sapiens hypothetical pro	1.85	2.35
449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.85	1.59
410418	D31382	Hs.63325	transmembrane protease, serine 4	1.84	1.90
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.84	1.03
414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.84	1.54
432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.83	1.74
452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.82	1.84
431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.82	1.83
427239	BE270447	Hs.174070	ubiquitin carrier protein	1.82	1.74
402424			NM_024901:Homo sapiens hypothetical prot	1.81	1.61
418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	1.81	3.67
431846	BE019924	Hs.271580	uroplakin 1B	1.80	4.11
410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.80	9.00
408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.80	1.02
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.80	2.26
451541	BE279383	Hs.26557	plakophilin 3	1.79	1.16
415786	AW419196	Hs.257924	hypothetical protein FLJ13782	1.79	5.59
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.79	8.95
425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.79	2.08
437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.77	2.96
437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	1.76	1.43
439606	W79123	Hs.58561	G protein-coupled receptor 87	1.76	8.80
424098	AF077374	Hs.139322	small proline-rich protein 3	1.76	0.57
430890	X54232	Hs.2699	glypican 1	1.73	1.39
452862	AW378065	Hs.8687	ESTs	1.73	1.99
427335	AA448542	Hs.251677	G antigen 7B	1.73	8.65
425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.72	2.07
414907	X90725	Hs.77597	polo (Drosophia)-like kinase	1.72	1.65
428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	1.72	1.03
453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.71	1.66
448993	AI471630	Hs.8127	KIAA0144 gene product	1.71	1.52
422406	AF025441	Hs.116206	Opa-interacting protein 5	1.71	5.52
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.71	8.55
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.71	8.55
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.71	8.55
424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.71	13.98
447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.70	1.84
414053	BE391635	Hs.75725	transgelin 2	1.69	1.51
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	1.69	8.45
426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcript	1.69	1.60
448262	AW880830	Hs.186273	ESTs	1.67	2.07
452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.66	0.70
452240	AI591147	Hs.61232	ESTs	1.66	1.23
417151	AA194055	Hs.293858	ESTs	1.65	2.08
452461	N78223	Hs.108106	transcription factor	1.65	8.25
418462	BE001596	Hs.85266	integrin, beta 4	1.65	1.78
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.64	1.59
438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	1.64	1.13
423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	1.63	1.81
453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	1.62	1.51
402777			C1002652*:gi|544327|sp|Q04799|FMO5_RABIT	1.62	2.33
436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	1.62	2.18
417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.62	1.27
413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	1.61	2.05
410407	X66839	Hs.63287	carbonic anhydrase IX	1.60	1.78
450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75	1.60	1.63
437016	AU076916	Hs.5398	guanine monphosphate synthetase	1.59	1.50
451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	1.58	1.92
422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	1.57	1.79
408908	BE296227	Hs.250822	serine/threonine kinase 15	1.56	7.80
433159	AB035898	Hs.150587	kinesin-like protein 2	1.56	7.80
443211	AI128388	Hs.143655	ESTs	1.56	7.80
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.55	1.44

426900	AW163564	Hs.142375	ESTs	1.54	1.93
421066	AU076725	Hs.101408	branched chain aminotransferase 2, mitoc	1.54	1.71
413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	1.53	1.55
418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.53	1.59
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	1.52	7.60
414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	1.49	0.52
418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.48	1.54
429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.48	1.39
402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.47	1.48
424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304814	1.47	7.35
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.47	1.37
422164	NM_014312	Hs.112377	cortic al thymocyte receptor (X. laevis	1.46	1.80
444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.45	1.58
452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.45	1.58
445182	AW189787		ESTs	1.43	7.15
408930	AA146721	Hs.334686	hypothetical protein FLJ21588	1.43	1.53
429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.43	1.34
406467			Target Exon	1.42	7.10
424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	1.42	1.32
422094	AF129535	Hs.272027	F-box only protein 5	1.41	4.55
431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	1.39	10.36
401760			Target Exon	1.37	1.16
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.36	1.39
424420	BE614743	Hs.146688	prostaglandin E synthase	1.33	1.49
421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.31	1.44
422119	AI277829	Hs.111862	KIAA0590 gene product	1.31	1.22
418729	AB028449	Hs.87889	helicase-moi	1.30	0.84
418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1.30	1.32
453028	AB006532	Hs.31442	RecQ protein-like 4	1.29	1.42
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	1.29	0.61
453321	AI984381	Hs.232521	ESTs	1.27	6.35
421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.26	6.30
425726	AF085808	Hs.159330	uroplakin 3	1.26	2.26
406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.26	1.11
429413	NM_014058	Hs.201877	DESC1 protein	1.25	1.01
418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	1.23	1.17
431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	1.22	1.59
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.20	1.38
422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	1.19	1.23
403903			C5001632*:gi|10645308|gb|AAG21430.1|AC00	1.19	1.98
425721	AC002115	Hs.159309	uroplakin 1A	1.17	2.30
413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	1.17	5.85
431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.17	1.39
443859	NM_013409	Hs.9914	follistatin	1.17	1.17
419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	1.13	2.83
422330	D30783	Hs.115263	epiregulin	1.13	5.65
420281	AI623693	Hs.323494	Predicted cation efflux pump	1.11	5.55
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	1.08	5.40
440304	BE159984	Hs.125395	ESTs	1.06	5.30
422170	AI791949	Hs.112432	anti-Mullerian hormone	1.06	1.55
417599	AA204688	Hs.62954	ESTs	1.05	1.02
411874	AA096106	Hs.20403	ESTs	1.04	7.20
449961	AW265634	Hs.133100	ESTs	1.03	0.65
418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.03	0.92
432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	1.02	5.10
453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	1.02	0.60
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	1.00	0.05
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	1.00	0.25
453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	1.00	0.25
439239	AI031540	Hs.235331	ESTs	1.00	0.27
450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	0.45
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	1.00	0.72
404403			Target Exon	1.00	1.00
406974	M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
410348	AW182663	Hs.95469	ESTs	1.00	1.00
412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	1.00	1.00
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
426320	W47595	Hs.169300	transforming growth factor, beta 2	1.00	1.00
426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	1.00	1.00
432097	X51730	Hs.2905	progesterone receptor	1.00	1.00
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	1.00
453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal ki	1.00	1.00
419078	M93119	Hs.89584	insulinoma-associated 1	1.00	1.25
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	1.00	1.35
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.75
451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00	1.80
415178	D80503	Hs.322850	ESTs	1.00	2.20

410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	2.25
425048	H05468	Hs.164502	ESTs	1.00	2.25
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	1.00	2.60
449448	D60730	Hs.57471	ESTs	1.00	2.70
417791	AW965339	Hs.111471	ESTs	1.00	2.95
421373	AA808229	Hs.167771	ESTs	1.00	3.00
427356	AW023482	Hs.97849	ESTs	1.00	3.15
421070	AA283185	Hs.19327	ESTs	1.00	3.25
415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypotheti	1.00	3.35
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	1.00	3.55
402075			ENSP00000251056*:Plasma membrane calcium	1.00	3.95
419559	Y07828	Hs.91096	ring finger protein	1.00	4.00
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	1.00	4.00
418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	1.00	4.35
412723	AA648459	Hs.335951	hypothetical protein AF301222	1.00	4.40
404877			NM_005365:Homo sapiens melanoma antigen,	1.00	4.45
443054	AI745185	Hs.8939	yes-associated protein 65 kDa	1.00	4.45
403047			NM_005656*:Homo sapiens transmembrane pr	1.00	4.50
406434			NM_030579*:Homo sapiens cytochrome b5 ou	1.00	4.65
412530	AA766268	Hs.266273	hypothetical protein FLJ13346	1.00	4.65
433365	AF026944	Hs.293797	ESTs	1.00	10.05
427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	0.99	0.60
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.99	1.00
431474	AL133990	Hs.190642	CEGP1 protein	0.94	9.14
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	0.93	21.15
414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	0.91	2.60
444649	AW207523	Hs.197628	ESTs	0.89	11.15
456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	0.89	5.13
414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	0.84	0.85
439569	AW602166	Hs.222399	CEGP1 protein	0.84	2.42
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	0.81	6.75
407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	0.80	0.57
457292	AI921270	Hs.281462	hypothetical protein FLJ14251	0.77	1.40
431089	BE041395		ESTs, Weakly similar to unknown protein	0.76	14.88
459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	0.74	11.03
424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.56	0.80
406964	M21305		gb:Human alpha satellite and satellite 3	0.53	11.16
416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	0.48	3.01
400288	X06256	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	0.40	0.70
421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.40	0.61

TABLE 3B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
411880	1263110_1	AW872477 BE088101 T05990
413804	1390710_1	T64682 BE168190 BE168256
414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
436608	42361_3	AA628980 AI126603 BE504035
439780	47673_1	AL109688 R23665 R26578
444163	593658_1	AI126098 AI184746 AI148521
445182	632151_1	AW189787 AI215430 AW268499 AW205930 AI392907 BE093017 BE093019 BE093010
451844	888230_1	T61430 AI820546 AI821336
456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 3C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400773	8131629	Minus	44116-44238,48208-48321

400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
400845	9188605	Plus	34428-34612
400846	9188605	Plus	39310-39474
401093	8516137	Minus	22335-23166
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
402239	7690131	Plus	38175-38304,42133-42266
402260	3399665	Minus	113765-113910,115653-115765,116808-116940
402305	7328724	Plus	40832-41362
402424	9796344	Minus	64925-65073
402777	9588235	Plus	126786-126948
402901	8894222	Minus	175426-175667
403047	3540153	Minus	59793-59968
403381	9438267	Minus	26009-26178
403903	7710671	Minus	101165-102597
404403	7272157	Minus	72053-72238
404440	7528051	Plus	80430-81581
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
405932	7767812	Minus	123525-123713
406081	9123861	Minus	38115-38691
406399	9256288	Minus	63448-63554
406434	9256651	Minus	17803-17931
406467	9795551	Plus	182212-182958

TABLE 4A: Preferred diagnostics for bladder cancer

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 80th percentile of muscle-invasive bladder tumor (stage T2-T4) AIs divided by the 80th percentile of exophytic non-invasive carcinoma (stage Ta) AIs
R2 90th percentile of bladder tumor AIs minus background divided by 90th percentile of normal body sample AIs minus background, where background equals the 15th percentile of all sample AIs
R3 90th percentile of bladder tumor AIs divided by the 90th percentile of normal body sample AIs

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3
423961	D13666	Hs.136348	periostin (OSF-2os)	11.22	1.40	1.44
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	8.40	1.31	1.38
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	7.88	2.06	2.44
408243	Y00787	Hs.624	interleukin 8	7.54	2.86	4.85
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.14	1.18	1.18
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.32	1.34	1.36
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	5.27	0.61	0.57
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.17	7.47	35.60
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.30	1.75	1.54
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	4.29	1.35	1.60
413324	V00571	Hs.75294	corticotropin releasing hormone	4.20	6.27	45.75
412429	AV650262	Hs.75765	GRO2 oncogene	4.00	0.94	0.93
406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	3.66	1.25	1.25
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.58	2.07	2.26
406687	M31126		matrix metalloproteinase 11 (stromelysin	3.41	4.37	3.37
422550	BE297626	Hs.296049	microfibrillar-associated protein 4	3.09	0.39	0.40
410867	X63556	Hs.750	fibrillin 1 (Marfan syndrome)	2.96	0.44	0.45
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	2.90	1.94	3.46
414812	X72755	Hs.77367	monokine induced by gamma interferon	2.80	1.67	3.10
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.77	5.62	26.07
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.71	2.26	2.91
429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	2.40	0.47	0.37
417849	AW291587	Hs.82733	nidogen 2	2.34	0.88	0.86
400419	AF084545		Target	2.33	1.54	2.12
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	2.10	1.01	1.01
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	1.99	3.19	17.50
414774	X02419	Hs.77274	plasminogen activator, urokinase	1.94	2.49	1.84
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	1.94	2.02	5.39
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.84	1.99	8.55
414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	1.76	0.33	0.31
431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	1.76	1.13	1.16
421958	AA357185	Hs.109918	ras homolog gene family, member H	1.75	1.33	1.27
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.58	2.42	1.39
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.57	2.02	8.55
421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	1.55	1.57	1.55
407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	1.41	0.79	0.67
429344	R94038	Hs.199538	inhibin, beta C	1.36	1.39	1.34
402727			NM_025065:Homo sapiens hypothetical prot	1.34	1.34	1.56
412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.31	1.63	2.22
423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.27	2.00	1.67
424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	1.25	0.16	0.30
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.23	1.70	4.34
424479	AF064238	Hs.149098	smoothelin	1.19	0.27	0.47
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.17	1.59	2.93
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	1.16	0.82	0.80
421634	AA437414	Hs.106283	hypothetical protein FLJ10262	1.16	1.05	1.05
439569	AW602166	Hs.222399	CEGP1 protein	1.15	2.01	2.42
431346	AA371059	Hs.251636	ubiquitin specific protease 3	1.10	1.64	1.52
448901	AK001021	Hs.22505	hypothetical protein FLJ10159	1.10	0.31	0.31
450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	1.03	1.51	1.42
422424	AI186431	Hs.296638	prostate differentiation factor	1.02	2.77	2.68
458781	AI444821	Hs.63085	ESTs, Weakly similar to MPP3_HUMAN MAGUK	1.00	1.64	5.45
445413	AA151342	Hs.12677	CGI-147 protein	1.00	1.51	5.20
432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	1.00	1.55	4.30
403106			C8000064*:gi|10432393|emb|CAC10283.1| (A	1.00	1.48	4.24
402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.67	3.95
404860			C1003394*:gi|12314272|emb|CAC00591.1| (A	1.00	1.40	3.90
434037	AF116601		WW domain-containing oxidoreductase	1.00	1.58	3.70
405738			CX000390*:gi|6014646|gb|AAF01438.1|AF187	1.00	1.36	2.95
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.00	1.45	1.60
439898	AW505514	Hs.209561	KIAA1715 protein	1.00	1.28	1.59
452567	D87120	Hs.29882	predicted osteoblast protein	1.00	1.10	1.31
401271			C9000559*:gi|12314195|emb|CAB99338.1| (A	1.00	2.12	1.00
411339	BE164598	Hs.274251	hypothetical protein FLJ20375; KIAA1797	1.00	2.05	1.00

403005			C21000027*:gi|1817556|dbj|BAA13672.1| (D	1.00	1.89	1.00
431146	Z83850		Human DNA sequence from PAC 82J11 and co	1.00	1.89	1.00
434939	AF161422	Hs.306567	Homo sapiens HSPC304 mRNA, partial cds	1.00	1.86	1.00
431753	X76029	Hs.2841	neuromedin U	1.00	1.82	1.00
419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.69	1.00
435505	AF200492	Hs.211238	interleukin-1 homolog 1	1.00	1.67	1.00
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	1.67	1.00
406397			C16001447*:gi|12053709|emb|CAC20419.1| (	1.00	1.66	1.00
404488			NM_030958*:Homo sapiens organic anion tr	1.00	1.56	1.00
441206	BE552314	Hs.131823	ESTs, Weakly similar to TERA HUMAN [H.sa	1.00	1.49	1.00
407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	1.00	1.47	1.00
446119	D29527	Hs.290931	ESTs	1.00	1.47	1.00
406471			Target Exon	1.00	1.44	1.00
402110			*C18000178:gi|11990779|emb|CAC19649.1| (A*	1.00	1.42	1.00
407911	AF104922	Hs.41565	growth differentiation factor 8	1.00	1.40	1.00
404829			C1002937*:gi|7499208|pir||T20993 hypothe	1.00	1.37	1.00
421925	S80310	Hs.109620	acidic epididymal glycoprotein-like 1	1.00	1.26	1.00
406076	AL390179		Homo sapiens mRNA; cDNA DKFZp547P134 (fr	1.00	1.19	1.00
458622	AA972412	Hs.13755	f-box and WD-40 domain protein 2	1.00	1.09	1.00
416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	1.00	1.04	1.00
409357	M73628	Hs.54415	casein, kappa	1.00	1.03	1.00
436684	AW976319	Hs.94806	ATP-binding cassette, sub-family A (ABC1	1.00	0.84	0.84
436178	BE152396	Hs.21590	hypothetical protein DKFZp564O0523	1.00	0.91	0.80
402522			C1000568*:gi|12697965|dbj|BAB21801.1| (A	1.00	0.80	0.67
405735			ENSP00000252164*:KIAA1578 protein (Fragm	1.00	0.86	0.56
401905			ENSP00000252232*:Sterol regulatory eleme	1.00	0.65	0.52
404152			C6000931*:gi|9558454|dbj|BAB03398.1| (AB	1.00	0.58	0.51
418693	AI750878	Hs.87409	thrombospondin 1	1.00	0.85	0.51
451375	AI792066	Hs.283902	Homo sapiens BAC clone RP11-481J13 from	1.00	0.46	0.38
430132	AA204686	Hs.234149	hypothetical protein FLJ20647	1.00	0.84	0.33
456983	AI081687	Hs.11355	thymopoietin	1.00	0.61	0.29
438681	AW384815	Hs.149208	KIAA1555 protein	1.00	0.60	0.28
409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.00	0.39	0.19
409196	NM_001874	Hs.334873	carboxypeptidase M	1.00	0.43	0.13
410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	1.00	0.30	0.12
420674	NM_000055	Hs.1327	butyrylcholinesterase	1.00	0.30	0.08
415165	AW887604	Hs.78065	complement component 7	1.00	0.08	0.06
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	1.00	0.10	0.01
448256	BE614149	Hs.20814	CGI-27 protein	0.96	1.32	1.55
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	0.95	3.15	2.34
403214			NM_016232*:Homo sapiens interleukin 1 re	0.94	1.63	2.51
414799	AI752416	Hs.77326	insulin-like growth factor binding prote	0.92	1.87	1.60
406665	U22961	Hs.184411	*albumin*	0.92	1.09	1.03
401519			C15000476*:gi|12737279|ref|XP_012163.1|	0.88	1.46	3.44
417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig),	0.87	0.41	0.50
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	0.85	1.38	1.43
405494			C2001837*:gi|12697903|dbj|BAB21770.1| (A	0.83	1.46	4.65
444171	AB018249	Hs.10458	small inducible cytokine subfamily A (Cy	0.80	0.91	0.91
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	0.79	0.58	0.43
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	0.77	1.47	2.37
426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	0.75	1.13	1.18
431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	0.68	2.61	1.87
413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	0.68	2.70	4.96
426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	0.67	1.50	1.36
426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	0.56	2.05	2.46
422282	AF019225	Hs.114309	apolipoprotein L	0.55	3.91	3.92
409757	NM_001898	Hs.123114	cystatin SN	0.53	2.72	2.93
427450	AB014526	Hs.178121	KIAA0626 gene product	0.52	1.34	1.97
414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	0.50	1.04	1.05
423774	L39064	Hs.1702	interleukin 9 receptor	0.49	2.81	6.46
404977			Insulin-like growth factor 2 (somatomedi	0.28	5.78	5.17
428336	AA503115	Hs.183752	microseminoprotein, beta-	0.21	1.47	1.56
451668	Z43948	Hs.326444	cartilage acidic protein 1	0.18	4.05	3.60
428651	AF196478	Hs.188401	annexin A10	0.17	5.14	27.75
421110	AJ250717	Hs.1355	cathepsin E	0.12	5.49	45.35

TABLE 4B

Pkey:	*Unique Eos probeset identifier number*
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Pkey	CAT Number	Accession
431146	32854_1	Z83850 AA459717 AW965384 AA333635
434037	37918_1	AF116601 AI110691 AF063566

TABLE 4C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401271	9797373	Minus	61292-61911
401519	6649315	Plus	157315-157950
401905	8671966	Plus	153965-154441,156599-156819
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402110	8131678	Minus	173889-174062
402522	9798493	Plus	20605-20731
402727	9211324	Plus	54596-54777
403005	5791501	Minus	16945-17053,20018-20403
403106	7331404	Plus	77162-77350,81338-81511
403214	7630945	Minus	76723-77027,79317-79484
404152	9884757	Plus	41111-41281,45495-45716,47801-47910
404488	8113286	Minus	64835-64994
404829	6624702	Minus	4913-5093,7310-7469,9472-9621,9951-10082
404860	8979555	Plus	65852-66081
404977	3738341	Minus	43081-43229
405494	8050952	Minus	70284-70518
405735	9931101	Minus	29854-29976
405738	9943998	Plus	44370-45410
406076	9123123	Plus	89972-90319
406397	9256243	Minus	127317-127454
406471	9795566	Plus	87383-87589

TABLE 5A: Genes upregulated in bladder cancer

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1 90th percentile of bladder tumor AIs divided by the 90th percentile of normal body sample AIs

Pkey	ExAccn	UnigeneID	Unigene Title	R1
459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	11.03
437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	10.40
404917			Target Exon	9.65
401066			C11000517*:gi|7293105|gb|AAF48490.1| (AE	9.00
447475	AI380797	Hs.158992	ESTs	8.92
427335	AA448542	Hs.251677	G antigen 7B	8.65
450061	AI797034	Hs.346238	ESTs	8.35
401335			Target Exon	7.95
424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	7.35
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	7.20
436608	AA628980		down syndrome critical region protein DS	4.86
451950	AW292317	Hs.213307	ESTs	4.45
406542			C19000728*:gi|12585552|sp|Q9Y2Q1|Z257_HU	3.73
437931	AI249468	Hs.124434	ESTs	3.70
443133	AI033878	Hs.41379	ESTs	3.60
434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	3.37
402239			Target Exon	3.37
443162	T49951	Hs.9029	DKFZP434G032 protein	3.21
403383			Target Exon	3.13
438315	R56795	Hs.82419	ESTs	3.04
452827	AI571835	Hs.55468	ESTs	3.01
416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	3.01
402948			NM_025206:Homo sapiens hypothetical prot	2.91
429983	W92620	Hs.260855	ESTs	2.84
429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor t	2.78
444371	BE540274	Hs.239	forkhead box M1	2.75
417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.70
414906	AA157911	Hs.72200	ESTs	2.70
425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	2.68
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.62
429345	R11141	Hs.199695	hypothetical protein	2.61
414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.60
402305			C19000735*:gi|4508027|ref|NP_003414.1| z	2.54
432842	AW674093	Hs.334822	hypothetical protein MGC4485	2.51
427719	AI393122	Hs.134726	ESTs	2.51
455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.50
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	2.49
456967	AW004056	Hs.168357	T-box 2	2.49
406387			Target Exon	2.48
417997	AA418189	Hs.23017	Homo sapiens cDNA: FLJ22747 fis, clone K	2.48
415752	BE314524	Hs.78776	putative transmembrane protein	2.46
411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	2.43
434293	NM_004445	Hs.3796	EphB6	2.42
433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	2.40
425997	AK000086	Hs.165948	hypothetical protein FLJ20079	2.38
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.35
452012	AA307703	Hs.279766	kinesin family member 4A	2.34
445600	AF034803	Hs.12953	PTPRF interacting protein, binding prote	2.33
418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.33
454609	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.28
444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	2.26
420005	AW271106	Hs.133294	ESTs	2.22
439826	NM_014965	Hs.6705	KIAA1042 protein	2.22
405531			Target Exon	2.21
436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	2.18
404394			ENSP00000241075:TRRAP PROTEIN.	2.17
427479	BE410092	Hs.178471	KIAA0798 gene product	2.17
435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.13
431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	2.12
426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.10
422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.10
451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	2.09
403477			C3002160*:gi|7662420|ref|NP_055738.1| KI	2.09
417151	AA194055	Hs.293858	ESTs	2.08
448262	AW880830	Hs.186273	ESTs	2.07
415192	D17793	Hs.78183	aldo-keto reductase family 1, member C3	2.04
402994			NM_002463*:Homo sapiens myxovirus (influ	2.04

426053	U68105	Hs.172182	poly(A)-binding protein, cytoplasmic 1	2.02
423271	W47225	Hs.126256	interleukin 1, beta	2.01
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.99
407581	R48402	Hs.173508	P3ECSL	1.95
410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.95
427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	1.93
436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.93
436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	1.89
401961			NM_021626:Homo sapiens serine carboxypep	1.86
434042	AI589941	Hs.8254	Homo sapiens, Similar to tumor different	1.85
447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.84
418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	1.83
429612	AF062649	Hs.252587	pituitary tumor-transforming 1	1.80
422164	NM_014312	Hs.112377	cortic al thymocyte receptor (X. laevis	1.80
422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	1.79
410407	X66839	Hs.63287	carbonic anhydrase IX	1.78
412115	AK001763	Hs.73239	hypothetical protein FLJ10901	1.77
414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	1.75
432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.74
427239	BE270447	Hs.174070	ubiquitin carrier protein	1.74
459198	AI086347	Hs.151138	ESTs	1.74
421066	AU076725	Hs.101408	branched chain aminotransferase 2, mitoc	1.71
424687	J05070	Hs.151738	*matrix metalloproteinase 9 (gelatinase B*	1.70
450663	H43540	Hs.25292	ribonuclease HI, large subunit	1.70
417324	AW265494		ESTs	1.67
453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.66
428000	R35145	Hs.291904	accessory proteins BAP31/BAP29	1.65
450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75	1.63
423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	1.62
415440	D83782	Hs.78442	SREBP CLEAVAGE-ACTIVATING PROTEIN	1.62
428028	U52112	Hs.182018	interleukin-1 receptor-associated kinase	1.62
426783	Z19084	Hs.172210	MUF1 protein	1.62
445937	AI452943	Hs.321231	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	1.61
445462	AA378776	Hs.288649	hypothetical protein MGC3077	1.60
400965			C11002190*:gi|12737279|ref|XP_012163.1|	1.59
432269	NM_002447	Hs.2942	macrophage stimulating 1 receptor (c-met	1.59
429578	AI969028	Hs.99389	ESTs	1.59
449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.59
431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	1.59
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.59
429002	AW248439	Hs.2340	junction plakoglobin	1.57
442410	AW996503	Hs.197680	ESTs	1.56
407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.55
418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.54
424611	NM_001421	Hs.151139	E74-like factor 4 (ets domain transcript	1.54
414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.54
408930	AA146721	Hs.334686	hypothetical protein FLJ21588	1.53
448993	AI471630	Hs.8127	KIAA0144 gene product	1.52
414053	BE391635	Hs.75725	transgelin 2	1.51
433662	W07162	Hs.150826	CATX-8 protein	1.50
432562	BE531048	Hs.278422	DKFZP586G1122 protein	1.50
402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.48
426127	L36983	Hs.167013	dynamin 2	1.48
427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	1.48
418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.47
418960	NM_004494	Hs.89525	hepatoma-derived growth factor (high-mob	1.46
428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	1.46
432344	AI476474	Hs.248156	ESTs	1.46
453449	W16752	Hs.32981	sema domain, immunoglobulin domain (Ig),	1.46
450690	AA296696	Hs.333418	FXYD domain-containing ion transport reg	1.46
441940	AW298115	Hs.128152	ESTs	1.45
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.44
439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.42
422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	1.41
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.41
445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.39
441565	AW953575	Hs.303125	p53-induced protein PIGPC1	1.37
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.35
418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1.32
432636	AA340864	Hs.278562	claudin 7	1.32
439053	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	1.32
413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	1.31
453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	1.28
430056	X97548	Hs.228059	KRAB-associated protein 1	1.24
451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.23
431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	1.20
439863	BE547830	Hs.9408	paired immunoglobulin-like receptor beta	1.19

451541	BE279383	Hs.26557	plakophilin 3	1.16
406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.11
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.00
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	0.86
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	0.61

TABLE 5B

Pkey: Unique Eos probeset identifier number
CAT *number*: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
417324	166714_1	AW265494 AA455904 AA195677 AW265432 AW991605 AA456370
436608	42361_3	AA628980 AI126603 BE504035
451385	86787_1	AA017656 AA017374 AA019761
454609	1226517_1	AW810204 AW810555 AW810196 AW810619 AW810507
455797	1366826_1	BE091833 BE091874 BE091871

TABLE 5C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400965	7770576	Minus	173043-173564
401066	8217436	Plus	71448-71574
401335	9884881	Plus	15736-16352
401961	4581193	Minus	124054-124209
402239	7690131	Plus	38175-38304,42133-42266
402260	3399665	Minus	113765-113910,115653-115765,116808-116940
402305	7328724	Plus	40832-41362
402948	9368458	Minus	143456-143626,143808-143935
402994	2996643	Minus	4727-4969
403383	9438267	Minus	119837-121197
403477	9958251	Plus	111834-112008
404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
404917	7341851	Plus	49330-49498
405531	9665194	Plus	35602-35803
406387	9256180	Plus	116229-116371,117512-117651
406542	7711499	Plus	117335-118473

TABLE 6A: Genes upregulated in bladder cancer

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1 90th percentile of bladder tumor AIs divided by the 90th percentile of normal urothelium biopsy AIs
R2 90th percentile of bladder tumor AIs divided by the 90th percentile of normal urothelium biopsy and normal bladder AIs

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
439926	AW014875	Hs.137007	ESTs	11.31	11.31
413324	V00571	Hs.75294	corticotropin releasing hormone	9.15	9.15
421110	AJ250717	Hs.1355	cathepsin E	9.07	9.07
417308	H60720	Hs.81892	KIAA0101 gene product	8.50	8.50
418406	X73501	Hs.84905	cytokeratin 20	8.10	8.10
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.98	7.98
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	7.67	7.67
408243	Y00787	Hs.624	interleukin 8	7.56	7.56
416065	BE267931	Hs.78996	proliferating cell nuclear antigen	7.17	5.17
425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	7.17	8.24
414183	AW957446	Hs.301711	ESTs	7.14	4.62
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.12	7.12
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	6.90	3.38
427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, r	6.85	4.98
441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.42	6.42
438091	AW373062		nuclear receptor subfamily 1, group I, m	6.32	6.32
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.09	3.67
414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	5.93	4.68
405033			C1002652*:gi|544327|sp|Q04799|FMO5_RABIT	5.84	5.84
413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	5.79	5.68
428336	AA503115	Hs.183752	microseminoprotein, beta-	5.78	4.57
449230	BE613348	Hs.211579	melanoma cell adhesion molecule	5.69	5.82
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	5.69	7.30
415511	AI732617	Hs.182362	ESTs	5.65	5.65
426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	5.60	5.60
421948	L42583	Hs.334309	keratin 6A	5.59	14.20
428651	AF196478	Hs.188401	annexin A10	5.55	5.55
424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.38	5.59
406687	M31126		matrix metalloproteinase 11 (stromelysin	5.36	5.34
439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	5.35	5.35
408246	N55669	Hs.333823	mitochondrial ribosomal protein L13	5.20	3.50
427678	BE267756	Hs.180312	mitochondrial ribosomal protein S16	5.13	4.10
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	4.97	3.71
442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	4.90	4.90
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.90	4.77
417720	AA205625	Hs.208067	ESTs	4.84	7.34
423979	AF229181	Hs.136644	CS box-containing WD protein	4.81	4.81
420981	L40904	Hs.100724	peroxisome proliferative activated recep	4.81	4.43
433470	AW960564		transmembrane 4 superfamily member 1	4.72	4.72
429138	AB020657	Hs.197298	NS1-binding protein	4.71	4.71
408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	4.71	4.71
452714	AW770994	Hs.30340	hypothetical protein KIAA1165	4.69	4.69
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.68	4.68
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	4.65	4.65
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	4.64	4.64
427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	4.63	5.12
412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.61	4.61
418030	BE207573	Hs.83321	neuromedin B	4.60	4.60
401192			Target Exon	4.60	4.29
426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	4.59	3.51
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	4.58	5.33
449618	AI076459	Hs.15978	KIAA1272 protein	4.58	4.58
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.55	4.55
415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.52	4.70
446742	AA232119	Hs.16085	putative G-protein coupled receptor	4.49	4.11
419433	AA814807	Hs.7395	hypothetical protein FLJ23182	4.48	4.48
412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	4.47	4.47
427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.45	4.45
444371	BE540274	Hs.239	forkhead box M1	4.44	3.87
444006	BE395085	Hs.10086	type I transmembrane protein Fn14	4.43	3.63
424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	4.43	4.43
401093			C12000586*:gi|6330167|dbj|BAA86477.1| (A	4.40	4.40
447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.39	4.39
417933	X02308	Hs.82962	thymidylate synthetase	4.38	4.35
409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.36	3.68
401451			NM_004496*:Homo sapiens hepatocyte nucle	4.35	4.35
450746	D82673	Hs.278589	general transcription factor II, I	4.35	3.36

414683	S78296	Hs.76888	hypothetical protein MGC12702	4.34	4.74
434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.31	4.31
417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	4.30	4.30
416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.30	4.30
440086	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom	4.29	4.29
417715	AW969587	Hs.86366	ESTs	4.27	7.45
409757	NM_001898	Hs.123114	cystatin SN	4.24	3.39
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	4.24	4.24
432842	AW674093	Hs.334822	hypothetical protein MGC4485	4.21	4.12
446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	4.20	4.20
436856	AI469355	Hs.127310	ESTs	4.19	4.19
428450	NM_014791	Hs.184339	KIAA0175 gene product	4.16	4.90
425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.14	4.14
409231	AA446644	Hs.692	*GA733-2 antigen; epithelial glycoprotein*	4.14	5.99
426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	4.12	4.12
446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	4.12	3.43
400843			NM_003105*:Homo sapiens sortilin-related	4.11	5.51
449722	BE280074	Hs.23960	cyclin B1	4.09	4.09
405506			Target Exon	4.09	3.75
420344	BE463721	Hs.97101	putative G protein-coupled receptor	4.07	4.07
426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	4.05	4.80
456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.03	7.64
437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.02	4.02
413794	AF234532	Hs.61638	myosin X	4.02	4.02
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	4.02	4.72
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.01	3.99
416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.01	4.01
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.00	4.00
400277			Eos Control	4.00	3.47
415791	H09366	Hs.78853	uracil-DNA glycosylase	3.99	3.37
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.98	4.77
427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	3.98	3.95
413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	3.96	6.95
420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.92	5.04
400409	AF153341		Homo sapiens winged helix/forkhead trans	3.91	3.88
408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	3.90	3.90
411678	AI907114	Hs.71465	squalene epoxidase	3.89	3.89
429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	3.87	3.87
428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	3.87	3.87
442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	3.85	4.50
429083	Y09397	Hs.227817	BCL2-related protein A1	3.85	3.85
439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.82	3.77
441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.82	3.82
430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.81	3.81
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.81	3.62
430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	3.80	3.80
447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.77	3.77
404875			NM_022819*:Homo sapiens phospholipase A2	3.77	3.46
411299	BE409857	Hs.69499	hypothetical protein	3.76	3.76
418827	BE327311	Hs.47166	HT021	3.76	3.76
446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.75	3.75
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.73	3.73
433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.71	3.71
400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	3.70	3.45
409518	BE384836	Hs.3454	KIAA1821 protein	3.69	3.69
430024	AI808780	Hs.227730	integrin, alpha 6	3.69	3.69
426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	3.68	3.68
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.68	3.66
414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.67	3.67
413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	3.67	3.41
424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	3.67	3.88
434263	N34895	Hs.44648	ESTs	3.65	3.65
438280	AW015534	Hs.217493	annexin A2	3.63	3.36
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.63	3.68
408989	AW361666	Hs.49500	KIAA0746 protein	3.61	3.66
416640	BE262478	Hs.79404	neuron-specific protein	3.60	4.22
416926	H03109	Hs.108920	HT018 protein	3.59	3.59
414368	W70171	Hs.75939	uridine monophosphate kinase	3.59	3.53
402727			NM_025065:Homo sapiens hypothetical prot	3.58	3.58
419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.56	3.77
416114	AI695549	Hs.183868	glucuronidase, beta	3.55	3.55
424941	AA128376	Hs.153884	ATP binding protein associated with cell	3.55	3.55
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	3.54	4.63
429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor t	3.53	3.92
420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	3.51	5.77
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.50	3.50
418203	X54942	Hs.83758	CDC28 protein kinase 2	3.50	3.50

415220	AA431880	Hs.181174	ESTs, Weakly similar to T19201 hypotheti	3.50	3.50
428371	AB012193	Hs.183874	cullin 4A	3.46	3.46
418663	AK001100	Hs.41690	desmocollin 3	3.45	4.74
404977			Insulin-like growth factor 2 (somatomedi	3.45	3.89
422663	AW500087	Hs.119014	zinc finger protein 175	3.44	3.44
434061	AW024973	Hs.283675	NPD009 protein	3.41	5.64
418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.41	4.32
431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.40	3.40
411943	BE502436	Hs.7962	ESTs, Weakly similar to S44608 C02F5.6 p	3.39	4.27
420005	AW271106	Hs.133294	ESTs	3.38	3.40
453450	AW797627	Hs.347459	ADP-ribosylation factor 6	3.38	3.87
410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	3.36	3.36
428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.35	3.35
437469	AW753112	Hs.15514	hypothetical protein MGC3260	3.35	3.35
407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.34	3.34
428157	AI738719	Hs.198427	hexokinase 2	3.33	3.73
450293	N36754	Hs.171118	hypothetical protein FLJ00026	3.33	3.33
400750			Target Exon	3.33	3.33
450139	AK001838	Hs.296323	serum/glucocorticoid regulated kinase	3.33	3.33
412636	NM_004415		desmoplakin (DPI, DPII)	3.30	4.81
447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28/cdc	3.27	3.38
430315	NM_004293	Hs.239147	guanine deaminase	3.26	4.30
421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	3.26	3.41
443030	R68048	Hs.9238	hypothetical protein FLJ23516	3.19	3.34
436911	AA142984	Hs.5344	adaptor-related protein complex 1, gamma	3.17	3.40
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	3.06	3.52
443171	BE281128	Hs.9030	TONDU	3.05	3.83
429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	3.01	3.53
408380	AF123050	Hs.44532	diubiquitin	2.99	4.11
421508	NM_004833	Hs.105115	absent in melanoma 2	2.99	3.67
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.97	4.55
452046	AB018345	Hs.27657	KIAA0802 protein	2.95	3.39
451940	AI735759	Hs.52620	integrin, beta 8	2.93	3.58
407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	2.90	3.68
422282	AF019225	Hs.114309	apolipoprotein L	2.89	3.57
402230			Target Exon	2.88	5.36
406685	M18728		gb:Human nonspecific crossreacting antig	2.80	5.80
417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.79	3.89
447957	NM_014821	Hs.20126	KIAA0317 gene product	2.75	3.45
418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.75	3.46
417275	X63578	Hs.295449	parvalbumin	2.73	3.54
431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	2.72	8.39
401781			Target Exon	2.62	4.15
407242	M18728		gb:Human nonspecific crossreacting antig	2.54	5.96
428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	2.52	4.27
430200	BE613337	Hs.234896	geminin	2.52	4.19
451035	AU076785	Hs.430	plastin 1 (I isoform)	2.51	4.15
443162	T49951	Hs.9029	DKFZP434G032 protein	2.48	3.66
441495	AW294603	Hs.127039	ESTs	2.45	3.60
449246	AW411209	Hs.23363	hypothetical protein FLJ10983	2.45	3.52
401780			NM_005557*:*Homo sapiens* keratin 16 (foca	2.22	4.49
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.20	3.55
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	2.15	6.08
439394	AA149250	Hs.56105	ESTs	2.05	3.95
427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.79	3.88

TABLE 6B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
412636	13165_1	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365163 AW365166 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674 BE184924 C04715 W39488 AW995615 BE184948 BE159646 AW606653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467 AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029

		AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975 AI470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI306554 AI686869 AI568892 AW190555 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070 AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA961816 AA283207 AI076962 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861 AW860878
433470	3672_1	AW960564 AA092457 T55890 D56120 T92525 AI815987 BE182608 BE182595 AW080238 M90657 AA347236 AW961686 AW176446 AA304671 AW583735 T61714 AA316968 AI446615 AA343532 AA083489 AA488005 W52095 W39480 N57402 D82638 W25540 W52847 D82729 D58990 BE619182 AA315188 AA308636 AA112474 W76162 AA088544 H52265 AA301631 H80982 AA113786 BE620997 AW651691 AA343799 BE613669 BE547180 BE546656 F11933 AA376800 AW239185 AA376086 BE544387 BE619041 AA452515 AA001806 AA190873 AA180483 AA159546 F00242 AI940609 AI940602 AI189753 T97663 T66110 AW062896 AW062910 AW062902 AI051622 AI828930 AA102452 AI685095 AI819390 AA557597 AA383220 AI804422 AI633575 AW338147 AW603423 AW606800 AW750567 AW510672 AI250777 AA083510 AW629109 AW513200 AA921353 AI677934 AI148698 AI955858 AA173825 AA453027 AI027865 AW375542 AA454099 AA733014 AI591384 R79300 R80023 AA843108 AA626058 AA844898 AW375550 AA889018 AI474275 AW205937 AI052270 AW388117 AW388111 AA699452 AI242230 N47476 H38178 AA366621 AA113196 AA130023 H39740 T61629 AI885973 AW083671 AA179730 AA305757 AI285455 N83956 AA216013 AA336155 AW999959 T97525 AA345349 T91762 AA771981 AI285092 AI591386 BE392486 BE385852 AA682601 AI682884 AA345840 T85477 AA292949 AA932079 AA098791 D82607 T48574 AW752038 C06300
438091	44964_1	AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616 AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571 AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994 AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096

TABLE 6C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400750	8119067	Plus	198991-199168,199316-199548
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
401093	8516137	Minus	22335-23166
401192	9719502	Minus	69559-70101
401451	6634068	Minus	119926-121272
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
402230	9966312	Minus	29782-29932
402727	9211324	Plus	54596-54777
404875	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
405506	6466489	Plus	80014-80401,80593-81125

TABLE 7A: Genes downregulated in bladder cancer

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1 90th percentile of normal urothelium biopsy AIs divided by 75th percentile of bladder tumor AIs
R2 90th percentile of normal urothelium biopsy and normal bladder AIs divided by the 90th percentile bladder tumor AIs

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
403010			C21000152:gi|6226483|sp|Q52118|YMO3_ERWS	4.86	2.49
426796	S78234	Hs.172405	cell division cycle 27	4.28	2.48
416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	4.04	2.07
459006	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	3.82	2.66
404917			Target Exon	3.78	2.00
426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	2.64	1.79
419543	AA244170		gb:nc05h02.s1 NCI_CGAP_Pr1 Homo sapiens	2.63	3.42
453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	2.32	3.24
428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	2.20	3.80
451529	AI917901	Hs.208641	ESTs	2.18	3.69
417076	AW973454	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN A	2.03	3.03
425438	T62216	Hs.270840	ESTs	2.00	5.17
450515	AW304226		*biphenyl hydrolase-like (serine hydrolas*	1.89	2.46
432873	AW837268	Hs.279639	Homo sapiens mRNA; cDNA DKFZp586M2022 (f	1.70	2.79
452123	AI267615	Hs.38022	ESTs	1.69	2.46
424378	W28020	Hs.167988	neural cell adhesion molecule 1	1.65	4.67
437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50	3.34
402096			ENSP00000217725*:Laminin alpha-1 chain p	1.48	3.02
439563	AI018768	Hs.12482	glyceronephosphate O-acyltransferase	1.47	3.22
412810	M21574	Hs.74615	platelet-derived growth factor receptor,	1.46	2.30
458651	AW612481	Hs.104105	ESTs	1.39	2.89
414033	AL079707	Hs.207443	hypothetical protein MGC10848	1.36	2.80
433572	AL046859	Hs.3407	protein kinase (cAMP-dependent, catalyti	1.35	3.49
413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	1.34	2.93
420412	AW976674	Hs.125103	ESTs	1.32	5.13
421406	AF179897	Hs.104105	Meis (mouse) homolog 2	1.31	4.07
417446	AL118671	Hs.82163	monoamine oxidase B	1.27	2.86
452886	AI478250	Hs.13751	ESTs	1.26	1.95
446808	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	1.25	3.44
443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	1.24	2.07
421348	M94048	Hs.103724	peripheral myelin protein 22	1.24	2.63
433070	N75346	Hs.306121	CDC20 (cell division cycle 20, S. cerevi	1.23	2.80
420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	1.22	3.43
408491	AI088063	Hs.7882	ESTs	1.20	6.01
447384	AI377221	Hs.40528	ESTs	1.00	7.92
421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	1.00	7.38
409619	AK001015	Hs.55220	*BCL2-associated athanogene 2*	1.00	6.40
444795	AI193356	Hs.160316	ESTs	1.00	5.53
408495	W68796	Hs.237731	ESTs	1.00	5.05
417124	BE122762	Hs.25338	ESTs	1.00	4.73
443998	AI620661	Hs.296276	ESTs	1.00	4.39
406303			C16000922:gi|7499103|pir||T20903 hypothe	1.00	4.37
422994	AW891802	Hs.296276	ESTs	1.00	4.37
422195	AB007903	Hs.113082	KIAA0443 gene product	1.00	4.35
452877	AI250789	Hs.32478	ESTs	1.00	3.90
452487	AW207659	Hs.6630	*Homo sapiens cDNA FLJ13329 fis, clone OV*	1.00	3.90
417159	R01761		gb:ye81f10.s1 Soares fetal liver spleen	1.00	3.82
445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	1.00	3.62
406274			Target Exon	1.00	3.59
410611	AW954134	Hs.20924	KIAA1628 protein	1.00	3.06
426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial	1.00	2.89
422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	1.00	2.61
413040	AA193338	Hs.12321	sodium calcium exchanger	1.00	2.51
429623	NM_005308	Hs.211569	G protein-coupled receptor kinase 5	1.00	2.05
456607	AI660190	Hs.106070	cyclin-dependent kinase inhibitor 1C (p5	1.00	2.01
429143	AA333327	Hs.197335	plasma glutamate carboxypeptidase	0.97	2.45
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.90	2.47
442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	0.88	5.08
414449	AA557660	Hs.76152	decorin	0.88	3.13
412014	AI620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	0.78	1.88
425100	AF051850	Hs.154567	supervillin	0.70	3.90
432094	AI658580	Hs.61426	Homo sapiens mesenchymal stem cell prote	0.68	3.41
427818	AW511222	Hs.193765	ESTs	0.63	3.75

TABLE 7B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
417159	1653899_1	R01761 R01760 N49787
419543	185745_1	AA244170 AI018087 AA244355
450515	83710_1	AW304226 AW008420 AA349212 H15015 AA317021 AI829484 H25661 H81744 AI906147 AA837938 AW167766 AW603578 AW842369 BE439926 AA902417 AW235409 AA010062 AW069319 AI280242 AW672925 H06848 H05608 R51905 R45023 AW675471 H28475 AI086597 AI197815 AI825355 N99134 AI075956 AI470122 AA449985 AW662833 AA860423 AA913342 T23825 AI394207 AI310319 T32467 AI589870 AI682293 AI810633 BE223045 H14620 AA626645 AA876023 T33571 AA953982 AI138631 H15016 AI304356 AA983631 AI350990 AI143993 AI708171 AA526961 H26247 W38485 AA847598 H81745 AW855486 BE299605 AI079409 AI278050 AI223168 AI860904 AW025415 AI339003 AA393692 AI354302 AI492838 N80194 AI015651 N34543 BE295397 AI085154 W24135

TABLE 7C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: *Indicates nucleotide positions of predicted exons.*

Pkey	Ref	Strand	Nt_position
402096	8117697	Minus	24993-25186
403010	3132346	Plus	78385-79052
404917	7341851	Plus	49330-49498
406274	7543787	Plus	932-1123
406303	8575868	Plus	173622-173786

TABLE 8A: Genes predictive of bladder cancer progression

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1 80th percentile of Ta or T1 tumor AIs from patients who upstaged divided by 80th percentile of Ta or T1 tumor AIs from patients who did not upstage
R2 median of Ta or T1 tumor AIs from patients who upstaged divided by the median of Ta or T1 tumor AIs from patients who did not upstage

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
413324	V00571	Hs.75294	corticotropin releasing hormone	8.30	4.18
437802	AI475995	Hs.122910	ESTs	7.51	2.50
444444	AI149332	Hs.14855	ESTs	2.58	1.38
445033	AV652402	Hs.72901	mucin 13, epithelial transmembrane	2.26	1.13
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.27	5.33
449618	AI076459	Hs.15978	KIAA1272 protein	2.70	3.33
407242	M18728		gb:Human nonspecific crossreacting antig	3.58	1.90
418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	3.32	1.00
423441	R68649	Hs.278359	absent in melanoma 1 like	2.44	2.40
405033			C1002652*:gi|544327|sp|Q04799|FMO5_RABIT	1.75	3.48
423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.72	1.28
425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	2.40	2.78
437928	NM_005476	Hs.5920	UDP-N-acetylglucosamine-2-epimerase/N-ac	2.20	1.53
446584	U53445	Hs.15432	downregulated in ovarian cancer 1	1.38	2.33
436608	AA628980		down syndrome critical region protein DS	3.32	4.53
404440			NM_021048:Homo sapiens melanoma antigen,	2.64	1.00
435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.06	1.09
424098	AF077374	Hs.139322	small proline-rich protein 3	2.47	3.64
437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	2.09	0.91
428036	AW068302		Homo sapiens mRNA for caldesmon, 3' UTR	2.71	4.58
446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.18	2.33
448479	H96115	Hs.21293	UDP-N-acteylglucosamine pyrophosphorylas	2.61	1.81
412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferri	1.90	2.02
401241	AB028989		mitogen-activated protein kinase 8 inter	1.26	2.55
408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.12	1.23
415989	AI267700		ESTs	1.60	1.00
431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.73	1.50
452140	AB007928	Hs.28169	KIAA0459 protein	2.44	2.95
443162	T49951	Hs.9029	DKFZP434G032 protein	2.98	1.00
435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.56	1.20
407379	AA332127	Hs.325804	transcription factor 17	2.10	1.72
442712	BE465168	Hs.131011	ESTs	2.54	2.72
411678	AI907114	Hs.71465	squalene epoxidase	1.12	3.11
406791	AI220684	Hs.347939	hemoglobin, alpha 2	1.69	1.38
431805	NM_014053	Hs.270594	FLVCR protein	1.92	2.05
438414	AA806794	Hs.131511	ESTs	1.04	2.15
413924	AL119964	Hs.75616	seladin-1	1.69	2.05
437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	2.27	2.26
445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	1.42	2.74
408349	BE546947	Hs.44276	homeo box C10	1.60	2.05
422545	X02761	Hs.287820	fibronectin 1	1.77	3.02
406643	N77976	Hs.347939	hemoglobin, alpha 2	1.57	1.35
407228	M25079	Hs.155376	hemoglobin, beta	1.81	1.50
449644	AW960707	Hs.148324	ESTs	1.90	3.19
402305			C19000735*:gi|4508027|ref|NP_003414.1|z	2.25	1.49
427683	BE545490	Hs.15053	Homo sapiens HCMOGT-1 mRNA for sperm ant	1.08	2.25
441690	R81733	Hs.33106	ESTs	1.80	2.65
434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	2.13	1.63
403362			NM_001615*:Homo sapiens actin, gamma 2,	2.33	2.22
445496	AB007860	Hs.12802	development and differentiation enhancin	1.12	2.60
425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	1.83	3.05
402366	AV648601		apolipoprotein B (including Ag(x) antige	1.32	2.05
427254	AL121523	Hs.97774	ESTs	2.44	1.00
414533	AA149060	Hs.296100	ESTs	1.70	2.06
430157	BE348706	Hs.278543	ESTs	2.54	3.00
413433	NM_003199	Hs.326198	transcription factor 4	2.26	1.41
410532	T53088	Hs.155376	hemoglobin, beta	1.52	1.56
405779			NM_005367:Homo sapiens melanoma antigen,	2.42	1.22
450455	AL117424	Hs.25035	chloride intracellular channel 4	2.48	2.13
414081	AW969976	Hs.279009	matrix Gla protein	1.81	1.53
414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	1.65	2.08
415062	H45100	Hs.49753	uveal autoantigen with coiled coil domai	1.62	3.75
406317			C2002658*:gi|6625694|gb|AAF19354.1|AF185	1.68	2.11
453259	R93125	Hs.124187	ESTs	1.08	2.25
445937	AI452943	Hs.321231	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	1.76	1.01
434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	1.12	2.08
418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.02	2.40

432331	W37862	Hs.274368	MSTP032 protein	4.36	2.18
451736	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.51	3.45
413109	AW389845	Hs.110855	ESTs	4.34	5.98
413643	AA130987	Hs.188727	ESTs	1.30	2.42
433217	AB040914	Hs.278628	KIAA1481 protein	1.70	2.49
435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	1.79	1.66
438006	BE148799	Hs.127951	hypothetical protein FLJ14503	1.76	2.04
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	2.32	2.45
433656	AW974941	Hs.292385	ESTs, Weakly similar to I78885 serine/th	1.14	2.50
415714	NM_002290	Hs.78672	laminin, alpha 4	2.52	1.13
450282	AA007655	Hs.93523	ESTs	1.40	2.58
442855	AI074465	Hs.133469	ESTs	1.54	2.20
432917	NM_014125	Hs.241517	PRO0327 protein	2.24	3.03
429041	AJ132820	Hs.194768	a disintegrin and metalloproteinase doma	1.61	2.60
442807	AL049274	Hs.8736	Homo sapiens mRNA; cDNA DKFZp564H203 (fr	1.73	1.19
427719	AI393122	Hs.134726	ESTs	1.46	2.00
408778	AI500519	Hs.63382	hypothetical protein PRO2714	1.46	2.58
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.40	2.03
424425	AB031480	Hs.146824	SPR1 protein	1.60	1.11
445391	T92576	Hs.191168	ESTs	1.69	2.40
446899	NM_005397	Hs.16426	podocalyxin-like	1.22	2.42
420996	AK001927	Hs.100895	hypothetical protein FLJ10462	2.68	2.98
424909	S78187	Hs.153752	cell division cycle 25B	2.18	1.33
413593	AA205248		gb:zq78c12.r1 Stratagene hNT neuron (937	1.69	2.00
408734	AW264996	Hs.254299	ESTs	2.06	2.94
413880	AI660842	Hs.110915	interleukin 22 receptor	1.24	2.20
437063	AA351109	Hs.5437	Tax1 (human T-cell leukemia virus type I	1.78	2.60
418044	AI640532	Hs.119830	ESTs, Weakly similar to ALUF_HUMAN !!!!	1.54	2.53
441971	W27060	Hs.265855	ESTs	1.62	2.13
450401	AW959281	Hs.8184	ESTs	1.42	2.30
440157	AA868350	Hs.343636	ESTs	1.38	2.60
457587	AA992841	Hs.27263	KIAA1458 protein	1.47	2.42
440707	BE256751	Hs.22867	Homo sapiens cDNA: FLJ22073 fis, clone H	1.18	2.10
402241			Target Exon	2.58	2.52
413428	AA430155	Hs.151343	KIAA1524 protein	1.22	2.45
416735	R11275	Hs.194485	ESTs	1.14	2.14
421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.25	1.03
431031	AA830335	Hs.105273	ESTs	2.35	2.95
433336	AF017986	Hs.31386	secreted frizzled-related protein 2	3.72	1.00
420786	AW296466	Hs.43628	deleted in lymphocytic leukemia, 2	1.23	2.60
401335			Target Exon	1.18	1.68
417670	R07785		gb:yf15c06.r1 Soares fetal liver spleen	1.56	2.00
406314			C14001020:gi|12597441|gb|AAG60049.1|AF31	1.60	3.08
458981	AW968318	Hs.285996	hypothetical protein FLJ23375	1.70	2.50
417509	AA203414	Hs.42009	ESTs	1.82	2.05
452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	1.34	1.37
418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	1.37	1.02
457871	AI168278		ESTs	1.20	2.19
444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.43	1.22
413276	Z24725	Hs.75260	mitogen inducible 2	1.78	2.28
421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	2.55	2.60
417151	AA194055	Hs.293858	ESTs	1.68	1.67
453556	AA425414	Hs.33287	nuclear factor I/B	2.06	2.40
440859	AW070865	Hs.346390	ESTs	1.12	1.70
420629	AW204343	Hs.156823	ESTs, Weakly similar to T30868 RhoA-bind	1.21	2.38
422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	1.58	2.15
434831	AA248060	Hs.273397	KIAA0710 gene product	1.69	1.78
412055	AA099907	Hs.271806	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.36	2.65
445468	AW450439		ESTs	1.52	2.50
444550	BE250716	Hs.87614	ESTs	1.30	2.28
417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.50	3.02
430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (f	1.24	2.95
413444	BE141019		gb:MR0-HT0067-201099-002-b10 HT0067 Homo	1.68	2.80
433844	AA610175	Hs.179647	Homo sapiens cDNA FLJ12195 fis, clone MA	1.49	2.01
427055	AI301740	Hs.173381	dihydropyrimidinase-like 2	1.11	2.58
454244	R51604	Hs.300842	KIAA1608 protein	1.00	2.02
429503	AA394183	Hs.26873	ESTs	2.58	4.08
422940	BE077458		gb:RC1-BT0606-090500-015-b04 BT0606 Homo	3.48	2.46
407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.13	1.48
437312	AA809350	Hs.246180	ESTs	1.10	2.05
449426	T92251	Hs.198882	ESTs	1.22	2.08
447620	AW290951	Hs.224965	ESTs	1.80	2.18
444700	NM_003645	Hs.11729	fatty-acid-Coenzyme A ligase, very long-	1.72	2.81
436258	AW867491	Hs.107125	plasmalemma vesicle associated protein	1.99	1.80
415712	AW249188	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	1.66	2.98
432877	AW974111	Hs.292477	ESTs	1.63	2.79
412085	AW891667		gb:CM3-NT0089-110500-179-h09 NT0089 Homo	1.40	2.08

431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	1.96	3.58
409714	AW367812	Hs.199961	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.24	2.10
423013	AW875443	Hs.22209	secreted modular calcium-binding protein	1.49	2.09
422663	AW500087	Hs.119014	zinc finger protein 175	1.01	2.78
439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	1.54	2.57
413196	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma	1.04	2.18
439349	AI660898	Hs.195602	ESTs	2.03	2.43
443005	AI027184	Hs.200918	ESTs	1.42	2.10
424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.58	3.43
427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	2.08	1.70
413916	N49813	Hs.75615	apolipoprotein C-II	0.70	0.42
418332	R34976	Hs.78293	ESTs	2.74	2.43
426552	BE297660	Hs.170328	moesin	1.28	1.52
456583	AF179897	Hs.104105	Meis (mouse) homolog 2	1.42	2.02
447214	AI367288	Hs.273621	Homo sapiens cDNA: FLJ21350 fis, clone C	1.14	2.10
449254	W26908	Hs.172762	ESTs	2.04	2.50
443651	W22152	Hs.282929	ESTs	2.94	3.08
421021	AA808018	Hs.109302	ESTs	1.41	2.04
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.61	1.21
432027	AL096678	Hs.272353	KIAA0957 protein	1.70	2.76
452688	AA721140	Hs.49930	ESTs, Weakly similar to putative p150 [H	1.80	2.95
417042	C75563	Hs.113029	ribosomal protein S25	2.22	3.20
443574	U83993	Hs.321709	purinergic receptor P2X, ligand-gated io	1.21	2.51
429372	AA451859	Hs.99253	ESTs	1.28	2.43
424290	AA338396		gb:EST43386 Fetal brain I Homo sapiens c	1.82	2.03
428518	AW969656		gb:EST381733 MAGE resequences, MAGK Homo	1.72	2.52
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	1.65	3.03
414665	AA160873	Hs.332053	serum amyloid A1	1.36	1.08
418298	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	1.04	2.03
429655	U48959	Hs.211582	myosin, light polypeptide kinase	4.94	4.34
433924	AA618304	Hs.258785	ESTs	1.44	2.40
452683	AI089575	Hs.9071	progesterone membrane binding protein	1.48	2.48
439437	AI207788	Hs.343628	sialyltransferase 4B (beta-galactosidase	1.36	2.33
432314	AA533447	Hs.312989	ESTs	0.96	2.78
400881			NM_025080:Homo sapiens hypothetical prot	1.70	3.15
426477	AA379464		gb:EST92386 Skin tumor I Homo sapiens cD	2.01	2.37
454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	2.12	3.44
423977	AA333232		gb:EST37283 Embryo, 8 week I Homo sapien	1.38	2.13
450396	AU077002	Hs.24950	regulator of G-protein signalling 5	2.13	3.28
431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	1.90	2.23
415157	D63257		gb:HUM514B08B Clontech human placenta po	1.29	2.90
418236	AW994005	Hs.337534	ESTs	1.74	2.37
454390	AB020713	Hs.56966	KIAA0906 protein	1.47	1.38
436143	AA705245	Hs.192189	ESTs	1.46	2.45
436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	1.43	2.07
450735	AI732321		SRY (sex determining region Y)-box 4	1.36	2.02
420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	2.70	1.68
447100	AI361801	Hs.167130	hypothetical protein	1.66	2.03
453577	AL043049		gb:DKFZp434A1523_r1 434 (synonym: htes3)	1.41	2.75
408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.59	1.38
412632	AL120379	Hs.74294	aldehyde dehydrogenase 7 family, member	1.81	2.51
423291	NM_004129	Hs.126590	guanylate cyclase 1, soluble, beta 2	1.54	2.83
456172	R99050		gb:yq65c02.r1 Soares fetal liver spleen	1.46	2.68
452123	AI267615	Hs.38022	ESTs	1.24	1.93
433900	AA721668	Hs.257761	ESTs	1.78	2.66
408436	R31954	Hs.7885	phosphatidylinositol binding clathrin as	1.21	2.35
417123	BE326521	Hs.159450	ESTs	1.46	2.09
436023	T81819	Hs.302251	ESTs	2.68	2.70
454150	AA131893	Hs.154088	hypothetical protein FLJ22756	1.40	2.50
444094	AI695764	Hs.202394	ESTs	1.28	4.03
429176	AW975021	Hs.193800	ESTs	1.08	2.53
422259	AA307584		gb:EST178498 Colon carcinoma (HCC) cell	1.80	3.03
451164	AA015912	Hs.60659	ESTs, Weakly similar to T46471 hypotheti	1.47	1.17
417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (Ig),	2.92	2.70
455642	BE063965		gb:QV3-BT0296-140200-085-h01 BT0296 Homo	1.70	2.70
443387	BE139135	Hs.254629	ESTs	1.48	2.32
420995	AA282495	Hs.89014	ESTs	1.45	1.51
407329	AA576061	Hs.269834	ESTs, Weakly similar to ALUD_HUMAN !!!!	1.13	2.38
438797	C16161	Hs.283040	hypothetical protein PRO2543	0.99	2.75
443357	AW016773		low molecular mass ubiquinone-binding pr	1.60	2.08
412656	AF006011	Hs.74375	dishevelled 1 (homologous to Drosophila	1.32	1.13
427377	AU077029	Hs.177543	antigen identified by monoclonal antibod	1.24	0.79
412200	R08110	Hs.187462	ESTs, Weakly similar to I38022 hypotheti	1.35	1.54
432586	AA568548		ESTs	1.50	2.25
411590	T96183		gb:ye09f07.s1 Stratagene lung (937210) H	1.22	2.53
422672	X12784	Hs.119129	collagen, type IV, alpha 1	2.27	2.20
420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	1.59	2.11

419900	AI469960	Hs.170698	ESTs	1.30	2.68
410805	AW804742	Hs.84264	acidic protein rich in leucines	1.16	2.28
452560	BE077084	Hs.99969	ESTs	1.44	2.58
448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	4.02	1.00
424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	1.10	2.00
447400	AK000322	Hs.18457	hypothetical protein FLJ20315	1.45	1.28
422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	1.82	2.10
443696	AW607444	Hs.134622	ESTs	1.98	2.01
436094	AI798701	Hs.222222	ESTs	1.34	2.40
420168	AF217508	Hs.95594	serine carboxypeptidase vitellogenic-lik	1.58	2.45
430325	AF004562	Hs.239356	syntaxin binding protein 1	1.34	2.43
439022	AA356599	Hs.173904	ESTs	2.76	2.40
420563	AA278327	Hs.136237	ESTs, Moderately similar to Y140_HUMAN H	1.78	2.65
429494	AA769365	Hs.126058	ESTs	1.50	2.40
420689	H79979	Hs.88678	ESTs	1.26	2.28
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.72	1.29
439943	AW083789	Hs.124620	ESTs	1.45	2.84
442300	AI765908	Hs.129166	ESTs	1.24	2.35
449614	AI989490	Hs.197703	ESTs	1.12	2.22
444363	AI142827	Hs.143656	ESTs	1.32	2.08
424479	AF064238	Hs.149098	smoothelin	1.59	1.10
437321	AA768966	Hs.292026	ESTs, Weakly similar to 2109260A B cell	1.28	2.07
431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	1.52	2.63
433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	1.69	1.30
415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.71	2.19
437199	AL110175	Hs.306337	*Homo sapiens mRNA; cDNA DKFZp564H0616 (f*	1.48	2.50
457450	AW294163	Hs.146127	ESTs	1.07	2.60
456678	AF141305	Hs.173736	ancient ubiquitous protein 1	1.44	2.35
451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	0.95	3.00
405944			Target Exon	1.48	2.45
408877	AA479033	Hs.130315	ESTs, Weakly similar to A47582 B-cell gr	1.38	2.20
446682	AW205632	Hs.211198	ESTs	1.38	3.00
431380	AW610282	Hs.291003	ESTs	1.43	2.64
442027	AI652926	Hs.128395	ESTs	1.18	2.43
423578	AW960454	Hs.222830	ESTs	1.56	2.18
441495	AW294603	Hs.127039	ESTs	2.80	1.73
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.36	1.18
443949	AW827419	Hs.235070	ESTs	1.30	2.28
440495	AA887212	Hs.14161	hypothetical protein DKFZp434I1930	1.74	2.78
449948	R19156	Hs.20798	ESTs	1.12	2.23
439564	W77911	Hs.110006	ESTs	1.34	2.85
423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.24	1.09
436139	AA765786	Hs.120936	ESTs	1.30	2.10
456968	AI174861	Hs.190623	ESTs	1.14	2.15
437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	1.21	2.18
411652	AW855393		gb:CM3-CT0275-191099-024-f10 CT0275 Homo	1.85	1.94
420732	AA789133	Hs.88650	ESTs	1.66	2.71
409291	AW373472		gb:RC3-BT0523-181299-011-d12 BT0523 Homo	1.56	2.30
424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.56	1.39
424927	AW973666	Hs.153850	hypothetical protein C321D2.4	1.58	1.24
450946	AA374569	Hs.127698	ESTs, Moderately similar to 2109260A B c	1.02	2.25
428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	1.70	2.39
415361	F06724		gb:HSC1IG021 normalized infant brain cDN	1.34	2.40
406490			C5001926:gi|7511572|pir||T42245 probable	1.28	2.40
410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	1.52	2.00
440010	AA534930	Hs.127236	hypothetical protein FLJ12879	1.12	2.20
429508	AW369620	Hs.33944	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.33	2.28
426340	Z97989	Hs.169370	FYN oncogene related to SRC, FGR, YES	1.88	2.18
416889	AW250318	Hs.80395	mal, T-cell differentiation protein	1.65	1.16
451870	AI820991	Hs.8377	ESTs	1.24	2.03
444091	AV647924	Hs.282376	ESTs	1.05	2.13
410793	AW581906	Hs.66392	*intersectin 1 (SH3 domain protein)*	2.00	3.13
452222	AW806287	Hs.21432	SEX gene	1.25	1.10
433010	AW970018		gb:EST382097 MAGE resequences, MAGK Homo	1.36	2.41
432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	1.14	2.03
438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	2.24	1.77
448718	AA220235	Hs.153959	hypothetical protein MGC15436	1.52	2.65
402685			Target Exon	2.04	2.46
424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.66	2.05
422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	1.89	4.98
451225	AI433694	Hs.293608	ESTs	1.79	2.70
441078	AI453268	Hs.323409	Homo sapiens cDNA FLJ14113 fis, clone MA	1.44	2.58
409406	H83092	Hs.49605	ESTs	1.38	2.05
422297	AW961290		p30 DBC protein	1.20	2.73
408711	AW376061	Hs.63335	ESTs, Moderately similar to A46010 X-lin	1.20	2.08
426696	AW363332	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H	1.35	2.68
417324	AW265494		ESTs	1.68	1.25

408283	BE141579		gb:QV2-HT0083-071299-018-b05 HT0083 Homo	1.25	2.65
415166	NM_003652	Hs.78068	carboxypeptidase Z	1.34	1.09
406300			Target Exon	1.61	2.47
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	3.60	4.03
422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	2.16	1.44
422567	AF111178	Hs.118407	glypican 6	1.57	2.03
436855	AA732624	Hs.165852	ESTs	1.08	2.75
403536			Target Exon	0.93	2.13
447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.18	1.07
417117	N46778		gb:yy52b02.r1 Soares_multiple_sclerosis_	1.70	2.85
411690	AA669253	Hs.136075	RNA, U2 small nuclear	2.12	2.78
443243	AI452496	Hs.132056	ESTs	1.15	2.83
423074	AL109963		FSH primary response (LRPR1, rat) homolo	1.37	1.43
408916	AW295232	Hs.429	*ATP synthase, H transporting, mitochondr*	1.63	2.23
449799	AI143466	Hs.125060	ESTs	1.40	2.08
415378	T16964		gb:NIB2079-5R Normalized infant brain, B	1.88	1.85
431089	BE041395		ESTs, Weakly similar to unknown protein	1.57	2.57
434959	AW974949	Hs.186564	ESTs, Weakly similar to I38022 hypotheti	1.30	2.30
416311	D80529		gb:HUM081H05B Human fetal brain (TFujiwa	1.58	4.35
444614	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	1.88	2.98
456206	NM_006895	Hs.81182	histamine N-methyltransferase	1.24	2.08
410583	AW770280	Hs.36258	ESTs, Moderately similar to JC5238 galac	1.56	4.33
430410	AF099144	Hs.334455	tryptase beta 1	1.91	1.58
408139	AA451966		RAB9-like protein	1.42	2.14
432621	AI298501	Hs.12807	ESTs, Weakly similar to T46428 hypotheti	2.08	1.94
441584	AW148329	Hs.175208	ESTs	1.12	2.05
445940	D60438	Hs.34779	ESTs	1.86	2.70
453022	AA031499	Hs.118489	ESTs	2.02	1.75
444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.54	1.29
442994	AI026718	Hs.16954	ESTs	3.60	3.78
402085			*C18000504*:gi|2627436|gb|AAB86683.1| (AF*	1.36	2.53
411918	AW876354		gb:PM4-PT0019-141299-009-F08 PT0019 Homo	2.00	2.63
455508	AW976165		gb:EST388274 MAGE resequences, MAGN Homo	1.70	3.04
426106	AI678765	Hs.21812	ESTs	1.49	2.11
425131	BE252230	Hs.99163	ESTs	2.04	2.65
440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	1.17	2.55
420447	AA687306	Hs.88448	ESTs	1.66	2.58
428055	AA420564	Hs.101760	ESTs	1.08	2.15
422110	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	1.76	1.82
438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serin	1.08	2.10
403290			C10001011*:gi|4758212|ref|NP_004411.1| d	0.97	2.48
408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	1.42	1.41
432390	AA936177	Hs.274460	olfactory receptor, family 5, subfamily	1.26	2.05
443441	AW291196	Hs.92195	ESTs	1.52	2.13
419925	AA159850	Hs.93765	lipoma HMGIC fusion partner	1.72	2.80
445256	AI858635	Hs.144763	ESTs	1.97	3.33
456381	AA236606		gb:zr99b10.r1 NCI_CGAP_GCB1 Homo sapiens	1.16	1.95
422433	AA310560	Hs.153746	hypothetical protein FLJ22490	1.06	2.20
432529	AI989507	Hs.162245	ESTs	1.36	2.25
424951	AW964082		gb:EST376155 MAGE resequences, MAGH Homo	2.22	2.58
420785	H89633	Hs.191346	ESTs	1.26	2.15
411347	AW838126		gb:QV2-LT0051-240300-097-f01 LT0051 Homo	1.38	2.38
438742	AW204126	Hs.196543	ESTs	1.10	2.30
414900	AW452420	Hs.248678	ESTs	2.01	3.08
443284	AI369813	Hs.64783	ESTs, Weakly similar to T42705 hypotheti	0.66	0.43
402049			Target Exon	2.28	2.00
429400	AW604940	Hs.201668	transcription factor 20 (AR1)	1.16	2.00
423916	AW993496	Hs.17235	Homo sapiens clone TCCCIA00176 mRNA sequ	1.59	1.05
432495	AW973537	Hs.186734	ESTs, Weakly similar to I61746 pheromone	1.50	2.05
414840	R27319	Hs.23823	hairy/enhancer-of-split related with YRP	1.89	2.09
428711	R46414	Hs.56828	trinucleotide repeat containing 5	1.77	1.83
448609	AW139420	Hs.7972	KIAA0871 protein	1.14	2.26
443859	NM_013409	Hs.9914	follistatin	1.17	1.05
411141	AW819561		gb:RC5-ST0293-140200-013-G04 ST0293 Homo	1.44	2.40
440116	AI798851	Hs.266959	hemoglobin, gamma G	1.18	2.08
417944	AU077196	Hs.82985	collagen, type V, alpha 2	2.10	1.37
429640	U83508	Hs.2463	angiopoietin 1	1.92	2.98
410064	X53416	Hs.195464	filamin A, alpha (actin-binding protein-	1.51	1.29
458218	AI435179	Hs.126820	ESTs	1.49	1.15
443114	AI033377	Hs.153298	ESTs	1.38	2.05
427788	AA412397	Hs.116858	ESTs	1.45	1.85
435913	W95006	Hs.269559	ESTs, Weakly similar to S65657 alpha-1C-	1.63	3.90
457949	W69171	Hs.71741	ESTs, Highly similar to I38945 melanoma	1.01	2.00
419203	AA488719	Hs.190151	ESTs	1.94	2.45
412510	AI056689	Hs.133538	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.91	2.20
413885	BE177442		gb:RC1-HT0595-200400-012-f01 HT0595 Homo	1.48	2.80
426239	AA669615	Hs.214226	ESTs	1.36	2.50

408866	AW292096	Hs.255036	ESTs	1.93	2.92
412857	AI703484	Hs.128052	ESTs	1.72	1.60
427340	BE167242	Hs.47099	hypothetical protein FLJ21212	1.46	2.13
412902	BE008018		gb:QV0-BN0147-290400-214-c01 BN0147 Homo	0.90	2.05
451141	AW772713	Hs.247186	ESTs	2.38	3.95
412626	AA114945	Hs.151839	ESTs	1.75	2.15
405667			Target Exon	2.62	3.79
417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	1.24	2.08
401400			Target Exon	1.16	1.90
426796	S78234	Hs.172405	cell division cycle 27	2.14	1.63
435046	AA662772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.14	2.28
448401	AI498509	Hs.346254	ESTs	2.50	2.83
450832	AW970602	Hs.105421	ESTs	0.55	0.39
441057	AL043897	Hs.126483	ESTs	1.08	2.13
438725	AA815163	Hs.127307	ESTs	1.31	2.65
450062	AW001043	Hs.200854	ESTs	1.30	2.48
441214	AI820648	Hs.129136	ESTs	1.43	1.71
431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.22	2.30
414907	X90725	Hs.77597	polo (Drosophia)-like kinase	1.35	1.49
423622	BE154847		gb:PM1-HT0345-121199-001-d05 HT0345 Homo	1.57	2.30
450835	BE262773	Hs.25584	hypothetical protein FLJ10767	1.40	1.12
444014	AI095718	Hs.135015	ESTs	2.30	1.78
431603	AA807955	Hs.325984	EST	1.28	2.03
408697	AW419069	Hs.209670	ESTs	1.35	2.60
444312	R44007		ESTs	1.95	2.07
404286			C6001909:gi|704441|dbj|BAA18909.1| (D298	2.29	2.22
438813	M27346		gb:Homo sapiens (clone HGP09/HGP32) T ce	1.03	2.43
445534	AL038823	Hs.12840	Homo sapiens germline mRNA sequence	1.00	2.16
426046	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	1.59	2.73
451907	AI822065	Hs.50749	ESTs, Moderately similar to ALU7_HUMAN A	1.74	2.65
418796	AA228351	Hs.34060	ESTs	1.28	2.12
422431	AI769410	Hs.221461	ESTs	1.80	3.58
417557	AA225622	Hs.293589	ESTs	1.32	2.14
455313	AW894409	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	1.48	2.57
415479	F10042	Hs.4840	ESTs	1.83	2.01
450433	AW444538	Hs.231863	ESTs	1.31	2.58
410581	AA018982	Hs.125036	tumor endothelial marker 7 precursor	1.54	1.62
455407	AW936813		gb:PM2-DT0023-050400-003-b10 DT0023 Homo	1.32	2.15
417552	R00916	Hs.166510	ESTs	1.50	2.63
428290	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	1.94	2.70
432391	AI732374	Hs.339827	Human DNA sequence from clone RP5-881L22	0.96	2.38
456283	U68162	Hs.84171	myeloproliferative leukemia virus oncoge	1.22	2.13
438535	L09078		gb:Homo sapiens mRNA fragment	2.14	1.95
416564	AW795793	Hs.2575	Homo sapiens cDNA FLJ12257 fis, clone MA	2.28	1.93
435200	AA670310	Hs.145903	ESTs	1.16	2.13
457635	AV660976	Hs.3569	hypothetical protein	1.37	3.10
444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	0.99	2.45
449319	AA373630	Hs.188750	ESTs	1.56	3.28
418992	AW074143	Hs.87134	ESTs	1.88	2.20
409367	AW382767		gb:PM0-HT0339-081199-001-h05 HT0339 Homo	1.30	2.50
434973	AW449285	Hs.313636	EST	1.11	2.65
408383	BE466959	Hs.144153	ESTs	1.30	2.44
440100	BE382685	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.23	2.71
431996	AL122087	Hs.272304	Homo sapiens mRNA; cDNA DKFZp564C0371 (f	1.24	2.27
427681	AB018263	Hs.180338	tumor necrosis factor receptor superfami	1.70	1.68
405146			C8001690*:gi|6754446|ref|NP_034760.1| ki	2.00	0.68
436154	AA764950	Hs.119898	ESTs	1.43	3.00
451233	AA047221	Hs.59752	ESTs	1.38	2.20
446856	AI814373	Hs.164175	ESTs	1.33	3.93
448211	BE384592	Hs.6451	PRO0659 protein	1.48	2.73
418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	1.33	2.68
409609	AW444670	Hs.335685	ESTs	1.27	1.51
450414	AI907735	Hs.21446	KIAA1716 protein	1.60	1.24
452929	AW954938	Hs.172816	neuregulin 1	2.01	3.70
435112	AW976145	Hs.143198	inhibitor of growth family, member 3	1.22	1.30
439806	AA846824	Hs.180908	ESTs	0.80	2.04
439910	H66765	Hs.339397	ESTs	1.28	2.16
437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	1.06	2.82
441354	AA931221	Hs.126813	ESTs	1.20	2.28
428951	AL138153	Hs.300410	ESTs, Moderately similar to A47582 B-cel	1.50	1.83
438272	AI167963	Hs.143700	ESTs, Weakly similar to S65824 reverse t	1.34	2.51
429642	X68264	Hs.211579	melanoma cell adhesion molecule	1.18	1.18
422121	AI767949	Hs.179833	ESTs	1.18	2.26
411184	AW821117		gb:PM2-ST0303-170100-003-g03 ST0303 Homo	1.18	2.21
435871	AF257077	Hs.283627	eukaryotic translation initiation factor	1.17	1.57
430570	AI417881	Hs.292464	ESTs	1.49	3.17
431995	AL080197	Hs.272302	hypothetical protein	1.52	2.11

451326	AW296946	Hs.256078	ESTs	1.19	2.18
437046	BE149154		gb:RC2-HT0252-271099-017-c11 HT0252 Homo	1.18	2.25
410154	F06959		gb:HSC1QD011 normalized infant brain cDN	1.41	2.05
434373	AI565566	Hs.168587	ESTs	1.39	1.33
444552	AW295211	Hs.230777	ESTs	1.36	2.20
411608	AW853441		gb:RC1-CT0252-030100-023-g09 CT0252 Homo	2.12	1.80
440573	BE550891	Hs.270624	ESTs	2.19	2.17
443047	AW157377	Hs.132910	ESTs	1.81	2.28
451473	AW298047	Hs.346198	ESTs	1.18	2.30
416265	AA177088	Hs.190065	ESTs	2.37	3.38
435375	AI733610	Hs.187832	ESTs	1.12	2.18
401469			NM_022137*:Homo sapiens secreted modular	1.32	1.61
456152	AA174126	Hs.332163	ESTs	1.26	2.50
415808	R21439	Hs.334578	Homo sapiens, clone IMAGE:3929520, mRNA	1.39	2.43
452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	0.92	2.20
435127	AI217926	Hs.179863	EST	1.36	2.65
420772	AW752656	Hs.222707	KIAA1718 protein	1.19	1.50
456332	AA228357		gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	1.45	3.57
444678	AI741513	Hs.143739	ESTs	1.43	1.62
446175	AL036568	Hs.291	glutamyl aminopeptidase (aminopeptidase	1.00	1.53
416463	H59241		Homo sapiens cDNA FLJ11095 fis, clone PL	1.44	2.13
405158			ENSP00000243337:CDNA FLJ13984 fis, clone	1.38	2.68
403903			C5001632*:gi|10645308|gb|AAG21430.1|AC00	1.32	1.43
407271	X98937		gb:H.sapiens rearranged Ig heavy chain (	1.40	2.68
413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.59	1.33
450778	U81375	Hs.25450	solute carrier family 29 (nucleoside tra	1.17	1.10
434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	1.92	2.80
400075			Eos Control	1.76	2.60
433694	AI208611	Hs.12066	Homo sapiens cDNA FLJ11720 fis, clone HE	1.48	2.33
454826	AW833676		gb:QV4-TT0008-181199-038-h04 TT0008 Homo	1.57	2.89
415168	AA160805	Hs.199832	ESTs, Weakly similar to I78885 serine/th	2.08	1.76
439486	AF086303	Hs.103185	ESTs	1.49	2.19
403291			Target Exon	1.36	2.28
438618	AA897673	Hs.123457	ESTs	0.75	0.79
455087	AW855389		gb:CM3-CT0275-191099-024-e06 CT0275 Homo	0.91	2.63
408075	AA382881	Hs.42409	CGI-146 protein	1.46	2.15
436826	AA731863	Hs.120276	ESTs	1.04	3.11
408961	AW297475	Hs.323180	ESTs	1.25	1.39
424408	AI754813	Hs.146428	collagen, type V, alpha 1	1.64	2.05
423300	AK000742	Hs.126774	L2DTL protein	1.47	3.44
403217	AL134878		ribosomal protein, large P2	1.70	2.22
437990	AI686579	Hs.121784	ESTs	2.14	1.69
419156	AC002366	Hs.46329	amelogenin (X chromosome, amelogenesis I	1.40	1.45
411817	BE302900	Hs.72241	mitogen-activated protein kinase kinase	1.18	1.12
425701	AA361850	Hs.322149	Human clone 137308 mRNA, partial cds	1.60	2.15
418757	AI864193	Hs.169728	hypothetical protein FLJ13150	1.57	2.23
415184	AA380436	Hs.211973	homolog of Yeast RRP4 (ribosomal RNA pro	1.32	2.09
414918	AI219207	Hs.72222	hypothetical protein FLJ13459	1.61	1.50
401723			Target Exon	1.01	2.68
439010	AW170332	Hs.75216	Homo sapiens cDNA FLJ13713 fis, clone PL	1.28	1.65
449166	BE168981	Hs.23131	kinesin family member C3	1.64	2.58
410642	AW792784		gb:CM0-UM0001-010300-258-h11 UM0001 Homo	1.54	1.90
409556	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	1.63	1.21
439894	AA853077	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.76	0.61
401913			ENSP00000249158*:CDNA	0.97	2.59
406097			Target Exon	1.11	1.23
414745	AA160511	Hs.5326	amino acid system N transporter 2; porcu	1.29	1.12
445752	AI733942	Hs.344887	ESTs	2.03	1.68
408052	AW501117	Hs.283585	ESTs	1.32	1.72
407256	AA204763	Hs.288036	tRNA isopentenylpyrophosphate transferas	1.01	2.09
423264	AJ133439	Hs.126076	Glutamate receptor interacting protein	1.51	2.39
418859	AA229558		gb:nc15d10.s1 NCI_CGAP_Pr1 Homo sapiens	1.40	2.35
410370	AB037753	Hs.62767	KIAA1332 protein	1.34	2.00
417264	AA195100	Hs.188695	ESTs	1.09	2.61
444909	AI933051	Hs.192280	ESTs	1.56	2.92
419386	AA236867		ESTs, Weakly similar to I38022 hypothetl	1.14	2.28
439212	AF087995	Hs.134877	ESTs	1.06	2.90
437766	W69171	Hs.71741	ESTs, Highly similar to I38945 melanoma	1.25	2.28
448951	AI611221	Hs.334802	hypothetical protein FLJ10101	1.88	2.17
401659			Target Exon	1.63	2.05
419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	2.63	3.85
444813	AW054834	Hs.210356	ESTs	1.73	2.14
433902	AW292820	Hs.144906	ESTs	1.88	2.46
403072			NM_003319*:Homo sapiens titin (TTN), mRN	1.32	2.91
452484	AB033042	Hs.29679	cofactor required for Sp1 transcriptiona	0.72	0.70
456788	AA724612	Hs.133130	Homo sapiens mRNA; cDNA DKFZp566H0124 (f	1.90	3.40
403315			Target Exon	1.22	2.00

406432	AJ289116		CD1E antigen, e polypeptide	2.31	2.63
457785	AA682670	Hs.160884	ESTs	0.96	2.38
433259	AA580665	Hs.326082	ESTs	1.46	1.07
436882	AW016722	Hs.194976	SH2 domain-containing phosphatase anchor	1.38	2.13
401473			Target Exon	1.47	2.04
444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	1.64	2.15
438029	H61502	Hs.10235	chromosome 5 open reading frame 4	1.44	2.25
431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	1.26	2.21
450817	N71597	Hs.29698	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.20	2.90
404427			C8000068*:gi|5453579|ref|NP_006120.1| bo	0.74	0.81
430658	AW970093	Hs.24453	ESTs	1.45	2.55
405723			Target Exon	1.60	2.28
436896	AW977385	Hs.278615	ESTs	1.17	1.64
411974	AW880414	Hs.84264	acidic protein rich in leucines	1.54	2.08
412528	AI123478	Hs.32112	ESTs	1.72	2.85
446425	AW295364	Hs.255418	ESTs	1.25	1.31
424991	AA775471	Hs.241467	ESTs	0.62	0.37
443100	AI033188		gb:ow94e08.s1 Soares_fetal_liver_spleen_	1.15	2.34
445332	AI220225	Hs.321057	ESTs	1.07	2.00
414781	D50917	Hs.77293	KIAA0127 gene product	1.04	3.43
421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	1.15	2.53
424265	AF173901	Hs.144287	hairy/enhancer-of-split related with YRP	1.26	2.00
446667	BE161878	Hs.224805	ESTs	1.12	2.13
426399	AA652588	Hs.301348	Homo sapiens cDNA FLJ13271 fis, clone OV	2.26	1.29
438190	AA780020	Hs.136798	ESTs, Moderately similar to KBF3_HUMAN N	1.44	2.07
406972	M32053		gb:Human H19 RNA gene, complete cds.	1.38	2.11
417086	AA194446		ESTs, Weakly similar to S55024 nebulin,	2.12	3.30
446410	AI361109	Hs.151721	ESTs, Weakly similar to I38022 hypotheti	1.14	2.33
427674	NM_003528	Hs.2178	H2B histone family, member Q	1.24	1.00
422526	AA311763	Hs.131056	ESTs	1.29	2.04
439317	AF086127	Hs.50600	ESTs, Weakly similar to T47156 hypotheti	1.26	2.12
409126	AA063426		gb:zf70c08.s1 Soares_pineal_gland_N3HPG	1.28	2.20
412093	BE242691	Hs.14947	ESTs	0.87	2.58
420169	AA256126	Hs.16179	hypothetical protein FLJ23467	1.38	2.07
426096	D87436	Hs.166318	lipin 2	2.00	2.25
402551			NM_005012*:Homo sapiens receptor tyrosin	0.80	0.82
405760			Target Exon	1.44	2.85
402901			NM_025206*:Homo sapiens hypothetical pro	1.63	1.27
453982	AW014252	Hs.252837	ESTs	1.44	2.03
424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	1.40	1.18
439984	BE559514	Hs.275425	hypothetical protein	1.30	2.15
457297	AW968188		gb:EST380383 MAGE resequences, MAGJ Homo	1.64	3.17
415054	AI733907		gb:zo86h09.y5 Stratagene ovarian cancer	1.00	2.20
426273	AI174861	Hs.190623	ESTs	1.19	1.16
405187			NM_014272:Homo sapiens a disintegrin-lik	1.31	1.35
413939	AL047051	Hs.199961	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.44	1.88
427596	AA449506	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.06	1.50
408049	AW076098	Hs.345588	desmoplakin (DPI, DPII)	2.01	3.90
406002			Target Exon	1.73	2.08
408284	AW248254	Hs.44101	protein kinase PKNbeta	1.28	1.31
431377	AW178807	Hs.246182	ESTs	1.40	2.70
451456	AW386183	Hs.210305	ESTs	1.44	2.08
427530	AA405093	Hs.126519	ESTs	1.07	1.12
431957	AK002104	Hs.272246	hypothetical protein FLJ11292	1.27	2.89
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.74	1.28
419600	AA448958	Hs.91481	NEU1 protein	1.13	1.15
423314	AI400661	Hs.127811	disintegrin metalloproteinase with throm	1.44	2.53
451690	AW451469	Hs.209990	ESTs	1.41	2.49
454662	AW812715		gb:RC4-ST0185-271099-011-g01 ST0185 Homo	1.35	2.86
454413	AI653672	Hs.40092	PNAS-123	1.79	2.03
416861	AW977206	Hs.151858	ESTs	1.52	2.10
415908	H08623	Hs.22833	ESTs	1.37	2.13
438942	AW875398	Hs.6451	PRO0659 protein	1.80	1.55
407618	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	2.16	3.18
429177	AA447527	Hs.207429	ESTs	1.74	3.19
448357	N20169	Hs.108923	RAB38, member RAS oncogene family	0.77	0.73
422008	AJ000534	Hs.110708	sarcoglycan, epsilon	1.52	4.08
434461	AA744046	Hs.133350	ESTs, Weakly similar to I78885 serine/th	1.66	2.16
413489	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	1.28	2.23
405551			Target Exon	1.11	1.19
441183	BE562910	Hs.92679	Homo sapiens clone CDABP0014 mRNA sequen	1.20	1.20
456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	1.98	2.53
420611	AA994635	Hs.129929	ESTs	1.46	2.15
422061	BE178434	Hs.267995	ESTs, Moderately similar to G02654 ribos	1.42	2.30
437908	AI082424		ESTs	1.38	2.21
423052	M28214	Hs.123072	RAB3B, member RAS oncogene family	0.74	0.43
401927			C17000914*:gi|8394367|ref|NP_058549.1| s	2.26	2.14

432967	AA572949	Hs.207566	ESTs	1.52	2.28
439159	AF087972	Hs.120938	ESTs	2.03	2.08
415357	H22757	Hs.13471	ESTs	1.82	2.07
442327	AA991745	Hs.42522	ESTs	1.48	2.88
430186	AB020696	Hs.234791	KIAA0889 protein	1.46	2.23
426971	AI809984	Hs.243209	ESTs, Weakly similar to NPA1_HUMAN NEURO	1.06	2.13
422687	AW068823	Hs.119206	insulin-like growth factor binding prote	1.61	1.37
432954	AI076345	Hs.214199	ESTs	1.19	2.84
429040	AL035542	Hs.248169	olfactory receptor, family 2, subfamily	1.25	1.44
414169	AA136169	Hs.149335	ESTs	1.59	2.51
419882	AA687313	Hs.190043	ESTs	1.20	2.50
426900	AW163564	Hs.142375	ESTs	1.87	1.77
418773	T39748	Hs.325474	Target CAT	1.35	2.02
439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	1.32	2.10
428712	AW085131	Hs.190452	KIAA0365 gene product	1.41	1.52
408839	AW277084		gb:xp61h09.x1 NCI_CGAP_Ov39 Homo sapiens	1.14	2.03
450492	AW290961	Hs.201815	ESTs	1.17	2.21
434654	AI825942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	1.62	2.31
457567	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	1.80	3.73
452426	AI904823	Hs.31297	duodenal cytochrome b	2.15	1.84
418559	AA225048	Hs.104207	ESTs	1.84	2.33
439099	AB037800	Hs.6462	protein kinase C and casein kinase subst	1.07	1.15
451984	R60571	Hs.27406	Homo sapiens mRNA; cDNA DKFZp566F1946 (f	1.18	1.22
420789	AI670057	Hs.199882	ESTs	2.24	2.55
456396	AA236863	Hs.188894	ESTs, Weakly similar to APXL_HUMAN APICA	1.07	1.14
402948			NM_025206:Homo sapiens hypothetical prot	2.41	1.83
426405	AW296631	Hs.283403	ESTs	1.28	1.07
439732	AW629604	Hs.167641	hypothetical protein from EUROIMAGE 1703	0.85	0.77
416784	AA334592	Hs.79914	lumican	1.88	1.27
422531	AW967280	Hs.293894	ESTs, Weakly similar to HERC2 [H.sapiens	1.20	1.25
415608	F12795	Hs.12286	ESTs, Moderately similar to ALU1_HUMAN A	1.03	2.31
428671	BE297851	Hs.189482	zinc finger protein 179	1.26	2.20
420007	H13700	Hs.31235	ESTs, Weakly similar to Y934_HUMAN HYPOT	1.60	2.25
400850			Target Exon	1.22	1.03
404580			trichorhinophalangeal syndrome I gene (T	1.00	1.00
407680	AW064284	Hs.279153	ESTs	1.02	2.28
410420	AA224053	Hs.172405	cell division cycle 27	1.64	1.00
421234	AA907153	Hs.190060	ESTs	1.76	1.45
426791	AA384910	Hs.46519	ESTs	1.12	2.15
430439	AL133561		DKFZP434B061 protein	1.00	1.00
434036	AI659131	Hs.197733	hypothetical protein MGC2849	1.00	1.00
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.40	1.00
440304	BE159984	Hs.125395	ESTs	1.00	1.00
441699	AW511126	Hs.127572	ESTs	1.00	1.73
443383	AI792453	Hs.166507	ESTs	2.04	1.00
445660	AI702668	Hs.201955	ESTs	1.00	1.00
453160	AI263307	Hs.239884	H2B histone family, member L	1.00	1.00
456513	AA279143	Hs.88561	ESTs	1.00	1.40
457231	AI472022	Hs.301959	proline synthetase co-transcribed (bacte	0.98	0.63
459565	W27086	Hs.209694	ESTs	1.00	1.00
429317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ21243 fis, clone C	1.00	1.00
430971	M26150	Hs.248177	H3 histone family, member L	1.14	1.40
408376	AW971303	Hs.292601	ESTs	1.08	1.60
411920	AW876263		gb:PM4-PT0019-131299-006-E09 PT0019 Homo	0.82	0.45
457389	AW970989		gb:EST383074 MAGE resequences, MAGK Homo	0.92	0.71
408565	BE502544	Hs.282244	ESTs, Weakly similar to peptidoglycan re	1.00	2.10
438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	1.00	1.00
446779	AI341135	Hs.156084	ESTs	1.06	2.02
441691	AI015418	Hs.127556	ESTs	1.13	2.03
402039			Target Exon	0.44	0.36
437133	AB018319	Hs.5460	KIAA0776 protein	0.95	0.63
438089	W05391		nuclear receptor subfamily 1, group I, m	3.12	1.00
409582	R27430	Hs.271565	ESTs	1.00	1.00
428769	AW207175	Hs.106771	ESTs	1.00	1.48
442868	AI022701	Hs.336984	ESTs	1.27	1.62
439559	AW364675	Hs.173921	ESTs, Weakly similar to 2109260A B cell	1.00	1.33
426958	R18845	Hs.172979	zinc finger protein 177	1.24	2.25
419015	T79262	Hs.14463	ESTs	1.16	2.03
415806	AA169560		gb:zo89d08.r1 Stratagene ovarian cancer	1.00	1.33
436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypotheti	1.60	2.21
458760	AI498631	Hs.111334	ferritin, light polypeptide	1.10	1.43
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	1.28	1.00
438182	AW342140	Hs.182545	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.90	2.31
438091	AW373062		nuclear receptor subfamily 1, group I, m	4.70	1.00
441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	2.48	1.00
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.96	2.84
416055	Z45423	Hs.13349	Homo sapiens cDNA FLJ14647 fis, clone NT	1.52	1.46

417895	AA836392	Hs.56237	hypothetical protein FLJ20495	1.05	1.18
422959	AV647015		paired immunoglobulin-like receptor beta	1.33	1.25
408969	AW297929	Hs.328317	EST	1.88	2.07
409536	H59024	Hs.14485	Homo sapiens cDNA: FLJ23220 fis, clone A	1.18	2.38
447449	AW137091	Hs.18624	KIAA1052 protein	1.07	1.13
437315	AW976247	Hs.153248	ESTs	1.16	2.53
459317	BRCA1b		Eos Control	1.36	1.32
405137			Target Exon	1.11	1.18
400366	M22333		Target	1.55	1.42
423413	AA325560	Hs.346401	ESTs	1.78	1.57
433972	AI878910	Hs.278670	cisplatin resistance-associated overexpr	1.62	2.98
440748	AW451780	Hs.130363	ESTs	1.42	2.14
422637	AA399024	Hs.118836	myoglobin	1.46	2.38
432342	AL036128	Hs.274404	plasminogen activator, tissue	1.67	1.10
442820	AW293459	Hs.172681	ESTs	1.02	1.13
436573	AA723297	Hs.127138	ESTs	1.18	1.15
403779			Target Exon	1.13	1.15
447686	AI939440	Hs.345192	ESTs	1.66	2.78
447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	1.44	2.48
425853	BE348404	Hs.24740	ESTs	1.40	2.75
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	1.52	2.00
424132	AA335715	Hs.200299	ESTs	1.34	1.32
421707	NM_014921	Hs.107054	lectomedin-2	1.09	1.14
442871	AI290691	Hs.131393	ESTs	1.40	2.50
448489	AI523875		gb:tg97d04.x1 NCI_CGAP_CLL1 Homo sapiens	1.31	2.20
436365	AW444548	Hs.163118	ESTs	1.07	1.12
415733	AI052628	Hs.271570	ESTs, Weakly similar to 2109260A B cell	1.91	2.01
413888	AA580288		gb:nn12d01.s1 NCI_CGAP_Co12 Homo sapiens	1.75	1.93
408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	1.92	1.73
442959	AI025248	Hs.6927	ESTs	1.05	1.12
409610	AW444736	Hs.27864	ESTs	1.62	2.45
424793	AI559696	Hs.298885	ESTs	1.37	2.78
449977	C16939	Hs.297848	ESTs	1.52	4.57
414051	BE244127		gb:TCBAP1E0661 Pediatric pre-B cell acut	1.68	2.84
422400	AA974434	Hs.128353	ESTs	1.04	2.20
443908	AW295791	Hs.13040	G protein-coupled receptor 86	1.47	2.10
439316	AF086126	Hs.118208	Homo sapiens cDNA FLJ11727 fis, clone HE	2.08	0.59
438505	AA808948	Hs.173776	ESTs, Moderately similar to ALU1_HUMAN A	1.44	2.73
436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.17	1.00
453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	1.88	2.58
431756	R69465	Hs.255889	ESTs	1.12	1.30
424487	T08754	Hs.6259	KIAA1698 protein	1.15	1.15
435392	R07195	Hs.19918	ESTs	1.38	2.64
430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	0.92	2.12
418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	1.44	2.51
411664	BE065069	Hs.270833	*amphiregulin (schwannoma-derived growth*	1.94	2.33
416586	D44643	Hs.14144	secreted modular calcium-binding protein	1.72	2.68
419612	AI498267	Hs.110613	KIAA0421 protein	2.28	2.46
435800	AI248285	Hs.118348	ESTs	1.42	2.45
433363	AA584829	Hs.275163	non-metastatic cells 2, protein (NM23B)	2.07	2.53
422936	AA319278		gb:EST21478 Adrenal gland tumor Homo sap	1.46	1.22
413358	BE259160	Hs.75313	aldo-keto reductase family 1, member B1	1.43	1.43
435357	N71620	Hs.118173	ESTs	1.44	2.93
441063	AA913819	Hs.188025	ESTs	1.20	2.80
450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	1.44	4.18
430446	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	1.03	2.34
401577			NM_000761:Homo sapiens cytochrome P450,	1.13	1.22
403978			C5000010*:gi|10440464|dbj|BAB15765.1| (A	1.22	1.66
459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.72	4.60
416708	H78836	Hs.181900	ESTs, Moderately similar to ALU1_HUMAN A	1.36	2.03
451410	AL110235	Hs.26358	*DKFZP566K1924 protein*	1.51	2.28
451159	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	1.33	1.09
448455	AI252625	Hs.269860	ESTs, Moderately similar to S65657 alpha	0.83	0.40
444020	R92962	Hs.35052	ESTs	1.66	2.50
414623	BE391050		gb:601285674F1 NIH_MGC_44 Homo sapiens c	1.84	3.88
454915	AW841619		gb:RC1-CN0017-120200-012-b09 CN0017 Homo	1.14	2.10
444064	W85970	Hs.16292	ESTs	0.80	0.63
454353	AW389693	Hs.300700	hypothetical protein FLJ20727	1.30	2.10
447794	AI424999	Hs.161445	EST	1.26	2.05
426686	AI362802	Hs.171814	parathymosin	1.16	1.11
435815	AA700482	Hs.113157	ESTs	1.66	2.73
432482	L19267	Hs.275924	dystrophia myotonica-containing WD repea	1.10	1.15
431062	AA491270	Hs.187946	ESTs	1.44	2.60
429191	AF065215	Hs.198161	*phospholipase A2, group IVB (cytosolic)*	1.35	1.06
424456	AA341017	Hs.25549	hypothetical protein FLJ20898	1.21	3.45
451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	1.23	2.10
432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	1.11	2.71

431868	BE246400	Hs.285176	acetyl-Coenzyme A transporter	1.03	3.10
429321	AA449921		gb:zx37g07.r1 Soares_total_fetus_Nb2HF8_	1.68	2.93
417890	R79048		gb:yi87g02.r1 Soares placenta Nb2HP Homo	1.32	1.80
439590	AF086410		gb:Homo sapiens full length insert cDNA	1.32	2.43
420232	AW450051	Hs.256295	ESTs	1.28	2.26
418927	BE349635	Hs.190284	ESTs	1.46	1.23
441940	AW298115	Hs.128152	ESTs	1.34	1.34
401090			C9000193*:gi|6330729|dbj|BAA86547.1| (AB	1.50	1.40
409136	AW206670	Hs.50748	chromosome 21 open reading frame 18	1.02	2.38
438267	AW205708	Hs.292725	ESTs, Weakly similar to T18818 hypotheti	1.28	2.25
422482	AI439905	Hs.344476	gb:ti57g08.x1 NCI_CGAP_Lym12 Homo sapien	1.05	2.81
420067	T52431	Hs.94795	Homo sapiens mRNA; cDNA DKFZp564O222 (fr	1.77	2.40
442180	AA983913	Hs.128929	ESTs	1.76	2.38
434256	AI378817	Hs.191847	ESTs	1.05	2.06
444519	AI160304	Hs.28313	ESTs	0.55	0.63
454459	AW855738	Hs.17767	KIAA1554 protein	1.10	2.05
455988	BE177983		gb:RC3-HT0600-230300-021-g10 HT0600 Homo	1.70	2.64
444510	AI367823	Hs.146872	ESTs	1.44	2.08
456210	N49729	Hs.156875	ESTs	1.64	2.65
450569	AW192334	Hs.38218	ESTs	1.78	2.71
414921	BE390551	Hs.77628	steroidogenic acute regulatory protein r	1.05	1.12
401381			C14000165:gi|12698069|dbj|BAB21853.1| (A	0.63	0.85
439998	BE559554	Hs.61790	hypothetical protein FLJ23338	1.06	1.14
453762	AW977286	Hs.17428	RBP1-like protein	1.42	2.68
419403	AA744520	Hs.87734	ESTs, Weakly similar to nonsyndromic hea	0.99	2.17
423736	AW936874		gb:RC1-DT0029-120100-011-f07 DT0029 Homo	2.05	1.56
421186	AI798039	Hs.270563	ESTs, Moderately similar to T12512 hypot	1.29	1.31
426435	AI827946	Hs.124854	hypothetical brain protein my040	1.36	1.59
439312	AA833902	Hs.270745	ESTs	1.60	2.50
407924	BE537128	Hs.299797	ESTs	1.51	1.15
409692	AI500724		KIAA1550 protein	1.72	2.21
415449	H15034		gb:ym20a03.s1 Soares infant brain 1NIB H	1.50	2.13
423436	R21176	Hs.100926	ESTs	1.18	2.60
458697	AI797713	Hs.156471	ESTs	1.54	2.20
415770	M79237		gb:EST01385 Subtracted Hippocampus, Stra	1.49	1.55
449279	AI962312	Hs.224976	ESTs, Weakly similar to CRX_HUMAN CONE-R	2.50	3.60
429735	AA458759	Hs.188794	ESTs	1.84	2.31
442124	R66412	Hs.129013	Homo sapiens cDNA FLJ14309 fis, clone PL	1.10	1.19
412557	AA761612	Hs.291557	ESTs	1.10	1.18
409335	NM_001502	Hs.53985	glycoprotein 2 (zymogen granule membrane	1.18	1.12
430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	1.35	2.39
420855	AA281092	Hs.33417	Homo sapiens cDNA: FLJ22806 fis, clone K	1.22	2.09
450567	AA033904	Hs.269235	ESTs	1.60	2.20
414197	W44877	Hs.55501	ESTs	1.06	2.08
448800	AI571294	Hs.298889	ESTs, Moderately similar to ALU1_HUMAN A	1.65	2.79
421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	1.47	2.90
412679	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	1.32	2.53
417882	R22311		gb:yh26c09.r1 Soares placenta Nb2HP Homo	1.58	2.43
425112	AW953291	Hs.64211	hypothetical protein MGC5601	0.70	0.63
401658			C16000210:gi|12585542|sp|O14771|Z213_HUM	1.68	2.04
409325	AW377549	Hs.17865	ESTs	1.68	2.21
437402	AI553976	Hs.121191	ESTs	1.20	2.35
433455	AA360439	Hs.89319	ESTs	0.98	2.53
457329	AI634860	Hs.247043	type 1 tumor necrosis factor receptor sh	0.59	0.43
434830	AW852235		gb:QV0-CT0225-230300-169-e11 CT0225 Homo	1.24	1.12
450696	AI654223	Hs.16026	hypothetical protein FLJ23191	1.44	2.53
446098	AW072215	Hs.208470	ESTs	1.38	2.93
443310	BE552018	Hs.133152	ESTs	0.85	0.83
424015	N95696	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.42	2.25
420229	AA256675	Hs.194058	ESTs, Weakly similar to AF252293 1 PAR3	1.70	2.39
403371			Target Exon	1.50	3.43
410744	H86002		gb:ys92b01.r1 Soares retina N2b5HR Homo	1.32	2.13
424160	T74062		gb:yc81f01.r1 Soares infant brain 1NIB H	1.30	2.17
438818	AW979008	Hs.222487	ESTs	1.98	2.43
438791	AA825750	Hs.129983	ESTs	1.12	2.15
411206	AW827390	Hs.16899	ESTs	1.17	2.58
432211	BE274530	Hs.273333	hypothetical protein FLJ10986	0.42	0.30
448918	AB011152	Hs.22572	KIAA0580 protein	1.54	2.63
424496	AI733451	Hs.167165	hypothetical protein FLJ12975	1.39	2.25
410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	1.84	3.23
457581	AA578512		gb:nh22e11.s1 NCI_CGAP_Pr1 Homo sapiens	1.21	1.09
435353	AW243062	Hs.190348	ESTs	1.90	2.98
417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	1.21	1.24
433682	AA642418	Hs.17381	ESTs	1.18	2.23
424915	R42755	Hs.23096	ESTs	1.60	2.73
442201	AW516704	Hs.208726	ESTs	1.74	3.20
429111	AI870811	Hs.7579	KIAA1151 protein	1.27	1.40

429282	N27596	Hs.21342	ESTs	1.84	3.73
436604	AW105129	Hs.242158	ESTs	1.27	2.70
448712	W01046	Hs.333371	Homo sapiens clone TA40 untranslated mRN	0.79	2.70
412274	AA101443		gb:zn74a07.r1 Stratagene NT2 neuronal pr	1.40	2.53
403859			C5001408*:gi|12621134|ref|NP_075244.1| M	1.76	2.00
451521	AA018237	Hs.128189	gb:ze53a02.r1 Soares retina N2b4HR Homo	1.48	2.51
443210	AI692649	Hs.9451	hypothetical protein MGC13168	1.44	2.60
442722	AL048889	Hs.131029	ESTs, Weakly similar to B28096 line-1 pr	1.20	2.25
400840			Target Exon	0.66	0.60
454639	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	1.23	1.41
439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	1.77	2.12
410725	AW799279		gb:RC0-UM0051-210300-012-h06 UM0051 Homo	1.08	2.55
423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	1.94	2.29
450717	T94709		gb:ye35d09.r1 Stratagene lung (937210) H	1.56	2.64
400314	NM_018949	Hs.192720	G protein-coupled receptor 14	0.89	0.87
434947	AA654320	Hs.183819	Homo sapiens cDNA FLJ12304 fis, clone MA	1.19	2.14
453582	AW854339	Hs.33476	hypothetical protein FLJ11937	1.24	2.19
409005	AW299806	Hs.297256	ESTs	1.24	2.03
406584			Target Exon	1.52	2.37
420203	AA256374	Hs.191069	ESTs	1.16	1.37
406156			Target Exon	1.18	1.17
422132	AB002337	Hs.112078	KIAA0339 gene product	1.08	1.16
441371	AW452292	Hs.197354	ESTs	1.19	2.00
434807	AA364183	Hs.323443	hypothetical protein FLJ11806	1.30	2.76
424542	AI860558	Hs.272009	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.48	2.48
450893	AK002185	Hs.25625	hypothetical protein FLJ11323	1.15	1.57
418481	M81945	Hs.85289	CD34 antigen	2.16	1.76
443077	AI459490	Hs.60090	Homo sapiens cDNA FLJ13595 fis, clone PL	1.36	2.41
437521	AA758756	Hs.121380	ESTs	1.07	2.05
430265	L36033	Hs.237356	stromal cell-derived factor 1	2.34	1.35
446898	AV660906	Hs.184411	albumin	1.52	1.33
429725	AA457367	Hs.191638	ESTs	1.38	3.00
425114	AW409763	Hs.50699	ESTs, Weakly similar to 2109260A B cell	1.13	2.34
419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	1.62	1.71
435284	AA879470	Hs.96849	Homo sapiens cDNA FLJ11492 fis, clone HE	1.20	2.50
415634	F13165	Hs.12549	ESTs, Weakly similar to 2109260A B cell	1.46	2.35
420565	AI806770	Hs.30258	ESTs	1.39	3.85
419494	W01060	Hs.34382	ESTs	1.10	1.75
458183	AL031591	Hs.7370	phosphotidylinositol transfer protein, b	1.28	2.24
416620	R93080	Hs.35035	ESTs	1.81	2.58
431356	AW499632	Hs.288512	Homo sapiens cDNA FLJ11632 fis, clone HE	1.42	2.03
433282	BE539101	Hs.5324	hypothetical protein	0.33	0.20
456898	NM_001928	Hs.155597	D component of complement (adipsin)	1.50	0.95
458126	AW979136	Hs.124629	ESTs	1.34	1.32
414005	AA134489	Hs.269379	ESTs	1.52	2.07
411496	AW849241		gb:IL3-CT0215-210200-088-E03 CT0215 Homo	1.10	2.21
451147	AA016982	Hs.64341	ESTs	1.53	2.29
450238	T89693	Hs.138777	ESTs	1.32	2.28
449284	BE502240	Hs.38592	hypothetical protein FLJ23342	1.46	1.40
449479	AI797619	Hs.197659	ESTs	0.72	0.66
403066			Target Exon	1.32	1.19
410118	AW590680	Hs.110802	von Willebrand factor	1.72	2.54
437674	AI749921	Hs.205377	ESTs	1.38	2.21
431065	AA491286	Hs.128792	ESTs	1.30	2.08
416352	H78006	Hs.19553	ESTs	1.05	1.14
452565	BE066552		gb:RC3-BT0333-300300-017-h08 BT0333 Homo	1.46	2.53
418115	AW005376	Hs.173280	ESTs	1.20	0.98
422031	R66895	Hs.28788	ESTs	1.37	1.37
446269	AW263155	Hs.14559	hypothetical protein FLJ10540	1.64	2.20
457683	AI821877	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN A	1.03	2.35
435521	W23814	Hs.6361	mitogen-activated protein kinase kinase	0.73	0.59
438874	H02780	Hs.347520	gb:yj41a11.r1 Soares placenta Nb2HP Homo	1.56	2.73
441167	AA921754	Hs.211781	ESTs	1.74	2.12
455917	BE156765		gb:RC1-HT0370-120100-012-c09 HT0370 Homo	1.29	1.35
419058	AW675039	Hs.1227	aminolevulinate, delta-, dehydratase	2.04	1.83
408651	BE266928	Hs.17126	hypothetical protein MGC15912	1.30	1.23
442737	AB002319	Hs.8663	KIAA0321 protein	0.85	0.79
407134	T51588		gb:yb27e06.s1 Stratagene fetal spleen (9	1.23	0.97
447492	AI381619	Hs.20188	ESTs	1.26	2.28
437840	AA884836	Hs.292014	ESTs	2.05	2.29
412294	AA689219	Hs.117176	poly(A)-binding protein, nuclear 1	1.47	3.55
419909	AL136653	Hs.93675	decidual protein induced by progesterone	1.10	2.18
432569	AI131140	Hs.152434	ESTs	1.34	1.83
412252	AW903782		gb:CM4-NN1032-190400-527-g09 NN1032 Homo	1.26	2.00
444298	Z17870		gb:HSDHII020 Stratagene cDNA library Hum	1.36	2.68
445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	0.95	2.23
418315	T06475	Hs.124962	Homo sapiens, clone IMAGE:3510191, mRNA,	0.82	0.82

440357	AA379353	Hs.20950	phospholysine phosphohistidine inorganic	0.83	0.68
440867	AI417007	Hs.166338	ESTs	1.45	1.50
410956	AW938322		gb:PM1-DT0054-231299-002-c02 DT0054 Homo	1.06	2.95
446574	AI310135	Hs.335933	ESTs	1.54	2.45
447912	AW576549	Hs.165728	ESTs, Weakly similar to I38022 hypotheti	1.22	2.07
457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	1.89	2.08
433762	AA732484	Hs.169399	ESTs	1.24	2.58
418156	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m	3.71	1.38
409282	AW966480		gb:EST378554 MAGE resequences, MAGI Homo	1.70	1.70
425169	AW292500	Hs.128514	ESTs	1.13	1.12
458497	AI161428	Hs.75916	splicing factor 3b, subunit 2, 145kD	1.26	2.28
405673			NM_022775:Homo sapiens hypothetical prot	2.00	1.00
442691	AW341438	Hs.278036	ESTs	1.38	2.28
424316	AA676403	Hs.145078	regulator of differentiation (in S. pomb	1.06	2.10
444608	AI174683	Hs.329863	ESTs	1.95	1.82
447345	BE247767	Hs.18166	KIAA0870 protein	1.26	2.10
439848	AW979249		gb:EST391359 MAGE resequences, MAGP Homo	1.68	2.63
428946	D42046	Hs.194665	DNA2 (DNA replication helicase, yeast, h	1.32	2.33
403214			NM_016232*:Homo sapiens interleukin 1 re	1.02	2.15
404495			C8001441*:gi|8923061|ref|NP_060114.1| hy	2.20	2.49
443471	AW236939	Hs.172154	Homo sapiens clone FLB3442 PRO0872 mRNA,	1.58	1.74
437116	AL049253	Hs.190162	ESTs	1.22	2.53
451357	AB020640	Hs.26319	Human DNA sequence from clone RP3-467L1	0.94	2.35
408255	AW807321		gb:MR4-ST0062-240300-003-g05 ST0062 Homo	1.12	1.39
448931	AI597806	Hs.192671	ESTs	1.30	3.29
422343	AI628633	Hs.346823	gb:ty77d05.x1 NCI_CGAP_Kid11 Homo sapien	1.86	2.32
407140	AA059106	Hs.271780	ESTs, Weakly similar to I38022 hypotheti	1.37	1.01
429187	AA447648	Hs.163872	ESTs, Weakly similar to S65657 alpha-1C-	1.74	1.55
423614	AI457640	Hs.206632	ESTs	1.48	2.83
429073	AA446167	Hs.47385	ESTs	1.24	2.00
415732	AA167566	Hs.271570	ESTs, Weakly similar to 2109260A B cell	1.31	2.34
412634	U55984	Hs.289088	heat shock 90kD protein 1, alpha	0.42	0.22
415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.94	1.27
415007	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2	0.78	0.71
402654			Target Exon	0.90	0.85
457974	AW842353	Hs.321717	ESTs, Weakly similar to S22765 heterogen	0.86	0.90
405340			C2002952:gi|1345964|sp|P10079|FBP1_STRPU	1.46	2.33
426259	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	1.63	2.75
442237	AW905607	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCLE	1.08	3.38
456370	AA234938	Hs.87384	ESTs	0.77	2.83
407041	X15673		gb:Human pTR2 mRNA for repetitive sequen	2.00	1.84
452001	AI827675	Hs.274281	fidgetin	1.38	2.03
445137	AI733837	Hs.145661	ESTs	1.60	3.00
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	1.17	2.10
404418			Target Exon	1.90	3.36
447658	AI916872	Hs.213424	ESTs	1.90	2.21
434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	1.58	1.24
400834			NM_002240*:Homo sapiens potassium inward	1.25	2.33
449542	AW857362	Hs.268855	ESTs, Weakly similar to I38022 hypotheti	1.46	1.28
441043	AA913422	Hs.192104	ESTs	1.26	1.09
403391			C3001164*:gi|1730196|sp|P50573|GAR3_RAT	1.46	2.55
449129	AI631602	Hs.258949	ESTs	1.27	2.48
418321	D63477	Hs.84087	KIAA0143 protein	0.56	0.52
426789	F06596	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	1.31	2.06
443679	AK001810	Hs.9670	hypothetical protein FLJ10948	1.34	1.22
428554	R46070	Hs.6407	ESTs	1.04	2.08
401890			Target Exon	1.24	1.14
419501	AW843822		gb:CM4-CN0045-010200-514-f08 CN0045 Homo	1.74	1.38
457096	AI809202	Hs.208343	ESTs, Weakly similar to cerebroside sulf	0.82	0.87
426123	AA370352		gb:EST82246 Prostate gland I Homo sapien	1.28	2.35
449445	AW197349	Hs.232197	ESTs	1.24	2.13
430683	AC004862	Hs.247768	Homo sapiens PAC clone RP4-697H17 from 7	1.30	2.00
440642	AI744995		ESTs, Moderately similar to ALU4_HUMAN A	1.29	2.44
455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	1.78	2.95
449622	AW013915	Hs.196578	ESTs	1.42	2.20
415116	AA160363	Hs.269956	ESTs	2.02	1.03
457269	AI338993	Hs.134535	ESTs	1.93	1.35
427877	AW138725	Hs.178067	ESTs	1.91	2.42
454631	AW811324		gb:IL3-ST0141-131099-017-A02 ST0141 Homo	1.00	3.13
458390	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN !!!!	1.02	2.21
435844	AA700856	Hs.59651	ESTs, Weakly similar to I78885 serine/th	0.85	0.81
427237	AA399964	Hs.97763	ESTs	1.57	1.44
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	1.20	3.13
442151	AI733404	Hs.128865	ESTs	1.50	2.13
412708	R26830	Hs.106137	ESTs, Weakly similar to CGHU7L collagen	1.16	3.00
417262	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot	1.25	2.40
419362	N64116	Hs.24624	hypothetical protein FLJ21945	1.38	2.48

447248	AW295831	Hs.6496	ESTs	1.56	2.03
415622	F13010	Hs.12400	ESTs	1.48	2.30
414065	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PL	1.26	2.88
414585	W46954	Hs.334716	hypothetical protein MGC16291	1.24	2.05
443197	Z43613		gb:HSC1GD091 normalized infant brain cDN	1.11	2.04
428266	AI382001	Hs.43590	ESTs	1.09	2.03
447083	AI472124	Hs.157757	ESTs	1.66	3.53
412302	AW936334		gb:QV4-DT0021-281299-070-g05 DT0021 Homo	1.74	3.00
445555	AW974013		ESTs	1.32	1.29
453117	AW162044	Hs.104203	hypothetical protein MGC12981	0.73	0.81
436757	AW975663	Hs.293404	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.21	1.88
431976	AA719001	Hs.291065	ESTs	1.23	2.01
430657	AA482910	Hs.279664	ESTs	1.64	2.65
438744	BE314727	Hs.75721	profilin 1	0.85	0.85
439325	AF086139	Hs.150423	cyclin-dependent kinase 9 (CDC2-related	1.16	2.05
438117	AA328041	Hs.194329	hypothetical protein FLJ21174	0.79	0.76
401686			NM_014587*:Homo sapiens SRY (sex determi	1.32	2.31
420269	U72937	Hs.96264	alpha thalassemia/mental retardation syn	0.78	0.53
434288	AW189075	Hs.116265	fibrillin3	2.42	4.23
433215	AB040912	Hs.191098	hypothetical protein FLJ11598	1.36	1.36
413429	BE139117	Hs.278881	ESTs	1.30	2.98
426417	AA377908	Hs.13254	ESTs	1.36	1.77
413882	AA132973	Hs.184492	ESTs	1.55	2.10
413346	AA128586		gb:zl24h06.r1 Soares_pregnant_uterus_NbH	1.29	1.77
445020	AI205655	Hs.147221	ESTs	1.90	2.00
418175	AW967054	Hs.206312	ESTs, Weakly similar to I38022 hypotheti	1.60	3.70
429582	AI569068	Hs.22247	ESTs	1.06	2.38
409134	AW340389	Hs.250585	ESTs	1.64	2.57
415642	U19878	Hs.336224	transmembrane protein with EGF-like and	0.73	2.33
435667	F13625	Hs.124183	ESTs	1.10	2.33
440513	BE407106	Hs.65907	Homo sapiens, clone IMAGE:3959816, mRNA,	0.85	2.03
419711	C02621	Hs.159282	ESTs	1.22	2.00
434249	AA987537	Hs.129875	ESTs	1.29	2.48
437355	AL359557	Hs.306508	Homo sapiens mRNA; cDNA DKFZp762O1415 (f	1.86	2.08
428360	H10291	Hs.30974	ESTs	1.40	2.05
435339	AI358300	Hs.129827	ESTs	1.38	2.18
435345	AW360966	Hs.6653	ESTs	1.49	2.27
435105	AI878982	Hs.131859	Homo sapiens F-box protein FBX11 mRNA, p	1.78	2.33
459645	AA074346	Hs.250715	ESTs	1.50	2.40
449691	AA002143	Hs.21413	solute carrier family 12, (potassium-chl	0.74	0.69
425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	1.42	2.76
437272	AW975957		gb:EST388066 MAGE resequences, MAGN Homo	1.00	2.16
456955	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	0.84	0.81
421362	AK000050	Hs.103853	hypothetical protein FLJ20043	1.30	2.21
457926	AA452378	Hs.11637	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	1.27	2.12
444557	AI167637	Hs.146924	ESTs	1.83	2.35
434476	AW858520	Hs.84264	acidic protein rich in leucines	1.43	3.80
458059	AW015588	Hs.137232	ESTs, Weakly similar to S65657 alpha-1C-	1.30	2.23
413595	AW235215	Hs.16145	ESTs	2.10	2.43
417281	R98773	Hs.268883	ESTs	1.26	2.10
445689	BE158869		gb:QV0-HT0398-210100-096-f08 HT0398 Homo	1.15	2.15
423249	AA323682	Hs.125374	ESTs, Weakly similar to S26689 hypotheti	1.76	1.50
408366	AW511255	Hs.346442	ESTs	1.74	2.91
441359	AI435179	Hs.126820	ESTs	2.43	1.59
413068	BE063792		gb:QV3-BT0295-260100-066-d06 BT0295 Homo	1.52	2.09
441322	AW071851	Hs.130628	ESTs	1.42	2.10
409124	AW292809	Hs.50727	N-acetylglucosaminidase, alpha- (Sanfili	1.11	2.20
432413	AK000257	Hs.274505	Homo sapiens mRNA; cDNA DKFZp564A216 (fr	1.10	2.25
425391	AI248252	Hs.160672	ESTs	1.17	2.38
443861	AW449462	Hs.134743	ESTs	1.44	2.30
454609	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.30	1.33
425893	AA629695		gb:ad43b07.s1 Stratagene lung carcinoma	1.76	2.51
443611	NM_014397	Hs.9625	NIMA (never in mitosis gene a)-related k	1.81	2.90
410359	R38624	Hs.106313	ESTs	1.78	2.05
406308			NM_025192:Homo sapiens hypothetical prot	1.92	2.24
432476	T94344	Hs.326263	ESTs	1.40	2.45
435073	AA664078		gb:ac04a05.s1 Stratagene lung (937210) H	1.66	2.26
420581	AA278459	Hs.151940	ESTs	1.48	2.58
435579	AI332373	Hs.156924	ESTs	1.46	2.68
439633	AF086464	Hs.86248	ESTs	1.40	2.48
430551	AA481150	Hs.136343	ESTs	1.40	2.28
450855	T97988	Hs.295605	mannosidase, alpha, class 2A, member 2	1.48	2.40
444326	AI939357	Hs.270710	ESTs	0.88	2.28
412149	R49355	Hs.273824	ESTs	1.58	2.19
455116	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	1.56	2.50
449626	AA774247	Hs.301637	zinc finger protein 258	0.60	0.53
410047	AI167810	Hs.132390	zinc finger protein 36 (KOX 18)	0.66	0.58

418865	AW117500	Hs.104241	ESTs	1.58	2.63
402762			ENSP00000235171*:GAP junction beta-4 pro	0.81	0.82
436449	AI418027	Hs.120361	ESTs	1.46	1.46
403488			ENSP00000201948:KARYOPHERIN BETA2B HOMOL	1.38	2.23
431235	AA318271	Hs.250905	hypothetical protein	1.14	2.55
448576	AB026730	Hs.21495	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	0.70	0.78
408100	AW205382	Hs.42676	KIAA0781 protein	1.36	2.66
433436	AW162474		Bruno (Drosophila) -like 6, RNA binding	1.50	2.15
422337	R38572		gb:yc87c11.s1 Soares infant brain 1NIB H	2.23	1.71
426160	AA206020	Hs.167460	splicing factor, arginine/serine-rich 3	1.08	2.09
447008	BE010189		nuclear receptor subfamily 1, group I, m	1.26	1.27
420141	AA702961	Hs.124103	ESTs, Weakly similar to I38344 titin, ca	1.46	2.60
423840	AA332434	Hs.72465	ESTs, Weakly similar to non-lens beta ga	1.26	2.47
447793	AI424924	Hs.211203	ESTs	2.38	1.83
407328	AA508857	Hs.187748	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.11	2.54
432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.63	2.05
421311	N71848	Hs.283609	hypothetical protein PRO2032	0.51	0.44
444649	AW207523	Hs.197628	ESTs	1.21	2.24
448688	R94570	Hs.266869	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.91	3.25
428847	AI954833	Hs.98881	ESTs	1.48	2.66
413750	BE161453		gb:IL2-HT0437-290200-045-A06 HT0437 Homo	1.22	1.00
429355	AW973253	Hs.292689	ESTs	1.86	2.35
427798	AA412499	Hs.104779	ESTs	1.82	2.33
431179	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	0.80	2.00
451719	AI373532	Hs.157910	ESTs	1.29	3.85
438094	AI821755	Hs.131805	ESTs, Weakly similar to A56194 thromboxa	1.74	2.54
418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	0.52	0.49
407414	AF072164		gb:Homo sapiens HSFE-1 mRNA, partial cds	1.67	2.28
416410	H53777	Hs.36822	ESTs	1.85	2.28
439141	AI241470	Hs.268982	ESTs	1.08	2.28
441181	AA416925	Hs.121076	peptidylprolyl isomerase (cyclophilin)-H	1.81	2.02
434482	AF143331	Hs.16073	ESTs	1.22	2.00
455757	BE079531		gb:RC5-BT0624-240300-013-D08 BT0624 Homo	1.53	2.16
425787	AA363867	Hs.155029	ESTs	0.76	2.13
405727			CX001244:gi|11420428|ref|XP_004814.1| be	1.70	2.21
441846	AW850980		gb:IL3-CT0220-150200-068-B03 CT0220 Homo	1.16	2.14
451945	BE504055	Hs.211420	ESTs	0.84	2.73
438432	AW444990	Hs.258800	ESTs, Weakly similar to I38022 hypotheti	1.60	2.43
451140	AW411354	Hs.26002	LIM domain binding 1	1.14	1.20
407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.03	2.42
453041	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	1.69	3.43
437613	R19892	Hs.10267	MIL1 protein	1.16	2.11
451507	AW291109	Hs.208787	ESTs, Weakly similar to T31611 hypotheti	1.22	2.05
430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	2.85	1.00
453669	AL049029	Hs.7258	hypothetical protein FLJ22021	0.75	0.64
455065	AW854352		gb:RC3-CT0255-200100-024-g10 CT0255 Homo	1.49	2.20
442220	AL037800	Hs.8148	selenoprotein T	0.50	0.18
437936	AW798475	Hs.288549	hypothetical protein FLJ14710	1.50	2.44
442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	0.54	0.37
405223			Target Exon	1.09	2.80
437225	AW975982	Hs.292935	ESTs	1.03	2.47
421101	AF010446	Hs.101840	major histocompatibility complex, class	0.72	0.57
436200	R51386	Hs.124881	ESTs	1.64	2.93
402025			NM_021624:Homo sapiens histamine H4 rece	1.52	2.28
407019	U49973		gb:Human Tigger1 transposable element, c	2.40	2.12
451305	AW003571	Hs.211191	ESTs, Weakly similar to A46010 X-linked	1.24	3.23
423450	AJ290445	Hs.128759	KIAA0524 protein	1.64	2.13
423139	AW402725	Hs.288560	hypothetical protein FLJ21106	1.61	2.28
451763	AW294647	Hs.233634	hypothetical protein FLJ14220	1.39	2.08
458915	AI915689	Hs.212781	EST	1.62	2.02
452829	AI955579	Hs.63368	ESTs, Weakly similar to TRHY_HUMAN TRICH	0.60	0.41
446383	T05816	Hs.92511	ESTs	2.08	1.48
432576	AW157424	Hs.165954	ESTs, Weakly similar to I38022 hypotheti	1.88	2.49
433820	AI401627	Hs.174067	ESTs	1.30	2.00
419719	AA844700	Hs.39297	ESTs, Moderately similar to ALU1_HUMAN A	1.33	2.00
415868	H06728	Hs.21017	ESTs	1.34	2.08
420738	NM_004185	Hs.258575	wingless-type MMTV integration site fami	1.42	2.29
446614	AK001733	Hs.15562	hypothetical protein FLJ10871	0.79	0.78
404167			NM_021956*:Homo sapiens glutamate recept	1.62	2.55
417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	0.72	0.75
401215			C12000457*:gi|7512178|pir||T30337 polypr	1.14	2.08
421600	AW893889	Hs.323231	Homo sapiens cDNA FLJ11946 fis, clone HE	1.88	2.66
426248	T18988	Hs.293668	ESTs	1.17	3.44
454523	AW803980		gb:PM0-UM0084-240300-001-G11 UM0084 Homo	1.34	2.40
420656	AA279098	Hs.187636	ESTs	1.22	2.43
402833			C1002508:gi|6691937|emb|CAB65797.1| (AL0	1.31	2.00
438910	AA827921	Hs.291858	ESTs, Weakly similar to ALUC_HUMAN !!!!	1.39	3.13

416170	H42454	Hs.220645	ESTs	0.99	2.18
433598	AI762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN A	2.04	1.28
417699	T91491	Hs.119670	ESTs	1.36	2.50
459605	AL045773		gb:DKFZp434F246_r1 434 (synonym: htes3)	1.21	2.13
453204	R10799	Hs.191990	ESTs	3.12	2.98
458971	AL119206	Hs.126257	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.34	2.09
457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	1.68	2.00
400414	AF083118	Hs.283968	Homo sapiens CATX-2 mRNA, complete cds	1.70	2.54
426263	AI908774	Hs.259785	carnitine palmitoyltransferase I, liver	0.96	2.14
439334	AI148976	Hs.112062	ESTs	1.50	2.45
455527	AW984479		gb:PM1-HN0012-220300-001-b12 HN0012 Homo	1.46	2.28
408084	AL040832	Hs.160422	Homo sapiens clone PP902 unknown mRNA	1.61	2.23
432059	AF227131	Hs.272387	taste receptor, type 2, member 4	1.66	2.15
429791	AW015667	Hs.119427	ESTs	1.51	2.83
438695	AI885190	Hs.156089	ESTs, Weakly similar to repressor protei	1.19	2.03
458139	AI525711	Hs.253147	ESTs	1.42	2.10
413035	BE155563		gb:PM4-HT0352-171199-001-C05 HT0352 Homo	1.62	2.30
422444	AA310688		gb:EST181501 Jurkat T-cells V Homo sapie	1.38	2.05
409546	AW410190	Hs.250624	hypothetical protein MGC4473	1.87	2.18
411432	AW846272		gb:QV0-CT0179-300999-024-d12 CT0179 Homo	1.04	2.03
445327	AI220082	Hs.147722	ESTs	1.16	2.10
424628	AB011136	Hs.151385	KIAA0564 protein	0.61	0.63
440197	AW340708	Hs.317714	pallid (mouse) homolog, pallidin	0.56	0.39
409894	BE081731		gb:QV2-BT0635-220400-158-e04 BT0635 Homo	1.50	2.45
422776	AA316987	Hs.129846	ESTs	1.36	2.20
428255	AI627478	Hs.187670	ESTs	1.34	2.40
412484	AA112090	Hs.269961	ESTs	0.97	2.00
432789	D26361	Hs.3104	KIAA0042 gene product	1.44	2.73
430100	AA766178	Hs.291601	ESTs, Highly similar to T00350 hypotheti	1.06	2.02
419528	AA244000	Hs.222365	ESTs	1.34	2.06
441793	AA968459	Hs.158785	ESTs	1.80	2.70
429468	AF033579		T-box 10	0.71	0.61
410248	AA166653	Hs.268171	ESTs	2.55	2.10
401818			NM_000664*:Homo sapiens acetyl-Coenzyme	1.76	2.58
451724	AI903765		gb:UI-BT037-301298-102 BT037 Homo sapien	1.64	2.28
431866	NM_012098	Hs.8025	angiopoietin-like 2	1.56	2.36
432719	AW935411	Hs.314460	ESTs	1.36	2.25
418977	AA233094	Hs.191517	ESTs	2.06	3.60
404220			C6000989*:gi|7573285|emb|CAB87644.1| (AL	1.54	2.23
446708	BE549905	Hs.231754	ESTs	1.35	2.16
453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	1.42	2.38
422050	AA302741	Hs.25786	ESTs, Moderately similar to JC5238 galac	1.40	2.50
400704			Target Exon	1.48	1.00
406104			Target Exon	1.22	2.03
411008	AW813238		gb:MR3-ST0191-020200-207-d04 ST0191 Homo	1.00	2.13
426582	AA381797	Hs.281121	ESTs	1.35	2.45
430853	AI734179	Hs.105676	ESTs	1.43	2.23
432420	AL044659	Hs.43791	ESTs	1.15	2.03
403197			C2002793*:gi|1353148|sp|Q09568|YR86_CAEE	0.52	0.47
432407	AA221036		gb:zr03f12.r1 Stratagene NT2 neuronal pr	1.93	2.23
414996	AW747800	Hs.55016	hypothetical protein FLJ21935	1.56	2.72
401016			ENSP00000227126:NAALADASE II PROTEIN.	1.25	2.45
433335	AA584134	Hs.269454	ESTs	1.31	2.24
459668	BE244127		gb:TCBAP1E0661 Pediatric pre-B cell acut	1.16	2.03
437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheti	3.75	2.72
452277	AL049013	Hs.28783	KIAA1223 protein	0.33	0.26
425712	AA412548	Hs.21423	ESTs, Moderately similar to ALU1_HUMAN A	1.34	2.21
427598	AA406057	Hs.97998	ESTs	1.06	2.05
412565	M85975	Hs.344069	gb:EST02500 Fetal brain, Stratagene (cat	1.24	2.59
422043	AL133649	Hs.110953	retinoic acid induced 1	0.48	0.41
421814	L12350	Hs.108623	thrombospondin 2	0.48	2.45
413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	1.32	2.45
435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	0.39	0.28
452396	H10302	Hs.112577	ESTs	1.60	2.45
440612	BE561384		gb:601344969F1 NIH_MGC_8 Homo sapiens cD	1.08	2.60
454721	AW815588		gb:QV0-ST0216-061299-066-a09 ST0216 Homo	1.44	1.65
417796	AA206141	Hs.6786	ESTs	1.68	3.85
432864	D16217	Hs.279607	calpastatin	0.43	0.35
454480	AA088375	Hs.22612	hypothetical protein DKFZp566D1346	2.19	1.91
434490	AF143870	Hs.15246	ESTs	2.26	2.07
418797	AA515814		gb:ng64b03.s1 NCI_CGAP_Lip2 Homo sapiens	1.42	2.55
403871			C5001783*:gi|780367|gb|AAB05844.1| (L416	1.60	2.63
441283	AA927670	Hs.131704	ESTs	1.31	3.63
442250	AW290871	Hs.129121	ESTs	1.14	2.38
456747	AL037357	Hs.125864	tropomodulin 2 (neuronal)	1.61	1.26
425757	AA363171		gb:EST72986 Ovary II Homo sapiens cDNA 5	1.29	2.95
405494			C2001837*:gi|12697903|dbj|BAB21770.1| (A	2.09	1.00

432250	AA452088	Hs.274170	Opa-interacting protein 2	1.26	2.71
431911	AK000156	Hs.272193	Homo sapiens cDNA FLJ20149 fis, clone CO	1.46	2.60
413923	AI733852	Hs.199957	ESTs	1.62	2.10
449590	AA694070	Hs.268835	ESTs	1.20	2.53
438467	AA808027	Hs.123277	ESTs	1.48	2.10
432121	AI824879	Hs.211286	ESTs, Weakly similar to 1207289A reverse	1.27	3.13
412298	AW936300		gb:QV4-DT0021-281299-070-a04 DT0021 Homo	1.42	2.60
408519	AA679082	Hs.43481	hypothetical protein DKFZp564K192	1.84	3.70
416067	T79732	Hs.14633	ESTs	1.11	3.08
420497	AW206285	Hs.253548	ESTs	1.90	2.48
405704			NM_001844*:Homo sapiens collagen, type I	1.42	2.90
423443	AI432601	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	1.42	2.03
415904	Z44679	Hs.336391	ESTs	1.62	2.94
413786	AW613780	Hs.13500	ESTs	0.33	0.17
404031			C5001700*:gi|9256616|ref|NP_061761.1| pr	1.94	2.29
457412	N40711	Hs.333300	hypothetical protein FLJ14026	1.92	3.20
439719	AF086554	Hs.326048	Homo sapiens mRNA; cDNA DKFZp434M0420 (f	1.62	2.30
418161	AI950754	Hs.81716	ESTs	1.81	2.42
425894	AW954011	Hs.180711	ESTs	0.92	2.20
419988	W39388	Hs.55336	Homo sapiens, clone MGC:17421, mRNA, com	1.34	2.57
439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	1.67	2.66
450177	AI698091	Hs.107845	ESTs	1.50	2.25
459704	AA719572	Hs.274441	Homo sapiens mRNA; cDNA DKFZp434N011 (fr	1.27	3.35
410357	AW663614		gb:hj22e04.x1 NCI_CGAP_Li8 Homo sapiens	0.69	0.59
459234	AI940425		gb:CM0-CT0052-150799-024-c04 CT0052 Homo	1.67	2.08
421313	NM_014923	Hs.103329	KIAA0970 protein	0.57	0.26
431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	1.80	2.73
423086	AB028984	Hs.123420	KIAA1061 protein	0.40	0.56
425980	AA366951		gb:EST77963 Pancreas tumor III Homo sapi	1.33	2.50
423185	BE299590	Hs.125078	ornithine decarboxylase antizyme 1	0.60	0.56
410840	AW806924		gb:QV4-ST0023-160400-172-h10 ST0023 Homo	1.50	2.88
403917			Target Exon	1.82	2.02
437384	AI674710	Hs.174397	ESTs	1.26	2.05
444389	AW439340	Hs.189720	ESTs	1.26	2.13
443318	AI051603	Hs.133141	ESTs	1.46	2.20
441093	AI698138	Hs.126918	ESTs	1.40	2.35
439432	AI984203	Hs.57874	ESTs	0.88	2.18
454629	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	1.96	2.31
406207			Target Exon	2.77	2.55
444872	AI936264		p30 DBC protein	1.48	2.45
401908			C17000154:gi|12003980|gb|AAG43830.1|AF21	1.15	2.28
404730			Target Exon	1.84	2.78
457498	AI732230	Hs.191737	ESTs	1.49	2.55
448471	AA158617	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	0.37	0.36
438978	AI095207	Hs.307972	ESTs	1.57	2.39
418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	2.86	3.34
400416	AF083130		Homo sapiens CATX-14 mRNA, partial cds	2.03	1.55
450446	AI696334	Hs.14450	ESTs	1.32	2.38
419791	AI579909	Hs.105104	ESTs	0.41	0.27
449436	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	2.01	1.50
430808	L08603	Hs.247980	melanocortin 4 receptor	1.09	2.18
443116	AI033397	Hs.132225	ESTs	1.30	2.25
437923	BE088433	Hs.334696	hypothetical protein KIAA1335	1.40	2.50
403294			Target Exon	0.98	2.18
436007	AI247716	Hs.232168	ESTs	1.38	1.00
430649	AB040941	Hs.247713	KIAA1508 protein	1.52	2.85
437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	1.29	2.59
444500	AV651273	Hs.282966	ESTs, Moderately similar to 2109260A B c	1.22	2.05
447434	R16890	Hs.137135	ESTs	1.72	2.85
400830			NM_025006:Homo sapiens hypothetical prot	2.04	2.68
428114	AI821548	Hs.98363	ESTs, Weakly similar to I38022 hypothetl	1.09	2.74
409688	AI150485		gb:qf36a10.x1 Soares_testis_NHT Homo sap	1.67	1.38
440781	BE561823	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.28	2.50
442662	U78168	Hs.8578	Rap1 guanine-nucleotide-exchange factor	1.92	2.28
443078	M78728	Hs.132694	Homo sapiens cDNA: FLJ23149 fis, clone L	1.42	2.03
440179	AI990151	Hs.125904	ESTs	1.49	2.63
446780	R31107		gb:yh61g01.s1 Soares placenta Nb2HP Homo	1.96	2.78
444173	AI126432	Hs.149493	ESTs	1.50	2.10
417939	R53863	Hs.337512	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.60	2.03
428490	BE301738	Hs.49806	ESTs, Weakly similar to A46010 X-linked	0.47	0.44
443869	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	1.25	2.68
426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.12	1.15
411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	0.64	0.48
454701	AW854930		gb:PM0-CT0263-201099-003-f06 CT0263 Homo	1.30	2.33
439795	N77294	Hs.194294	ESTs	1.17	2.33
425546	BE409762	Hs.26118	hypothetical protein MGC13033	1.17	2.85
411245	AW833441		gb:QV4-TT0008-271099-020-g01 TT0008 Homo	1.90	3.98

434957	AF283775	Hs.35380	x 001 protein	0.47	0.41
425724	AA362525		gb:EST72223 Namalwa B cells I Homo sapie	1.38	2.63
446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.34	0.28
453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	1.28	2.19
421718	AL117574		Homo sapiens mRNA; cDNA DKFZp434L2221 (f	2.04	1.79
415924	H18047	Hs.335821	ESTs	2.02	3.17
450850	AA648886	Hs.151999	ESTs	1.68	2.45
443153	AI371823	Hs.34079	ESTs	1.13	2.41
434420	AA688278	Hs.194864	hypothetical protein FLJ22578	1.34	2.38
426126	AL118747	Hs.26691	ESTs	1.31	2.25
421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	1.48	2.40
459563	AI590487	Hs.49760	gb:tt77d04.x1 NCI_CGAP_HSC3 Homo sapiens	1.74	3.33
453006	AI362575	Hs.303171	ESTs	1.17	2.24
437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	0.54	0.46
417016	AA837098	Hs.269933	ESTs	1.04	2.18
420223	N27807	Hs.286	ribosomal protein L4	2.08	3.10
425303	AA354785		gb:EST63098 Jurkat T-cells V Homo sapien	2.18	2.85
400375	NM_014115		NM_014115*:Homo sapiens PRO0113 protein	1.83	2.14
456169	Y07909	Hs.79368	epithelial membrane protein 1	1.54	2.08
409707	AA861773	Hs.313501	ESTs	0.79	0.84
422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.46	2.06
443152	AI803470	Hs.204529	KIAA1806 protein	1.07	2.43
452714	AW770994	Hs.30340	hypothetical protein KIAA1165	0.45	0.34
415110	H04043		gb:yj45c03.r1 Soares placenta Nb2HP Homo	1.62	2.07
443251	BE185436	Hs.278839	ESTs	1.34	2.05
433441	R37094	Hs.13742	ESTs	1.76	2.05
434612	R76513	Hs.301183	molecule possessing ankyrin repeats indu	0.83	2.88
417807	R17806	Hs.269452	gb:yg09b06.r1 Soares infant brain 1NIB H	1.30	2.23
426902	AI125334	Hs.97408	ESTs	1.94	2.20
436028	AA731124	Hs.120931	ESTs	2.01	1.73
428878	AA436884	Hs.48926	ESTs	1.22	2.17
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	1.32	2.75
442435	AI986208	Hs.244760	ESTs, Highly similar to 834087 hypotheti	2.09	3.13
416527	T62507	Hs.11038	ESTs	1.66	2.12
441808	AW118601	Hs.127887	ESTs, Moderately similar to 1609195B blo	1.22	2.58
417054	AF017060	Hs.174151	aldehyde oxidase 1	2.57	1.48
446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	1.16	2.23
418442	AI873471	Hs.186898	ESTs	1.39	2.26
416640	BE262478	Hs.79404	neuron-specific protein	0.31	0.26
403146			Target Exon	1.49	2.18
457397	AW969025	Hs.109154	ESTs	1.32	2.26
439189	AI951185	Hs.144630	nuclear receptor subfamily 2, group F, m	1.76	2.90
423969	AI830571	Hs.34969	hypothetical protein DKFZp566N034	1.18	2.00
459683	AI674906	Hs.199460	gb:wc73f02.x1 NCI_CGAP_Pan1 Homo sapiens	1.74	2.00
426826	AK001890	Hs.172654	guanine nucleotide binding protein beta	2.04	1.60
414462	BE622743	Hs.301064	arfaptin 1	0.40	0.29
438027	N93047	Hs.19131	transcription factor Dp-2 (E2F dimerizat	1.08	2.40
408623	AW811978	Hs.254037	ESTs	1.64	3.08
433765	AA909619	Hs.112668	ESTs	1.52	2.02
417132	N56605	Hs.269053	ESTs	1.64	2.51
416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	0.28	0.16
435186	AL119470	Hs.145631	ESTs	1.74	3.10
411107	AW958042	Hs.95870	PTD015 protein	0.49	0.24
406930	U04691		gb:Human olfactory receptor (OR17-219) g	2.21	3.88
411026	AW813786		gb:RC3-ST0197-120200-015-b05 ST0197 Homo	1.64	1.03
415766	H01613	Hs.50628	adaptor-related protein complex 4, sigma	1.64	2.51
446018	AW631111	Hs.249727	gb:hh92e12.y1 NCI_CGAP_GU1 Homo sapiens	1.56	2.48
440125	AW238410	Hs.253888	ESTs	1.46	2.25
449832	AA694264	Hs.60049	ESTs	1.27	2.33
431899	AA521381	Hs.187726	ESTs	1.11	2.53
431531	BE142052	Hs.62654	kringle-containing transmembrane protein	1.06	2.00
441077	AI241273	Hs.15312	ESTs	1.12	2.13
426799	H14843	Hs.303154	popeye protein 3	0.61	0.51
419480	BE536584	Hs.122546	hypothetical protein FLJ23017	1.88	2.38
455908	BE156306		gb:QV0-HT0367-150200-114-h04 HT0367 Homo	1.77	2.55
403332			Target Exon	1.46	2.60
455753	BE075124		gb:PM1-BT0585-110200-003-h02 BT0585 Homo	1.40	2.43
404429			Target Exon	1.31	2.01
438941	AF075047	Hs.31864	ESTs	1.34	2.21
428745	AA433896	Hs.201634	ESTs	1.72	2.06
411567	AW851630		gb:MR2-CT0222-211099-002-h06 CT0222 Homo	1.60	2.70
458714	R20916	Hs.344777	ESTs	0.93	2.07
426839	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	1.39	2.71
444539	AI955765	Hs.146907	ESTs, Weakly similar to 2004399A chromos	1.66	2.18
407322	AA171892	Hs.324570	ESTs, Weakly similar to ALU3_HUMAN ALU S	1.30	2.65
453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hfbr1)	1.52	2.73
435695	AA694324	Hs.257675	ESTs	1.24	2.00

402294			Target Exon	1.80	3.08
417759	R13567	Hs.12548	ESTs	1.63	2.58
417527	AA203524		gb:zx56e10.r1 Soares_fetal_liver_spleen_	1.52	2.02
427526	AA405062	Hs.345830	gb:zu12e04.r1 Soares_testis_NHT Homo sap	2.03	1.90
455300	AW891707		gb:CM3-NT0090-040500-171-e02 NT0090 Homo	1.12	2.20
448121	AL045714	Hs.128653	hypothetical protein DKFZp564F013	0.93	2.28
415855	AI921875		gb:wp07e04.x1 NCI_CGAP_Kid12 Homo sapien	1.43	2.08
425702	N59555		gb:yv76f05.s1 Soares fetal liver spleen	1.61	2.80
441056	H37860	Hs.125720	ESTs	1.11	2.10
400311	AF072164	Hs.137570	Homo sapiens HSFE-1 mRNA, partial cds	2.04	2.95
451478	NM_012331	Hs.26458	methionine sulfoxide reductase A	0.50	0.20
425288	AA354502		gb:EST62799 Jurkat T-cells V Homo sapien	0.99	2.08
456397	W28339	Hs.150580	PTD010 protein	1.11	2.29
405654			C12001521:gi|7513934|pir||T31081 cca3 pr	2.30	1.00
450151	AI088196	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	1.21	2.60
419851	AA287987	Hs.13477	ESTs, Weakly similar to 1207289A reverse	1.26	2.60
406016			Target Exon	0.57	0.48
440903	AI468079	Hs.126623	ESTs	2.02	1.61
445026	W90337	Hs.282966	ESTs, Moderately similar to 2109260A B c	1.56	2.23
414182	AA136301	Hs.344442	KIAA1105 protein	1.32	2.55
457048	AA400352	Hs.112861	ESTs	1.54	2.05
440542	AA889143	Hs.295655	ESTs, Weakly similar to PC4259 ferritin	1.48	2.15
422857	R71461		gb:yi51h07.r1 Soares placenta Nb2HP Homo	1.42	2.78
445948	AW444662	Hs.202247	ESTs	1.50	2.48
454002	BE299567	Hs.271749	ESTs, Moderately similar to ALU8_HUMAN A	1.31	2.25
413656	T91703		gb:ye20g09.s1 Stratagene lung (937210) H	2.10	1.69
420441	AI986160	Hs.180383	dual specificity phosphatase 6	0.99	2.33
412062	H09124	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	2.14	1.61
408991	BE501816	Hs.281927	ESTs	1.76	2.83
432534	AW361626	Hs.339833	hypothetical protein FLJ11240	0.41	0.28
435136	R27299	Hs.10172	ESTs	0.76	3.40
451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	2.16	1.85
413928	AA442498	Hs.6700	ESTs, Moderately similar to Z195_HUMAN Z	1.30	2.00
439448	AA970788	Hs.257586	ESTs	1.87	2.23
403344			NM_000341:Homo sapiens solute carrier fa	1.36	2.22
418056	AA524886		gb:nh34f02.s1 NCI_CGAP_Pr3 Homo sapiens	1.42	2.85
435428	AI791746	Hs.130293	ESTs	2.44	1.32
419964	AA811657	Hs.220913	ESTs	1.32	2.08
440926	AW196772	Hs.131323	ESTs	1.80	2.65
452625	AA724771	Hs.61425	ESTs	1.64	2.18
452797	AI369787	Hs.7146	ESTs	1.47	3.16
436120	AI248193	Hs.119860	ESTs	1.41	2.83
449567	AI990790	Hs.188614	ESTs	1.48	2.45
409628	AB021865	Hs.55276	potassium voltage-gated channel, Shal-re	1.70	2.23
416617	H69311	Hs.205980	ESTs	1.83	2.04
452266	AI767250	Hs.165240	ESTs	0.58	0.43
404606			Target Exon	1.47	3.75
401814			Target Exon	2.00	1.91
428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	0.33	0.21
433390	AA586950	Hs.260180	Homo sapiens mRNA; cDNA DKFZp761G18121 (	2.00	4.90
451443	AW295527	Hs.210303	ESTs	1.87	2.25
411188	BE161168		gb:PM0-HT0425-170100-002-a10 HT0425 Homo	2.15	1.69
452704	AA027823	Hs.149424	Homo sapiens PNAS-130 mRNA, complete cds	2.64	1.65
424060	X92108		H.sapiens mRNA for subtelomeric repeat s	2.40	2.58
433331	AI738815	Hs.117323	ESTs	1.46	2.10
428520	AA331901	Hs.184736	hypothetical protein FLJ10097	0.44	0.19
439492	AF086310	Hs.103159	ESTs	0.42	0.26
426736	AA431615	Hs.130722	ESTs	1.90	2.45
416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	2.72	6.25
404917			Target Exon	1.60	2.15
448955	AW207597	Hs.28102	ESTs	2.08	1.75
402797			Target Exon	2.12	1.37
457951	U23860		gb:Human clone mcag19 chromosome 16 CTG	1.72	2.00
426982	AA149707	Hs.173091	ubiquitin-like 3	0.36	0.17

TABLE 8B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408139	10421_1	AA451966 NM_016370 AB036693 AL139228 R58124 AI634847 AL119333 W07356 AI334284 H29050 AI192685 AA652438 AW172843 W19794 N21460 AI743862 AW130622 AA991348 AI204553 AA992664 N80848 AA699329 AI824676 R26624 R49653
408255	1049351_1	AW807321 AW807262 AW177104 AW807319 AW807115 AW807344 AW807324 AW178116 BE141575 AW845849 AW807105 AW845868 BE140942 AW807178 AW807167 AW807398 AW807320 AW807306 AW845866

408283	1050275_1	BE141579 AW807555 AW807502 BE141596 AW845845 AW807500 AW845864 AW807480 AW807486 AW807478 AW178109 AW807228 AW807374 AW807125 AW846124 AW807470 AW807477 AW807510 AW807208 BE141573 AW807465
408839	1085657_1	AW277084 R27662 R26970 D79194
409126	110159_1	AA063426 AW962323 AW408063 AA063503 AA772927 AW753492 BE175371 AA311147
409282	111512_1	AW966480 AA069840 AA384646
409291	1115745_1	AW373472 AW373484 BE071899 BE071898
409367	1123651_1	AW382767 BE153835 BE153702 BE153572
409688	114831_3	AI150485 AW938392 AA076894 AW883422
409692	114869_1	AI500724 AA399661 AA397891 AI471084 AI423511 T07531 AI094336
409894	1157906_1	BE081731 AW861738 AW503629 BE081969
410154	117950_1	F06959 Z43559 AA082002
410357	1197159_1	AW663614 BE046540 BE045760 AW827443 BE046544
410642	1213736_1	AW792784 Z44444 H06639
410725	1218207_1	AW799279 AW799395 AW799392 AW799276 AW799479 H57885
410730	121847_1	AW368860 AA457091 AI903441 AA088823 W88852 AW979154 AA826016 R94779
410744	1219485_1	H86002 W92289 AW801558 AW801324 AW801270 AW801307 AW801351 AW801357 AW801299 AW801609 AW801356 AW801420 AW801425 AW801358 AW801429 AW801428 AW801427 AW801424 AW801306
410840	1223800_1	AW806924 AW866537 AW866473 AW866298 AW866390 AW866478 AW866454 AW866309 AW866539 AW866521 AW866547 AW866517 AW866403 AW866369
410956	1227882_1	AW938322 AW938307 AW938320 AW938323 AW811840
411008	1229027_1	AW813238 AW813474 AW813334 AW816081 AW813296 AW813363 AW813397 AW813327 AW813328 AW816031 AW816140
411026	1229373_-1	AW813786
411141	1233793_1	AW819561 AW819682 AW819563 AW819688 AW819499 AW819498 AW819690 BE065081
411184	1234977_1	AW821117 AW855541 AW855405 AW855374
411188	1235093_1	BE161168 BE162466 AW821260
411245	1236412_1	AW833441 AW833552 AW833700 AW833610 AW833673 AW833675
411347	1239834_1	AW838126 AW838294 AW838247 AW838251 AW838292 AW838299 AW838374
411432	1245636_1	AW846272 AW846564 AW846545 AW846285 AW846135 AW846317 AW846200 AW846265 AW846326 AW846196 AW846357 AW846153 AW846286 AW846319 AW846277 AW846381 AW846438 AW846481 AW846352
411496	1248073_1	AW849241 AW849569 AW849243
411567	1249774_1	AW851630 AW851703 AW851735 AW851723 AW851708 AW851712
411590	125064_1	T96183 T64070 AA094134
411608	1251259_1	AW853441 BE145228 BE145218 BE145162 BE145283
411652	1252836_1	AW855393 AW855560 AW855424
411880	1263110_1	AW872477 BE088101 T05990
411918	1265807_1	AW876354 AW876179 AW876318 AW876290 AW876234 AW876125 AW876199 AW876198
411920	1265812_1	AW876263 AW876257 AW876261 AW876273 AW876231 AW876398 AW876334 AW876134 AW876371 AW876308 AW876314 AW876328 AW876169 AW876331 AW876426 AW876407 AW876412 AW876322 AW876363 AW876218 AW876240 AW876141 AW876138 AW876326 AW876181 AW876131 AW876378 AW876206 AW876191 AW876188 AW876376 AW876289 AW876415 AW876209 AW876366 AW876343 AW876347 AW876165
412085	1276467_1	AW891667 H93096
412252	1285293_1	AW903782 AW903668 AW903672 AW903763 AW903784
412274	128647_1	AA101443 R20332 F07484
412298	1288098_1	AW936300 AW936538 AW936386
412302	1288128_1	AW936334 AW936371 AW936474
412679	1321229_1	BE144762 AW979091
412902	1335166_1	BE008018 BE008025 BE008026 BE007959 BE007994 BE008016 BE008019 BE008024 BE008022 BE008027 BE008029 BE008020 BE008015 BE008021 BE008028 BE008023 BE008030 BE008014
413035	1346295_1	BE155563 BE155574 BE155556 BE061294
413068	1348104_1	BE063792 BE063803 BE063775 BE063801 BE063809 BE063777 BE063784 BE063808 BE066125 BE063782 BE063805 BE063812
413196	135322_1	AA127386 R15644 AA127404
413346	136323_1	AA128586 AA463667 AA235203
413444	1370831_1	BE141019 BE141473 BE141529
413489	1373392_1	BE144228 BE144291
413593	137891_1	AA205248 AA130658 AA204737
413645	138145_1	AA130992 AA503835 AW969537
413656	1381628_1	T91703 BE155222 BE155240 BE155274 BE155275 T92469
413750	1386250_1	BE161453 W28808
413885	1397288_1	BE177442 BE177439 BE177445 BE177440 BE177448 BE177444 BE177433
413888	139750_1	AA580288 AA315655 AA133031 AA377748
414051	1413185_1	BE244127 BE246216
414623	1466952_1	BE391050 BE389191 BE389697
415054	151827_1	AI733907 AA159708 AI732614
415110	1522905_1	H04043 D60988 D60337
415157	1525616_1	D63257 D78918 D63214
415361	1534970_1	F06724 Z43690 R21681
415378	1535274_1	T16964 F07075 H10256
415449	1537026_1	H15034 T17195 F09069
415770	155437_1	M79237 AI267298 AA169260
415806	155668_1	AA169560 AA169840
415855	155930_1	AI921875 AA170835 AA866613
415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
416311	158797_1	D80529 D81719 C14833 AA179446 AA357794
416463	1595999_1	H59241 H57540 R00795
417086	164830_1	AA194446 AA194603 AA193162 AA196396 Z24810
417117	1651230_1	N46778 W86339 N75221
417324	166714_1	AW265494 AA455904 AA195677 AW265432 AW991605 AA456370

417527	168576_1	AA203524 W88451
417670	1692163_1	R07785 T85948 T86972
417882	1705458_1	R22311 R23982 R23997
417890	1706141_1	R79048 R23111
418056	171841_1	AA524886 AW971347 AA211537
418797	179095_1	AA515814 AA515037 AA230024 AA228343
418859	179717_1	AA229558 AA345492 AA229582
419145	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
419501	185354_1	AW843822 AW844020 AA825923 AW968657 AW854173 BE084673
421338	201378_1	AA287443 AA419385 BE084078 AI478347
421582	2041_1	AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539 BE074045 AI307407 AW602303 BE073575 AI202532 AA524242 AI970839 AI909751 BE076078 AI909749 R55292
421718	20595_1	AL117574 AI681945 BE503055 AW015330 C16652 AA441855 AA329853 AW962502 AA441830 AF114049
421926	209246_1	AA300591 AW963893 AA300493
422259	214322_1	AA307584 AW795791 AW795790
422297	214851_1	AW961290 AA308338 R60841 BE378716 R13001
422337	215447_1	R38572 R49597 H51730 F10468 AA309198 BE011889 AA613236
422444	216595_1	AA310688 AA355321 AW962134
422857	222190_1	R71461 AA328744 AA318128 BE081817 BE081587 BE081751
422936	223099_1	AA319278 AA319712 AW961504 AW954956
422940	223106_1	BE077458 AA337277 AA319285
422959	22327_3	AV647015 AV647162 AA477047 AW392066 BE168052 AA657684 AL040747 AL043589 AL041618 W24630 AA419002 AA778650 AI028269 AW378085 AW780241 AI984255 AW129462 AI271476 AL040967 AA836991 AL040910 AW273346 AA132452 AI375545 AI436321 N53166 AA598667 AA423804 AA889495 AI954063 AI923968 AW194576 AI400578 AA748499 AA860230 AW519209 AA339537 AA476935 AA767391 AI017695 AI860419 N93437 AW452389 AI051533 AA806940 AA609569 AI624860 AI356952 AI811516 AI439198 AA749268 AI206880 AI784422 AI431957 AI187038 AI678429 AI273421 AI358604 AI691155 AA586499 AA897667 AA524576 AI417772 AW799936 BE241923 AA013428 BE164987 AW602710 AI933540 AA757772 AW015132 AI954159 AW956377 W69468 AI807580 AI871746 AI922524 N80292 AI676213 BE467086 N92405 AV656311 AI678172 AW339455 AI949278 AI872882 AI123785 AA016267 AI961623 AW168519 F28686 F37181 AA908333 AW020788 AW374027
423074	22470_1	AL109963 AA134692 BE273642 M78295 AI825179 AA228029 BE538677 AW589948 AW241564 AA732224 AA228030 AW977225
423622	230333_1	BE154847 BE154890 AA328702
423736	231511_1	AW936874 AW936923 AW936924 AA330274
423977	233868_1	AA333232 AW962695 R54896
424060	23490_1	X92108 AW295478 AI768675 AI086644 AW190160 AA313783 AA322741 AA354698 AW962099 AL044667 AA282648 AA973897 AL036586 AA386055 AL135179 AW882199
424160	236151_1	T74062 F12441 AA336207 BE185031
424290	237857_1	AA338396 AW966247 AW753612
424951	245273_1	AW964082 AA348838 AA348839
425288	249569_1	AA354502 AA355215 AW962122
425303	249780_1	AA354785 AA354792 AW958427
425702	255206_1	N59555 AA362113 AA362136
425724	255509_1	AA362525 AW979199 AA857501
425757	255956_1	AA363171 AW963347 AA371863
425893	257742_1	AA629695 AA365582 AA365581 AW959799 AW876559 AW876588
425980	258778_1	AA366951 AA470999 AA469425
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426477	267804_1	AA379464 AA379611 AA379463
428036	28620_1	AW068302 AI754558 AI750727 AI752631 AA302174 AA327522 M64110 AW859944 AW859989 AI751995 AA769620 AI858829 AI924875 AI888836 AA864291 AI685060 AW088029 AI924908 AW466328 AI093800 AA991651 AI254501 BE004703 AA334442 AW938852 AA194330 AL046953 AA852866 AW391995 W30846 AW662928 W25261 AA042863 R99045 H97060 W03910 H94687 T88984 AL048165 T29632 N31556 N36484 AI798679 AA989355 W23832 AA873789 AI743646 AA363587 AI814748 AW338990 N73740 N83666 AL047816 R24137 R63433 AA524984 AA234043 AA195131 N99903 AA453669 AI240302 AA370271 AI950026 AW771049 AA121476 AA569557 AI752632 AI355594 AI471993 AI159941 N94555 AI753138 N21537 H97881 N25769 AW068044 AA808425 R63380 AA384736 AA384738 AA852352 AI073645 AA527960 AA525036 AA044414 AI752460 AA703064 R01216 AA897183 AI751996 T81078 H95047 AA573642 D58348 N20953 AA437143 N95439 AA579540 AW867056 AA770090 AI085180 AI806799 AA426421 AI572513 R24081 AA853189 AA295620 AA234044 AA371020 AW994984 H20896 AW964438 AA318516 AA318499 AA318727 AA318211 AA318478 AA318444 AA318307 AA318497 AA318448 AA318309 AA318496 AA318213 AA318435 AA318424 AA318217 AA318523 AA318438 AA318487 AA318724 AA593185 AW994985 T69842 AI251813 AA478174 AA447737 T68350 F07712 AA121145 H08973 AA345212 BE000667 AW068210 AW608407 R05674 H16712 N85426 N42354 H85516 BE147991 T28113 R32662 AA384678 AW239275 H82382 AW840700 D58229 C04082 W45394 AW795667 R73973 BE002409 AA042828 AA363555 AJ223812 AA344709 BE149590 R70995 W46881 W90778 N71242 AA534826 AL040676 R23797 H96450 AA062957 D79947 W46960 AW959278 AA295997 AA026215 AW579469 AW365135 AW365134 AW994353 AW972886 AW069166 AA343690 AW888731 AI751527 AA937490 AA937506 AI826715 BE465604 AI925532 AI858109 AW339097 AI858524 AI720571 BE046506 AW384981 AA043908 AA375983 AA525181 AW068366 AW070577 AW891837 N83985 AW182753 AI422979 AI679733 BE006555 AL048166 AI081401 AI888821 AI626043 N37087 AI624140 AI801298 AA600048 AI753947 H89615 N66424 AW069756 AI814880 AI982806 AI754287 AI971816 AW069022 AW069069 AW069454 AA342989 AI077712 AI311467 AI087361 AI801015 W46993 AI281324 AW191963 AI421675 AI300881 AI356670 AA873156 AI004219 AI189685 AA478018 AA076063 AI445222 AI753124 AI521569 AI925026 AI022368 AI475993 H20846 AI223234 AI635123 AA579170 N30442 AW117889 AA807935 AA558975 AI306636 AA888963 AI952591 AI935835 AI445293 H16713 AW139833 AA622122 AA972051 AI280828 H09543 AI453725 AW069613 AI865615 AI753921 AI368782 AI633208 AI446651 W46961 N22201 H82276 C16555 AA291477 AW440535 AW517755 AA669921 AI926777 AW662118 AA553369 N67873 AW023948 C15861 C16601 AI251465 AW079187 BE045090 AI273006 C16390 C16503 AI620823 F13661 N66864 Z21311 C16108 C16089 C16400 AA758273 AI287781 AA864676 AW608074 AW385583 AI589944 AA665817 AW192979 AW469065 AA564048 H84715 C16417 AA731072 AA661674 C16487 N29477 AW189997 AI370492 C16471 AA652809 AA936687 AA506512 C16306 AW028413 AI537935 AA528347 C16255 AW029046 C16202 AI868152 AI524662 T94414 AI567041 AI619654 AW008486 AI075624 AA577434 AA345104 T30105 AA932002 C16585 AI750390 AW294265 AI619552 AA669781 AA026678 AW132002 AW263919 C16562 AA759137 AA693351 Z40779 C16577 AA885045 AW073763 R45484 AI520895 U54708 T49285

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431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
431926	339082_1	AW972724 AA522631 AA877998
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432407	34624_1	AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639 BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720 AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859
432586	350432_1	AA568548 AI050036 AA554053 AI911659 AI826259
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433436	366107_1	AW162474 AA588442 AI972440
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437272	435447_1	AW975957 AA747943 AA811289
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438091	44964_1	AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616 AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571 AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994 AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
438813	46553_-1	M27346
439590	47413_1	AF086410 W94386 W74609
439848	477806_1	AW979249 D63277 AA846968
440612	49847_1	BE561384 AW732707
440642	499098_1	AI744995 AI973099 R19291 AA935215 AA897534 AI698070 BE179102 AI694912
441846	527227_1	AW850980 AA969613 AW366793
443100	559752_1	AI033188 BE004743 AW804074 BE004795 BE178660 BE089438 BE089378 BE089439 BE089437 BE089423 BE089420 BE089425 BE089424 BE089426
443197	56261_1	Z43613 AA320191 AW954963 H15889 R83872
443357	567506_1	AW016773 AI052778 AI452937 AW085293
444163	593658_1	AI126098 AI184746 AI148521
444298	600160_1	Z17870 AL039867 AI139927
444312	600647_1	R44007 N54521 AI140476 AW418649 T95308
444872	623948_1	AI936264 AI219228 AI200740 BE300771 AI635739 AI690626 AW044010 R60842 R40388
445468	640681_1	AW450439 AW297340 AI239849 AI613119
445555	64334_1	AW974013 AA557257 N36812 AI597998 AA873565
445689	647829_1	BE158869 AI248241 BE158865 BE158868
446780	692897_1	R31107 AI341136 AI653198 H04953
447008	70358_1	BE010189 AW879041 BE008038 AW905325 AA343575 AW844209 AL038020 BE010133 BE010083 AW903901 BE174377 AI309717 AI349651 AI903726 BE176661 AW905394
448489	765247_1	AI523875 R45782 R45781
450717	844561_1	T94709 AI820675 AI732253
450724	844585_1	R55428 AI820704 AI732283 R54983
450735	844617_1	AI732321 R55640 R55639 AI820744
451724	882130_1	AI903765 AI811194 BE007147 AW130760
452565	922372_1	BE066552 BE066341 AI907683
453577	972216_1	AL043049 T95976
453823	982526_1	AL137967 BE064160 BE064186
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454457	1207274_1	AW753456 AW753036 AW854868 AW854862
454523	1221564_1	AW803980 AW803974
454609	1226517_1	AW810204 AW810555 AW810196 AW810619 AW810507
454629	1227240_1	AW811114 AW811095 AW811087 AW811124 AW811054 AW811094 AW811157
454631	1227443_1	AW811324 AW811325 AW811326 AW811333 AW811329 AW811328 AW811332 AW811339 AW811335
454639	1227728_1	AW811633 AW811652 AW811898
454662	1228537_1	AW812715 AW812646 AW812714
454701	1229702_1	AW854930 AW814431 AW814190 AW814115 AW854941
454721	1230747_1	AW815588 AW815671 AW815493 AW815898 AW815613 AW815490 AW815808 AW815426

454741	1232559_1	BE154396 AW817959 BE154393
454826	1236377_1	AW833676 AW833814 AW833798 AW833677 AW833449 AW833630 AW833626 AW833444 AW833366 AW833791 AW833659 AW833432 AW833534 AW833556 AW833553
454915	1242343_1	AW841619 AW851958 AW851851 AW851985
455065	1251980_1	AW854352 AW854311 AW854340 AW854461
455087	1252832_1	AW855389 AW855556 AW855420
455116	1254206_1	AW857271 AW857308 AW857296 AW857258
455236	1265662_1	AW875972 AW875983 AW875974 AW876000 AW875966 AW876050
455300	1276482_1	AW891707 AW891696 AW891917 AW891913 AW891912 AW891909 AW891890 AW891892 AW891889 AW891697 AW891880 AW891898
455407	1288347_1	AW936813 AW936731 AW936728 AW936600 AW936681 AW936651
455508	1318507_1	AW976165 C04000
455527	1322125_1	AW984479 AW984498 AW984495 AW984477 AW984480 AW984504
455642	1348163_1	BE063965 BE063968 BE064034 BE064028 BE063874 BE063966 BE063869 BE064043 BE064033 BE063884
455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
455753	1356070_1	BE075124 BE075229 BE075278
455757	1358657_1	BE079531 BE079371 BE079372 BE079593 BE079468 BE079504 BE079505
455908	1382301_1	BE156306 BE156188 BE156298 BE156377 BE156374
455917	1382784_1	BE156765 BE156770 BE156767 BE156769 BE156803 BE156802 BE156847 BE156853 BE156780 BE156836 BE156792 BE156834 BE156779 BE156789 BE156833 BE156844 BE156831 BE156849 BE156797 BE156784 BE156801 BE156843 BE156793 BE156852
455988	1397740_1	BE177983 BE178322
456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
456172	1603643_1	R99050 R99067 H67642
456332	179104_1	AA228357 AW841786 AW841716
456381	184123_1	AA236606 AA459341 AA237079
457297	313764_1	AW968188 AA468196 AA468269 AA468298
457389	331080_1	AW970989 AA502167 AA507546
457567	357346_1	AW939074 AW939073 BE160476 AW939938 AW939206 AW940012 AW939076 AA573577 AW750479 AA574383 AW970057
457581	359936_1	AA578512 AA595535 BE177533
457741	395767_1	BE044740 AW827360 AW827623 BE161439 BE044718 BE046207 BE046551 AA653908 BE166581
457871	426637_1	AI168278 AA868238 BE550792 AI522194 AI819707 AA973538 AI990086 AI628424 AI095270 AI991608 AA730741
457951	44251_1	U23860 U80739
459234	945240_-1	AI940425

TABLE 8C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400704	8118864	Minus	63110-63241
400830	8570385	Plus	157683-163035
400834	8705192	Plus	121963-122288
400840	9188586	Plus	113882-114121
400850	1927150	Minus	4506-4691
400881	2842777	Minus	91446-91603,92123-92265
401016	8117441	Plus	126234-126359,128050-128236
401090	8492704	Minus	201281-201460
401215	9858408	Plus	103739-103919
401241	4827300	Minus	30503-30844,31056-31248
401335	9884881	Plus	15736-16352
401381	8570226	Minus	118629-119146,119392-119657
401400	7708226	Minus	33028-33585
401469	6682292	Minus	125521-125639
401473	7249001	Plus	115142-117305
401577	9280797	Minus	139377-139674,141195-141281,142217-142340
401658	9100664	Plus	89638-90028
401659	7689875	Minus	183379-183521
401686	6468551	Plus	5005-5426,6810-7042
401723	7656694	Plus	147273-147503
401814	7408052	Plus	136003-136726
401818	7467933	Minus	10964-11084,11674-11817
401890	8516144	Plus	148955-149396,149569-150002
401908	8698760	Minus	126888-127024
401913	9369520	Minus	33753-33904
401927	3873185	Minus	112000-112137
402025	7547159	Plus	173835-173998
402039	7770432	Plus	560-1294
402049	8072512	Plus	100065-100419
402085	7249154	Plus	90533-90687,94949-95158
402241	7690131	Minus	125073-125206,130996-131125
402294	2282012	Minus	2575-3000
402305	7328724	Plus	40832-41362

402366	9454515	Plus	195808-196863
402551	9856793	Minus	37346-37633
402654	8076879	Plus	44058-44803
402685	8318556	Plus	58962-59294
402762	9230904	Minus	123298-124035
402797	3421043	Minus	15758-15930
402833	8918545	Plus	26987-27778
402901	8894222	Minus	175426-175667
402948	9368458	Minus	143456-143626,143808-143935
403066	8954202	Plus	158189-158433
403072	8954241	Plus	141829-142006
403146	9799812	Plus	162877-163118
403197	9930749	Plus	79990-80237
403214	7630945	Minus	76723-77027,79317-79484
403217	7630969	Plus	54089-54163,55427-55623
403290	8083176	Plus	19288-20076
403291	7230870	Plus	95177-95435
403294	8096496	Plus	41565-41881
403315	8247953	Minus	125117-125287
403332	8568139	Minus	31409-31674
403344	8569726	Plus	70823-70990
403362	8571772	Plus	64099-64260
403371	9087278	Plus	105655-106050
403391	9438337	Plus	42410-42544,83317-83540,86840-86922,87970-88110
403488	9966615	Minus	12450-12753
403536	8076924	Plus	34972-35182
403779	8018040	Minus	95602-95969
403859	7708954	Plus	113738-113858
403871	7709262	Plus	104545-104757
403903	7710671	Minus	101165-102597
403917	7710849	Plus	109718-109847,109927-110202
403978	8576014	Plus	97326-97808
404031	7671252	Plus	171477-172316
404167	9926594	Minus	77030-77280
404220	6706820	Plus	46107-46439
404286	2326514	Plus	51086-51301
404418	7382420	Minus	153339-153481,155099-155294
404427	7407959	Plus	127170-127358
404429	7407979	Plus	31352-31498
404440	7528051	Plus	80430-81581
404495	8151634	Minus	59449-60477
404580	6539738	Minus	240588-241589
404606	9212936	Minus	22310-23269
404730	8389582	Plus	119832-120016,124110-124275
404917	7341851	Plus	49330-49498
405033	7107731	Minus	142358-142546
405137	8570507	Plus	158969-159423
405146	9438278	Minus	102529-102633
405158	9966252	Plus	42873-43056,43815-43949
405187	7229826	Plus	117025-117170,118567-118736
405223	7239614	Plus	106184-106313
405340	6094635	Plus	49644-49760
405494	8050952	Minus	70284-70518
405551	1552506	Plus	12525-12997
405654	4895155	Minus	53624-53759
405667	4726099	Plus	5798-5914
405673	4589984	Plus	50700-50842
405704	4204244	Plus	138842-139051
405723	9801668	Plus	114896-115831
405727	9838331	Minus	78865-79664
405760	6066938	Minus	37424-38045
405779	7280331	Minus	33048-33856
405944	7883702	Minus	5143-5684
406002	8247797	Minus	154007-154579
406016	8272661	Plus	41341-41940
406097	7107918	Minus	36698-37269
406104	9124028	Plus	35309-35977
406156	7144867	Plus	379-597
406207	5923650	Minus	162607-162800
406300	6479046	Minus	19234-19401
406308	9211532	Plus	358408-358651
406314	9211609	Minus	12899-13011,18022-18136
406317	9211652	Plus	108018-108410
406432	9256504	Plus	3804-3930,4026-4120,4929-5109
406490	7711309	Minus	80295-80480
406584	3983530	Minus	3989-4497

TABLE 9A: Genes predictive of no bladder cancer progression

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1 80th percentile of Ta or T1 tumor AIs from patients who did not upstage divided by the 80th percentile of Ta or T1 tumor AIs from patients who did upstage
R2 median of Ta or T1 tumor AIs from patients who did not upstage divided by the median of Ta or T1 tumor AIs from patients who upstaged

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	4.64	5.88
412129	M21984	Hs.73454	troponin T3, skeletal, fast	4.54	5.10
459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	4.37	1.63
400844			NM_003105*:Homo sapiens sortilin-related	3.69	5.90
419555	AA244416		gb:nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens	3.61	2.03
414522	AW518944	Hs.76325	step II splicing factor SLU7	3.60	1.00
440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypotheti	3.58	1.04
445182	AW189787		ESTs	3.57	2.70
407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.56	1.48
421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	3.28	3.25
429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	3.25	2.50
430702	U56979	Hs.278568	H factor 1 (complement)	3.20	2.70
412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.20	2.30
420729	AW964897	Hs.290825	ESTs	3.20	1.53
433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.00	4.10
420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	2.94	2.78
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.93	1.43
426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	2.93	1.33
428030	AI915228	Hs.11493	Homo sapiens cDNA FLJ13536 fis, clone PL	2.92	2.47
419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	2.89	3.33
414407	AA147026	Hs.76704	ESTs	2.87	2.87
450779	AW204145	Hs.156044	ESTs	2.78	1.86
411243	AB039886	Hs.69319	CA11	2.73	1.00
417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.68	2.32
441619	NM_014056	Hs.7917	DKFZP564K247 protein	2.67	2.98
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.66	1.00
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.64	1.77
426252	BE176980	Hs.28917	ESTs	2.63	7.30
424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.60	2.53
429429	AA829725	Hs.334437	hypothetical protein MGC4248	2.59	3.34
427450	AB014526	Hs.178121	KIAA0626 gene product	2.57	2.28
420180	AI004035	Hs.25191	ESTs	2.56	1.68
434061	AW024973	Hs.283675	NPD009 protein	2.54	2.10
422070	AF149785	Hs.111126	pituitary tumor-transforming 1 interacti	2.54	3.25
419355	AA428520	Hs.90061	progesterone binding protein	2.53	3.63
446215	AW821329	Hs.14368	SH3 domain binding glutamic acid-rich pr	2.52	4.38
432442	AI672516	Hs.178485	ESTs, Weakly similar to S65657 alpha-1C-	2.50	4.60
447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	2.49	2.23
401155			Target Exon	2.48	2.30
404530			Target Exon	2.48	1.00
446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	2.48	2.35
436476	AA326108	Hs.33829	bHLH protein DEC2	2.47	2.88
446535	AF257175	Hs.15250	peroxisomal D3,D2-enoyl-CoA isomerase	2.46	2.19
408636	BE294925	Hs.46680	CGI-12 protein	2.45	1.60
420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	2.44	3.75
427008	Z45258	Hs.286013	short coiled-coil protein	2.42	3.40
459711	BE386801	Hs.21858	trinucleotide repeat containing 3	2.40	2.78
407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.40	1.00
410337	M83822	Hs.62354	cell division cycle 4-like	2.39	3.88
435029	AF167706	Hs.19280	cysteine-rich motor neuron 1	2.39	3.23
437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	2.39	1.00
410968	AA199907	Hs.67397	homeo box A1	2.38	1.33
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.38	6.40
450775	AA902384	Hs.73853	bone morphogenetic protein 2	2.38	2.71
442433	BE243044	Hs.8309	KIAA0747 protein	2.37	3.68
454000	AA040620	Hs.5672	hypothetical protein AF140225	2.36	1.14
447701	BE619526	Hs.255527	hypothetical protein MGC14128	2.36	2.02
427985	AI770170	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	2.36	2.18
442257	AW503831	Hs.323370	Human EST clone 25267 mariner transposon	2.35	3.53
454070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	2.35	3.60
418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.35	2.48
421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	2.35	1.00
407793	AW080879	Hs.236572	gb:xc38g04.x1 NCI_CGAP_Co20 Homo sapiens	2.35	1.21
442061	AA774284	Hs.285728	abl-interactor 12 (SH3-containing protei	2.34	3.03
402845			ENSP00000246267:KIAA0444 PROTEIN (FRAGME	2.34	1.52
411407	R00903	Hs.169793	ribosomal protein L32	2.34	0.77
418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.34	0.72

424637	NM_015057	Hs.151411	KIAA0916 protein	2.32	2.55
413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	2.32	1.46
411060	*NM_006074*	*Hs.318501*	*Homo sapiens mRNA full length insert cDN*	2.32	2.90
430028	BE564110	Hs.227750	Target CAT	2.32	2.28
417720	AA205625	Hs.208067	ESTs	2.32	2.09
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.31	1.13
454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.30	4.38
444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	2.30	1.86
408179	AL042465	Hs.43445	poly(A)-specific ribonuclease (deadenyla	2.29	2.19
442679	R53718	Hs.107882	hypothetical protein FLJ10659	2.29	2.79
458949	AW291777	Hs.346137	ESTs, Weakly similar to T08599 probable	2.28	1.85
407191	AA608751		gb:ae56h07.s1 Stratagene lung carcinoma	2.27	2.42
448367	AI955411	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	2.27	1.18
405155			Target Exon	2.26	1.94
445594	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	2.26	1.55
417458	NM_005655	Hs.82173	TGFB inducible early growth response	2.25	1.95
430315	*NM_004293*	*Hs.239147*	*guanine deaminase*	2.24	1.84
411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	2.24	2.73
408937	AA210734	Hs.291386	ESTs	2.24	3.18
431474	AL133990	Hs.190642	CEGP1 protein	2.23	1.00
434094	AA305599	Hs.238205	hypothetical protein PRO2013	2.22	4.08
420997	AK001214	Hs.100914	hypothetical protein FLJ10352	2.22	2.15
420164	AW339037	Hs.24908	ESTs	2.22	2.16
414099	U11313	Hs.75760	sterol carrier protein 2	2.21	4.05
424800	AL035588	Hs.153203	MyoD family inhibitor	2.21	3.53
459005	AA447679	Hs.144558	ESTs, *Weakly similar to ALU1_HUMAN ALU S*	2.21	2.90
416290	NM_000016	Hs.79158	acyl-Coenzyme A dehydrogenase, C-4 to C-	2.20	4.00
439208	AK000299	Hs.180952	dynactin 4 (*p62*)	2.20	1.88
401563			C15001262:gi|7304981|ref|NP_038528.1| ca	2.20	1.77
404687			C9000375*:gi|11994617|dbj|BAB02754.1| (A	2.19	2.60
443303	U67319	Hs.9216	caspase 7, *apoptosis-related cysteine pr*	2.19	2.08
439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	2.19	2.21
400835	AW853954		chromosome 2 open reading frame 2	2.18	3.00
456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	2.18	2.45
431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.17	1.83
418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	2.17	2.67
451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.17	1.71
406038	Y14443		zinc finger protein 200	2.17	1.71
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.17	1.00
441623	AA315805		desmoglein 2	2.17	1.81
459244	AW503990	Hs.142442	HP1-BP74	2.17	4.03
424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.17	2.93
404204			ENSP00000252204*:Zinc finger protein 165	2.17	1.02
453987	AA323750	Hs.235026	Homo sapiens, clone IMAGE:4247529, mRNA,	2.16	2.85
411400	*AA311919*	*Hs.69851*	*nucleolar protein family A, member 1 (H/*	2.16	3.60
454949	AW847318	Hs.290131	KIAA1819 protein	2.16	1.96
409223	AA312572	Hs.6241	phosphoinositide-3-kinase, regulatory su	2.16	1.48
418030	BE207573	Hs.83321	neuromedin B	2.16	2.07
433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	2.16	2.32
459511	AI142379		gb:qg64c01.r1 Soares_testis_NHT Homo sap	2.16	1.85
437559	AI678033	Hs.121476	ESTs	2.15	1.43
418827	BE327311	Hs.47166	HT021	2.15	3.84
417470	AF112219	Hs.82193	esterase D/formylglutathione hydrolase	2.15	1.74
421012	X53281	Hs.101025	basic transcription factor 3	2.15	1.26
448772	AW390822	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	2.15	4.05
439601	AB029032	Hs.6606	KIAA1109 protein	2.15	2.15
434417	AL110157	Hs.3843	Homo sapiens mRNA; cDNA DKFZp586F2224 (f	2.15	1.45
424865	AF011333	Hs.153563	lymphocyte antigen 75	2.15	2.63
400752			NM_003105*:Homo sapiens sortilin-related	2.14	2.67
438916	AW188464	Hs.101515	ESTs	2.14	2.38
430024	AI808780	Hs.227730	integrin, alpha 6	2.14	2.00
409345	AI949109		*hypothetical protein FLJ20783*	*2.14*	1.40
421939	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	2.13	1.58
442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.13	2.67
419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	2.13	2.00
458025	AI275406	Hs.32450	gb:ql63c10.x1 Soares_NhHMPu_S1 Homo sapi	2.12	0.89
428582	BE336699	Hs.185055	BENE protein	2.12	2.65
422749	W01076	Hs.278573	CD59 antigen p18-20 (antigen identified	2.12	2.73
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.11	0.91
456421	AL157485	Hs.91973	hypothetical protein	2.11	2.51
421508	NM_004833	Hs.105115	absent in melanoma 2	2.11	3.13
402760			NM_021797*:Homo sapiens eosinophil chemo	2.09	1.79
406274			Target Exon	2.09	1.60
406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	2.09	1.00
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	2.09	2.92
445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 fis, clone C	2.09	3.20
442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	2.09	1.90

428336	AA503115	Hs.183752	*microseminoprotein, beta-*	2.08	1.15
405165			ENSP00000238974*:Homeobox protein NKX2-3	2.07	2.83
416999	AW195747	Hs.21122	hypothetical protein FLJ11830 similar to	2.07	3.71
453865	AA307279	Hs.35947	methyl-CpG binding domain protein 4	2.07	1.71
439924	AI985897	Hs.125293	ESTs	2.07	1.00
439004	AW979062		gb:EST391172 MAGE resequences, MAGP Homo	2.07	2.13
407955	BE536739	Hs.109909	ESTs	2.06	1.91
412998	BE046254		gb:hn38g09.x2 NCI_CGAP_RDF2 Homo sapiens	2.06	2.58
414013	AA766605	Hs.47099	hypothetical protein FLJ21212	2.05	5.00
415249	R40515	Hs.21248	ESTs	2.05	2.18
427332	R09418	Hs.261101	ESTs, Weakly similar to I38022 hypotheti	2.05	3.35
426521	AF161445	Hs.170219	*hypothetical protein*	2.05	1.00
431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	2.05	6.03
423851	R39505	Hs.133342	*Homo sapiens clone 24566 mRNA sequence*	2.05	1.88
410028	AW576454	Hs.346502	ESTs	2.04	1.95
406575			Target Exon	2.04	1.56
457148	AF091035	Hs.184627	KIAA0118 protein	2.04	3.11
449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	2.04	2.42
429837	NM_003896	Hs.225939	sialyltransferase 9 (CMP-NeuAc:lactosylc	2.04	1.97
440675	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	2.04	2.06
411988	AA455459	Hs.164480	ESTs, Weakly similar to T50609 hypotheti	2.04	2.65
433293	AF007835	Hs.32417	hypothetical protein MGC4309	2.04	2.35
446187	AK001241	Hs.14229	hypothetical protein FLJ10379	2.04	2.03
420838	AW118210	Hs.42321	ESTs	2.03	1.00
445481	AW661846	Hs.346630	ESTs	2.03	2.49
448175	BE296174	Hs.225160	*hypothetical protein FLJ13102*	2.03	2.25
410600	AW575742		ESTs, Moderately similar to S65657 alpha	2.02	2.10
401177			Target Exon	2.02	2.59
448474	AI792014	Hs.13809	hypothetical protein FLJ10648	2.02	4.23
434782	NM_005032	Hs.4114	plastin 3 (T isoform)	2.02	1.48
424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	2.02	2.93
424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.02	2.63
424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypotheti	2.02	3.43
414721	X90392	Hs.77091	ribosomal protein L10	2.02	1.89
429869	AI907018	Hs.15977	Target CAT	2.02	1.47
439177	AW820275	Hs.76611	ESTs, Weakly similar to I38022 hypotheti	2.01	1.94
437175	AW968078	Hs.87773	*protein kinase, cAMP-dependent, catalyti*	2.01	1.64
452046	AB018345	Hs.27657	KIAA0802 protein	2.01	4.31
417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	2.01	6.75
420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.00	2.75
408232	AL137269	Hs.43899	Homo sapiens mRNA; cDNA DKFZp434C1714 (f	2.00	2.02
408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.00	1.95
433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypotheti	2.00	0.91
426969	AI936504	Hs.2083	CDC-like kinase 1	2.00	3.60
442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	2.00	1.95
444916	AB028956	Hs.12144	KIAA1033 protein	2.00	1.23
452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.00	5.30
414906	AA157911	Hs.72200	ESTs	1.99	1.22
414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	1.99	3.83
414557	AA340111	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	1.99	2.31
452846	AA082160	Hs.63368	ESTs, Weakly similar to TRHY_HUMAN TRICH	1.99	3.43
408437	AW957744	Hs.278469	lacrimal proline rich protein	1.98	2.15
439205	AF087990	Hs.42758	Homo sapiens, clone IMAGE:3354845, mRNA,	1.98	2.28
442506	BE566411		ESTs	1.98	3.95
447731	AA373527	Hs.19385	CGI-58 protein	1.98	2.67
410579	AK001628	Hs.64691	KIAA0483 protein	1.97	2.43
426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	1.97	2.50
456141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.97	3.03
419576	AK002060	Hs.91251	*hypothetical protein FLJ11198*	1.96	2.88
407241	M34516		gb:Human omega light chain protein 14.1	1.96	1.09
420664	AI681270	Hs.99824	BCE-1 protein	1.96	1.76
448586	AF285120	Hs.283734	CGI-204 protein	1.96	3.28
408089	H59799	Hs.42644	thioredoxin-like	1.95	4.00
421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.95	2.12
452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	1.95	3.45
432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	1.94	2.80
434263	N34895	Hs.44648	ESTs	1.94	4.60
409829	M33552	Hs.56729	lymphocyte-specific protein 1	1.94	1.79
425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	1.94	2.30
401835			Target Exon	1.94	2.27
406557			C5000893:gi|6226859|sp|P38525|EFG_THEMA	1.94	3.28
440062	AI350518	Hs.129692	ESTs	1.94	3.18
410442	X73424	Hs.63788	*propionyl Coenzyme A carboxylase, beta p*	1.94	2.70
457281	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.94	2.60
420230	AL034344	Hs.284186	forkhead box C1	1.93	2.28
452970	NM_012238	Hs.31176	sirtuin (silent mating type information	1.93	4.35
403728			Target Exon	1.92	1.70

415789	H01581		gb:yj33f08.r1 Soares placenta Nb2HP Homo	1.92	2.15
406759	AA654582	Hs.77039	ATP synthase, H transporting, mitochondr	1.92	2.10
442073	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase	1.92	4.43
438023	AF204883	Hs.6048	FEM-1 (C.elegans) homolog b	1.92	4.00
445502	AW379160	Hs.12813	DKFZP434J214 protein	1.92	2.13
405474			NM_001093*:Homo sapiens acetyl-Coenzyme	1.92	2.58
430007	NM_014892	Hs.227602	KIAA1116 protein	1.92	3.78
439937	AF151906	Hs.6776	CGI-148 protein	1.91	2.32
418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	1.91	1.88
444630	AI753230	Hs.323562	hypothetical protein DKFZp564K142	1.91	1.61
451184	T87943	Hs.173638	transcription factor 7-like 2 (T-cell sp	1.90	3.35
414715	AA587891	Hs.904	amylo-1,6-glucosidase, 4-alpha-glucanotr	1.90	3.55
445841	AL080115	Hs.13370	DKFZP564G0222 protein	1.90	1.46
425284	AF155568	Hs.348043	NS1-associated protein 1	1.90	3.65
437943	NM_016353	Hs.5943	rec	1.89	1.73
442426	AI373062	Hs.332938	hypothetical protein MGC5370	1.89	2.79
400111			Eos Control	1.89	3.84
437762	T78028	Hs.154679	synaptotagmin I	1.89	1.00
404069			Target Exon	1.89	2.51
434809	AW974687		gb:EST386776 MAGE resequences, MAGM Homo	1.88	2.35
414220	BE298094	Hs.323806	gb:601118231F1 NIH_MGC_17 Homo sapiens c	1.88	1.00
422506	R20909	Hs.300741	sorcin	1.87	2.99
417439	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	1.87	1.13
404391			Target Exon	1.87	3.00
420187	AK001714	Hs.95744	hypothetical protein similar to ankyrin	1.86	2.93
446950	AA305800	Hs.5672	hypothetical protein AF140225	1.86	1.90
400634			C10000818*:gi|7661882|ref|NP_055697.1| K	1.86	2.80
408455	C19034	Hs.288613	Homo sapiens cDNA FLJ14175 fis, clone NT	1.86	1.32
422366	T83882	Hs.97927	ESTs	1.85	1.44
452170	AF064801	Hs.28285	patched related protein translocated in	1.85	2.64
430604	AV650537	Hs.247309	succinate-CoA ligase, GDP-forming, beta	1.85	1.81
426484	AA379658	Hs.272759	KIAA1457 protein	1.85	2.60
411609	AW993680		gb:RC3-BN0034-290200-013-d08 BN0034 Homo	1.85	2.10
431129	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f	1.84	3.70
412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	1.84	2.58
401512			NM_014080:Homo sapiens dual oxidase-like	1.84	1.52
415969	H11294	Hs.31047	ESTs	1.84	3.08
444736	AA533491	Hs.23317	hypothetical protein FLJ14681	1.84	1.20
426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	1.84	2.35
416968	AA412686	Hs.97955	ESTs	1.84	2.18
442961	BE614474	Hs.289074	F-box only protein 22	1.84	2.18
418650	BE386750	Hs.86978	prolyl endopeptidase	1.84	1.98
420923	AF097021	Hs.273321	differentially expressed in hematopoieti	1.84	1.00
432834	F06459	Hs.289113	cytochrome b5 reductase 1 (B5R.1)	1.83	3.93
442485	BE092285	Hs.29724	hypothetical protein FLJ13187	1.83	3.10
427699	AW965076	Hs.180378	hypothetical protein 669	1.83	3.03
447387	AI268331	Hs.102237	tubby super-family protein	1.83	1.78
418663	AK001100	Hs.41690	desmocollin 3	1.82	1.53
419733	AW362955	Hs.224961	Homo sapiens cDNA FLJ14415 fis, clone HE	1.82	1.00
409267	NM_012453	Hs.52515	transducin (beta)-like 2	1.81	1.57
413341	H78472	Hs.191325	ESTs, Weakly similar to T18967 hypotheti	1.81	2.05
423810	AL132665	Hs.132955	BCL2/adenovirus E1B 19kD-interacting pro	1.81	1.98
416274	AW160404	Hs.79126	guanine nucleotide binding protein 10	1.80	1.91
400843			NM_003105*:Homo sapiens sortilin-related	1.80	4.88
442187	N23532	Hs.288963	Homo sapiens cDNA: FLJ23034 fis, clone L	1.80	2.61
458285	AW296984	Hs.255595	ESTs, Weakly similar to A46302 PTB-assoc	1.80	2.33
413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	1.80	3.17
428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.80	1.00
401613			Target Exon	1.79	2.66
407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	1.79	2.30
443145	AI049671	Hs.307763	EST, Weakly similar to I38022 hypothetic	1.79	2.00
418596	AW976721	Hs.293327	ESTs	1.79	3.92
437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	1.79	1.24
439569	AW602166	Hs.222399	CEGP1 protein	1.79	2.39
430677	Z26317	Hs.94560	desmoglein 2	1.78	2.02
436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.78	0.98
453016	AW295466	Hs.232051	ESTs, Weakly similar to dJ403A15.3 [H.sa	1.78	2.60
426885	AA393130	Hs.193894	ESTs, Weakly similar to A47582 B-cell gr	1.78	2.47
452848	AI417193	Hs.288912	hypothetical protein FLJ22604	1.78	2.17
412560	R24601		CCR4-NOT transcription complex, subunit	1.78	3.13
411821	BE299339	Hs.72249	three-PDZ containing protein similar to	1.78	1.55
428788	AF082283	Hs.193516	B-cell CLL/lymphoma 10	1.78	2.36
443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	1.78	2.20
435479	AF197137	Hs.259737	ATP synthase, H transporting, mitochondr	1.78	2.03
413073	AL038165	Hs.75187	translocase of outer mitochondrial membr	1.77	2.29
442473	W27992		gb:43d9 Human retina cDNA randomly prime	1.77	2.93
418060	AA211589	Hs.208047	ESTs	1.77	4.19

400773			NM_003105*:Homo sapiens sortilin-related	1.77	1.76
400175			Eos Control	1.77	2.04
421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	1.77	2.32
451234	AI914901	Hs.24052	ESTs, Weakly similar to I38022 hypotheti	1.77	2.43
423332	AI091466	Hs.127241	sorting nexin 7	1.76	1.82
423960	AA164516	Hs.136309	SH3-containing protein SH3GLB1	1.76	2.00
450489	AI697990	Hs.346002	ESTs	1.76	3.15
457265	AB023212	Hs.225967	KIAA0995 protein	1.76	2.37
413076	U10564	Hs.75188	wee1 (S. pombe) homolog	1.75	2.18
421948	L42583	Hs.334309	keratin 6A	1.75	1.00
453578	R06875	Hs.81810	ESTs	1.75	3.10
412430	AW675064	Hs.73875	fumarylacetoacetate hydrolase (fumarylac	1.75	2.14
439396	BE562958	Hs.74346	hypothetical protein MGC14353	1.75	1.78
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.75	2.36
449538	AI559444	Hs.104679	ESTs	1.75	3.07
453146	AI338952	Hs.32194	ESTs	1.74	2.82
426122	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	1.74	2.88
408989	AW361666	Hs.49500	KIAA0746 protein	1.74	2.07
441715	AI929453	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	1.74	2.06
412718	X79204	Hs.74520	spinocerebellar ataxia 1 (olivopontocere	1.74	2.46
450798	AW167780	Hs.50438	ESTs	1.74	2.02
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.73	2.58
400190			Eos Control	1.73	2.40
416309	R84694	Hs.79194	cAMP responsive element binding protein	1.73	1.48
410219	T98226	Hs.171952	occludin	1.73	2.75
419814	AW402478	Hs.93213	BCL2-antagonist/killer 1	1.73	2.70
448625	AW970786	Hs.178470	hypothetical protein FLJ22662	1.73	2.07
422387	AA309996	Hs.148656	ESTs, Weakly similar to T12453 hypotheti	1.73	2.02
417386	AL037228	Hs.82043	D123 gene product	1.73	2.44
405812			Target Exon	1.72	2.94
436270	C03769	Hs.339669	Homo sapiens, clone IMAGE:3947554, mRNA,	1.72	2.85
409855	AW502461		gb:UI-HF-BR0p-ajv-b-08-0-UI.r1 NIH_MGC_5	1.72	2.63
411442	N25956	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	1.72	1.88
400846			sortilin-related receptor, L(DLR class)	1.72	1.63
401660			Target Exon	1.72	2.63
402190			C19000835*:gi|10946730|ref|NP_067362.1|	1.72	3.33
439191	AA281177	Hs.41182	Homo sapiens DC47 mRNA, complete cds	1.71	2.17
410444	W73484	Hs.132554	gb:zd54e04.s1 Soares_fetal_heart_NbHH19W	1.71	2.70
430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.71	1.33
446066	AI343931	Hs.149383	ESTs	1.71	2.32
411299	BE409857	Hs.69499	hypothetical protein	1.71	2.92
408246	N55669	Hs.333823	mitochondrial ribosomal protein L13	1.71	2.00
454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT	1.71	1.93
417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	1.70	3.70
427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	1.70	1.60
400750			Target Exon	1.70	2.82
455842	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.70	2.17
429966	BE081342	Hs.283037	HSPC039 protein	1.70	1.18
418444	AI902899	Hs.85155	butyrate response factor 1 (EGF-response	1.70	2.47
437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	1.70	3.03
415738	BE539367	Hs.295953	ESTs, Weakly similar to AF220049 1 uncha	1.70	2.34
405245			Target Exon	1.70	1.99
408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypotheti	1.70	2.05
413611	BE153275		gb:PM0-HT0335-180400-008-e11 HT0335 Homo	1.70	2.05
410190	AW072328	Hs.59728	Homo sapiens mRNA; cDNA DKFZp566C0546 (f	1.69	2.20
434608	AA805443	Hs.179909	hypothetical protein FLJ22995	1.69	2.36
432170	T56887	Hs.18282	KIAA1134 protein	1.69	1.83
448182	AF244137	Hs.20597	host cell factor homolog	1.69	2.11
436293	AI601188	Hs.120910	ESTs	1.69	2.37
448524	AB032948	Hs.21356	hypothetical protein DKFZp762K2015	1.68	2.48
404231			Target Exon	1.68	2.50
453906	AW444952	Hs.257054	ESTs	1.68	2.45
437967	BE277414	Hs.5947	mel transforming oncogene (derived from	1.68	1.00
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.68	3.51
448813	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	1.68	1.69
429162	AK001250	Hs.197642	hypothetical protein FLJ10388	1.68	3.13
425556	H27225	Hs.9444	hypothetical protein FLJ13114	1.67	2.02
405630			Target Exon	1.67	3.00
421405	AA251944	Hs.104058	CGI-29 protein	1.67	3.25
422640	M37984	Hs.118845	troponin C, slow	1.67	1.23
450857	AA629075	Hs.190090	ESTs	1.67	2.48
451668	Z43948	Hs.326444	cartilage acidic protein 1	1.66	2.55
433821	AW182416		ESTs	1.66	2.65
405595			NM_000721*:Homo sapiens calcium channel,	1.66	2.23
433892	AI929357	Hs.323966	Homo sapiens clone H63 unknown mRNA	1.66	1.97
443558	AA376798	Hs.286122	MDS024 protein	1.66	2.00
412141	AI183838	Hs.48938	hypothetical protein FLJ21802	1.66	2.65

424685	W21223	Hs.151734	nuclear transport factor 2 (placental pr	1.66	2.88
400845			NM_003105*:Homo sapiens sortilin-related	1.66	1.61
447816	NM_007233	Hs.274329	TP53 target gene 1	1.66	2.63
404438			Target Exon	1.66	2.34
451543	AA397651	Hs.301959	proline synthetase co-transcribed (bacte	1.65	2.08
433233	AB040927	Hs.301804	KIAA1494 protein	1.65	3.13
420938	AL049698	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	1.65	1.37
435438	H84421	Hs.4890	ubiquitin-conjugating enzyme E2E 3 (homo	1.65	2.35
431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.65	1.00
433235	AB040929	Hs.35089	contactin 3 (plasmacytoma associated)	1.65	1.44
439632	AW410714	Hs.334437	hypothetical protein MGC4248	1.65	2.35
409324	W76202	Hs.343812	lipoic acid synthetase	1.65	2.00
452207	NM_014517	Hs.28423	upstream binding protein 1 (LBP-1a)	1.65	2.33
423630	AB011132	Hs.129952	KIAA0560 gene product	1.65	2.13
443358	H65417	Hs.17757	pleckstrin homology domain-containing, f	1.65	1.63
427417	AA341061	Hs.177861	CGI-110 protein	1.64	1.28
450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	1.64	1.60
445677	H96577	Hs.6838	ras homolog gene family, member E	1.64	1.91
447503	AA115496	Hs.336898	Homo sapiens, Similar to RIKEN cDNA 1810	1.64	2.04
431234	AL389985	Hs.301637	zinc finger protein 258	1.64	1.53
418032	AW964695	Hs.9436	Homo sapiens, clone MGC:15763, mRNA, com	1.64	2.05
407796	AA195509	Hs.39733	postsynaptic protein CRIPT	1.64	2.30
446298	AF187813	Hs.14637	kidney- and liver-specific gene	1.64	2.05
439578	AW263124	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	1.64	2.26
429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	1.64	2.10
433646	AA603319	Hs.155195	ESTs	1.64	2.05
407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	1.64	1.00
419982	AA252544	Hs.55610	solute carrier family 30 (zinc transport	1.64	2.16
401603			NM_022041*:Homo sapiens giant axonal neu	1.64	2.73
431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	1.64	2.75
400788			C6000994*:gi|10435784|dbj|BAB14668.1| (A	1.63	2.04
416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	1.63	2.64
422491	AA338548	Hs.117546	neuronatin	1.63	0.96
424737	BE301883	Hs.152707	glioblastoma amplified sequence	1.63	3.45
416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	1.63	1.39
403988			C5001831:gi|11056014|ref|NP_067651.1| ac	1.62	2.11
411486	N85785	Hs.181165	eukaryotic translation elongation factor	1.62	2.63
407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	1.62	2.19
446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	1.62	3.03
438184	AA779897	Hs.122125	ESTs	1.62	2.79
405502			C7000609*:gi|628012|pir||A53933 myosin I	1.62	2.55
447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	1.62	2.48
457961	AA772119	Hs.270721	ESTs, Weakly similar to I38022 hypotheti	1.62	2.30
436774	AW975810	Hs.159054	hypothetical protein FLJ13224	1.62	2.17
414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	1.62	2.03
458660	AI299739	Hs.99601	hypothetical protein FLJ12553	1.62	2.25
405806			Target Exon	1.62	2.15
421205	AL137540	Hs.102541	netrin 4	1.62	1.00
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	1.62	1.74
427016	AA397525	Hs.191579	ESTs	1.61	2.16
458182	AI147996	Hs.155833	ESTs, Weakly similar to spliceosomal pro	1.61	2.74
451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.61	2.59
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.61	1.78
456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	1.61	2.10
447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.61	1.75
439944	AA856767	Hs.124623	ESTs	1.61	2.41
414692	H06831	Hs.164557	ESTs, Moderately similar to ALUC_HUMAN !	1.60	3.05
433187	R53995	Hs.293381	ESTs, Moderately similar to ALU7_HUMAN A	1.60	2.63
446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	1.60	2.43
441166	AA921738	Hs.132473	ESTs	1.60	2.69
425571	AJ007292	Hs.158306	ephrin-A2	1.60	1.49
406836	AW514501	Hs.156110	immunoglobulin kappa constant	1.60	1.08
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.60	1.47
449268	AW369278	Hs.23412	hypothetical protein FLJ20160	1.60	2.89
400772			NM_003105*:Homo sapiens sortilin-related	1.60	2.57
445733	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	1.60	2.03
428172	U09367	Hs.182828	zinc finger protein 136 (clone pHZ-20)	1.60	2.68
421887	AW161450	Hs.109201	CGI-86 protein	1.59	1.39
418127	BE243982	Hs.83532	membrane cofactor protein (CD46, trophob	1.59	1.67
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	1.59	2.19
434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	1.59	2.26
417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	1.59	1.76
418067	AI127958	Hs.83393	cystatin E/M	1.59	1.26
427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	1.59	2.25
451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	1.59	2.10
407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	1.58	2.43
410796	Z44547	Hs.3731	ESTs, Moderately similar to I38022 hypot	1.58	1.26

417343	AA197132	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.58	2.84
416643	U62531	Hs.79410	solute carrier family 4, anion exchanger	1.58	1.26
400847			NM_003105*:Homo sapiens sortilin-related	1.58	1.48
436760	AW606927	Hs.5306	hypothetical protein DKFZp586F1122 simil	1.57	1.57
433427	AI816449	Hs.171889	cholinephosphotransferase 1	1.57	1.64
451986	BE246996	Hs.318401	hypothetical protein DKFZp564D1378	1.57	1.83
428901	AI929568	Hs.146668	KIAA1253 protein	1.57	2.23
426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	1.57	3.07
444604	AW327695	Hs.11441	chromosome 1 open reading frame 8	1.57	1.86
439686	W40445	Hs.235857	ESTs, Weakly similar to I38022 hypotheti	1.57	3.07
426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	1.57	2.01
447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	1.57	2.83
418942	AI566004	Hs.141269	Homo sapiens cDNA: FLJ21550 fis, clone C	1.57	1.21
418555	AI417215	Hs.87159	hypothetical protein FLJ12577	1.56	3.08
402368			NM_021155*:Homo sapiens CD209 antigen (C	1.56	2.05
419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	1.56	2.08
404977			Insulin-like growth factor 2 (somatomedi	1.56	5.50
441872	BE567100	Hs.154938	hypothetical protein MDS025	1.56	2.30
415503	U36601	Hs.78473	N-deacetylase/N-sulfotransferase (hepara	1.56	2.56
451743	AW074266	Hs.23071	ESTs	1.56	1.85
423184	NM_004428	Hs.1624	ephrin-A1	1.56	1.41
408041	AW138782	Hs.243607	ESTs	1.56	2.21
416777	AF146760	Hs.79844	DKFZP564M1416 protein	1.56	2.00
428013	AF151020	Hs.181444	hypothetical protein	1.56	1.53
410072	BE384447	Hs.16034	hypothetical protein MGC13186	1.55	1.52
411495	AP000693	Hs.70359	KIAA0136 protein	1.55	2.88
408162	AA993833	Hs.118527	ESTs	1.55	2.70
413350	U02556	Hs.75307	t-complex-associated-testis-expressed 1-	1.55	1.99
422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, clone C	1.55	1.60
425229	AU076961	Hs.155212	methylmalonyl Coenzyme A mutase	1.55	2.57
425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	1.55	1.45
419011	H56244	Hs.89552	glutathione S-transferase A2	1.55	2.77
417538	AW050865	Hs.275711	hypothetical protein MGC2452	1.55	2.76
409806	AW500960		gb:UI-HF-BP0p-aly-b-01-0-UI.r1 NIH_MGC_5	1.55	2.45
402737			Target Exon	1.54	2.58
419825	AI754011	Hs.7326	ESTs	1.54	1.00
410001	AB041036	Hs.57771	kallikrein 11	1.54	0.62
407813	AL120247	Hs.40109	KIAA0872 protein	1.54	2.33
415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.54	2.77
427886	AA417083	Hs.104789	ESTs	1.54	2.60
437018	AA889078	Hs.187033	ESTs	1.54	2.48
415049	N67334	Hs.50158	ESTs	1.54	2.57
422315	U16296	Hs.115176	T-cell lymphoma invasion and metastasis	1.54	2.57
413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	1.54	1.98
447144	AI630759	Hs.17481	Homo sapiens clone 24606 mRNA sequence	1.54	2.48
438924	BE535511		transmembrane trafficking protein	1.53	3.08
445166	AI656116	Hs.147451	ESTs	1.53	2.08
414073	AF068293	Hs.75737	pericentriolar material 1	1.53	1.70
402378			Target Exon	1.53	2.83
452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.53	1.60
450374	AA397540	Hs.60293	Homo sapiens clone 122482 unknown mRNA	1.53	3.59
402617			C1003551:gi|6678593|ref|NP_033547.1| win	1.53	2.75
406837	R70292	Hs.156110	immunoglobulin kappa constant	1.53	1.01
410573	AF151057	Hs.64595	aminoadipate-semialdehyde dehydrogenase-	1.53	1.23
426359	AA376409	Hs.10862	Homo sapiens cDNA: FLJ23313 fis, clone H	1.53	0.67
434445	AI349306	Hs.11782	ESTs	1.53	2.80
452717	AW160399	Hs.30376	hypothetical protein	1.53	2.01
420465	AL080276	Hs.70488	similar to prokaryotic-type class I pept	1.53	2.25
437404	AA868974	Hs.180992	ESTs	1.53	2.00
459192	AW176180		gb:RC2-BT0214-010999-001-E07 BT0214 Homo	1.52	3.20
446457	AI300580	Hs.345281	ESTs, Moderately similar to ALU1_HUMAN A	1.52	2.35
441466	AW673081	Hs.54828	ESTs	1.52	1.99
421810	AK001718	Hs.108530	hypothetical protein FLJ10856	1.52	2.98
447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	1.52	2.47
414882	D79994	Hs.77546	Homo sapiens cDNA: FLJ21983 fis, clone H	1.52	2.55
442169	W21813	Hs.8125	Homo sapiens mRNA; cDNA DKFZp586E1521 (f	1.52	1.31
404349			Target Exon	1.52	2.74
416278	AA356366	Hs.79137	protein-L-isoaspartate (D-aspartate) O-m	1.52	2.93
431846	BE019924	Hs.271580	uroplakin 1B	1.52	1.01
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.52	0.93
442670	BE410050	Hs.11859	hypothetical protein FLJ13188	1.52	2.70
441617	AA581863	Hs.178485	Homo sapiens cDNA FLJ13919 fis, clone Y7	1.52	1.65
440079	AI557284	Hs.6900	ring finger protein 13	1.52	1.76
432831	AI821702	Hs.115959	ESTs, Weakly similar to I38022 hypotheti	1.52	2.13
414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.52	2.13
442149	AB014550	Hs.8118	KIAA0650 protein	1.52	1.00
457747	AW975000		gb:EST387105 MAGE resequences, MAGN Homo	1.51	2.38

419433	AA814807	Hs.7395	hypothetical protein FLJ23182	1.51	2.50
431812	AA515902	Hs.130650	ESTs	1.51	1.64
415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	1.51	2.62
447580	AI953360	Hs.133487	ESTs	1.51	2.02
416926	H03109	Hs.108920	HT018 *protein*	1.51	2.22
442755	W57656	Hs.109701	ubiquitin-like 5	1.51	1.34
448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	1.51	2.24
422675	BE018517	Hs.119140	eukaryotic translation initiation factor	1.51	1.49
404397			ENSP00000251675*:KIAA1550 protein (Fragm	1.51	2.18
412927	AA284018	Hs.75063	human immunodeficiency virus type I enha	1.51	1.33
402371			Target Exon	1.61	3.22
431730	AF208856	Hs.268122	hypothetical protein	1.51	1.57
417715	AW969587	Hs.86366	ESTs	1.51	1.59
451117	AA015752	Hs.205173	ESTs	1.50	2.70
434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	1.50	3.53
442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-specific (dun	1.50	2.24
425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.50	1.13
452658	N88604	Hs.30212	thyroid receptor interacting protein 15	1.50	1.62
428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	1.50	1.00
438967	H30340	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H	1.50	1.05
419847	AW390601	Hs.184544	Homo sapiens, clone IMAGE:3355383, mRNA,	1.50	2.53
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	1.49	0.97
433265	AB040971	Hs.35096	KIAA1538 protein	1.49	1.44
408136	AL041135	Hs.42959	KIAA1012 *protein*	1.49	2.24
455485	AA102287	Hs.26756	hypothetical protein FLJ20896	1.49	2.40
418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.49	2.84
405193			C7000789:gi|1943947|gb|AAC48716.1| (U901	1.48	2.20
408948	AW296713	Hs.221441	ESTs	1.48	2.20
426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	1.48	2.24
405932			C15000305:gi|3806122|gb|AAC69198.1| (AF0	1.48	1.48
454034	NM_000691	*Hs.575*	*aldehyde dehydrogenase 3 family, member*	1.48	1.16
422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	1.48	1.20
428044	AA093322	Hs.301404	RNA binding motif protein 3	1.48	2.38
416166	AW501907	Hs.261734	Homo sapiens cDNA: FLJ22807 fis, clone K	1.48	1.28
430453	BE387060	Hs.3903	Cdc42 effector protein 4; binder of Rho	1.48	2.73
401600	BE247275		U5 *snRNP-specific protein,* 116 kD	1.48	2.53
432638	AI017717		chromosome 21 open reading frame 15	1.48	2.03
405194			C7000789:gi|1943947|gb|AAC48716.1| (U901	1.48	2.00
416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.48	1.25
450272	AI075170	Hs.20010	ESTs	1.48	2.35
413709	BE158687		gb:CM0-HT0395-280100-169-b09 HT0395 Homo	1.48	2.08
442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	1.48	1.00
410418	D31382	Hs.63325	*transmembrane protease, serine* 4	1.47	1.91
436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	1.47	2.26
404769			NM_007037*:Homo sapiens a disintegrin-li	1.47	1.24
420132	BE079847	Hs.301914	gb:RC6-BT0627-220300-012-D06 BT0627 Homo	1.47	2.00
448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.47	2.90
421628	*AL121317*	*Hs.106210*	*hypothetical protein* FLJ10813	1.47	4.08
449059	AK000566	Hs.98135	hypothetical protein FLJ20559	1.47	3.13
449029	N28989	Hs.22891	solute carrier family 7 (*cationic amino*	1.47	1.06
422119	AI277829	Hs.111862	KIAA0590 gene product	1.47	1.51
438713	H16902		ESTs	1.47	2.39
418248	NM_005000	Hs.83916	NM_005000*:Homo sapiens NADH dehydrogena	1.47	1.00
419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.46	2.20
420548	AA278246	Hs.920	ESTs	1.46	2.13
424258	AA433848	Hs.107882	hypothetical protein FLJ10659	1.46	1.98
414683	S78296	Hs.76888	hypothetical protein MGC12702	1.46	1.45
427045	H86504	Hs.173328	protein phosphatase 2, regulatory subuni	1.46	2.31
446646	BE552004	Hs.26192	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.46	1.30
427257	AI026805	Hs.97726	ESTs	1.46	2.48
422971	AI879223	Hs.145409	RAB, member of RAS oncogene family-like	1.46	1.05
451334	AI122691	Hs.13268	ESTs	1.46	2.12
403326			C2000428*:gi|7705383|ref|NP_057536.1| GC	1.46	2.40
453827	AF201948	Hs.35660	BUP protein	1.46	1.65
423599	AI805664	Hs.31731	peroxiredoxin 5	1.46	1.56
410691	AW239226	Hs.65450	reticulon 4	1.46	1.49
430688	AL022101	Hs.104991	hypothetical protein similar to preferen	1.46	2.45
438083	AI949940	Hs.121924	ESTs	1.46	2.00
430713	AA351647	Hs.2642	eukaryotic translation *elongation factor*	1.45	1.60
437325	AF142481	Hs.5548	f-box and leucine-rich repeat protein 5	1.45	1.26
403342			Target Exon	1.45	2.21
438808	M73980	Hs.129053	Homo sapiens NOTCH 1 (N1) mRNA, complete	1.45	2.40
446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	1.45	3.65
414895	AW894856	Hs.116278	Homo sapiens cDNA FLJ13571 fis, clone PL	1.44	2.71
442072	AI740832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	1.44	1.08
425723	NM_014420	Hs.159311	dickkopf (Xenopus laevis) homolog 4	1.44	2.24
432901	AI554929	Hs.281866	ATPase, H transporting, lysosomal (vacuo	1.44	1.63

412210	AW901492		gb:RC0-NN1012-270300-031-h10 NN1012 Homo	1.44	2.15
421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	1.44	1.83
428115	AB023194	Hs.300855	KIAA0977 protein	1.44	1.31
442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	1.44	2.47
414685	L39874	Hs.76894	dCMP deaminase	1.44	1.25
413798	AA336708	Hs.75546	capping protein (actin filament) muscle	1.44	1.26
410937	AA218564	Hs.67052	vacuolar protein sorting 26 (yeast homol	1.44	1.41
400397	AJ270770		transcription factor 7-like 2 (T-cell sp	1.44	3.43
405902			Target Exon	1.44	2.65
433976	AA620987	Hs.190268	ESTs	1.44	2.46
405376			Target Exon	1.44	2.28
436086	Z43133	Hs.9961	Homo sapiens cDNA: FLJ21954 fis, clone H	1.44	1.34
418182	AW016405	Hs.16648	ESTs	1.44	2.35
430307	BE513442	Hs.238944	hypothetical protein FLJ10631	1.43	1.55
434924	AA443164	Hs.23259	hypothetical protein FLJ13433	1.43	2.05
417821	BE245149	Hs.82643	protein tyrosine kinase 9	1.43	2.15
404744			Target Exon	1.43	1.99
405418			Target Exon	1.43	2.83
402869			Target Exon	1.43	2.40
451608	AA384525	Hs.26745	hypothetical protein	1.43	1.22
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1.43	2.45
401041			C11000425:gi|4507721|ref|NP_003310.1| ti	1.43	2.90
417839	AI815732	Hs.82712	fragile X mental retardation, autosomal	1.43	2.84
409245	AA361037	Hs.288036	tRNA isopentenylpyrophosphate transferas	1.43	2.65
447808	NM_007265	Hs.19673	suppressor of S. cerevisiae gcr2	1.43	2.00
456492	AA330047	Hs.191187	ESTs	1.43	2.73
449244	AW859979	Hs.32204	ESTs	1.42	1.57
413094	H24184	Hs.25413	TOLLIP protein	1.42	1.33
452407	AA682909	Hs.29353	brain-specific protein p25 alpha	1.42	2.50
407674	AW064061	Hs.279145	ESTs	1.42	2.35
441297	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	1.42	2.20
421932	W51778	Hs.323949	kangai 1 (suppression of tumorigenicity	1.42	1.48
426348	BE466586	Hs.17433	hypothetical protein FLJ20967	1.42	1.83
432554	AI479813	Hs.278411	NCK-associated protein 1	1.42	2.46
431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	1.42	1.30
429953	NM_004376	Hs.226581	COX15 (yeast) homolog, cytochrome c oxid	1.42	1.50
444037	AV647686	Hs.42733	CHMP1.5 protein	1.42	1.38
402144			Target Exon	1.42	2.38
456758	AA325170	Hs.224627	ESTs, Weakly similar to FAHUAA alpha-act	1.42	2.23
452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	1.42	2.18
426863	AL137657	Hs.172803	hypothetical protein MGC10327	1.41	1.38
410684	AA088500	Hs.170298	ESTs	1.41	1.28
401784			NM_002280*:Homo sapiens keratin, hair, a	1.41	1.37
427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	1.41	1.32
449269	AI564682	Hs.175870	ESTs	1.41	1.37
406467			Target Exon	1.41	1.80
444339	T96555	Hs.31562	ESTs	1.41	2.94
431563	AI027643	Hs.120912	ESTs	1.41	1.41
413343	BE392026	Hs.334346	hypothetical protein MGC13045	1.41	1.21
447537	AW295072	Hs.346408	ESTs, Weakly similar to AF193556 1 sacsi	1.41	2.07
428211	AA424211	Hs.183176	ESTs	1.41	1.25
406248			Target Exon	1.41	2.40
437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.41	1.39
414653	M24486	Hs.76768	procollagen-proline, 2-oxoglutarate 4-di	1.41	1.33
403885			Target Exon	1.41	2.58
439459	AF086279	Hs.58013	ESTs	1.41	2.08
419075	T84266	Hs.123927	ESTs	1.41	2.84
405022			Target Exon	1.40	2.55
401346	BE041451		hypothetical protein	1.40	2.38
415660	AI909007	Hs.78563	ubiquitin-conjugating enzyme E2G 1 (homo	1.40	2.38
448023	AI693299	Hs.170388	ESTs	1.40	2.38
435962	AA702820	Hs.291294	ESTs	1.40	2.10
432480	AA205475	Hs.275865	ribosomal protein S18	1.40	1.37
414309	AK000639	Hs.75884	DKFZP586A011 protein	1.40	1.18
440256	U23841	Hs.18851	hypothetical protein FLJ10875	1.40	1.91
413809	L25851	Hs.851	integrin, alpha E (antigen CD103, human	1.40	2.80
408176	AK001553	Hs.43436	adenylate kinase 3 alpha like	1.40	2.73
433960	AW629188	Hs.188929	ESTs	1.40	1.99
404178			C6001430*:gi|4503521|ref|NP_001559.1| mu	1.40	2.83
402449			Target Exon	1.40	1.51
455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	1.40	2.30
429221	AI821060	Hs.198271	Target CAT	1.40	1.22
422122	AA383642	Hs.111894	lysosomal-associated protein transmembra	1.40	1.42
406231			Target Exon	1.40	2.60
405879			Target Exon	1.40	2.73
450936	AI033745		gb:ow23a10.x1 Soares_parathyroid_tumor_N	1.40	1.13
403381			ENSP00000231844*:Ecotropic virus integra	1.39	6.03

453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	1.39	3.20
448261	BE244072	Hs.20815	macrophage erythroblast attacher	1.39	1.33
427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	1.39	2.30
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.39	1.53
407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.39	1.34
430138	AA936296	Hs.234265	DKFZP586G011 protein	1.39	2.38
432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	1.39	2.88
444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	1.39	1.34
440704	M69241	Hs.162	insulin-like growth factor binding prote	1.39	1.61
450092	AW139606	Hs.221057	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.39	2.78
400275			NM_006513*:Homo sapiens seryl-tRNA synth	1.39	2.03
403725			Target Exon	1.39	2.03
443211	AI128388	Hs.143655	ESTs	1.39	1.83
421510	AK000919	Hs.105191	hypothetical protein FLJ10057	1.39	2.83
430071	AA355986	Hs.232068	transcription factor 8 (represses interl	1.38	3.54
451545	AI802128	Hs.208647	ESTs	1.38	2.21
439897	NM_015310	Hs.6763	KIAA0942 protein	1.38	3.65
423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	1.38	1.00
410344	AW978436	Hs.62515	KIAA0494 gene product	1.38	2.25
404439			ENSP00000067222*:Mitochondrial 28S ribos	1.38	2.25
448581	NM_002709	Hs.21537	protein phosphatase 1, catalytic subunit	1.38	1.47
408569	BE066047	Hs.86412	chromosome 9 open reading frame 5	1.38	1.27
447643	H10767	Hs.238465	nGAP-like protein	1.38	1.22
401593			Target Exon	1.38	2.58
403807			NM_031889:Homo sapiens enamelin (ENAM),	1.38	2.38
406356	N47812		CGI-35 protein	1.38	2.25
401886			NM_021783:Homo sapiens XEDAR (XEDAR), mR	1.38	2.00
421110	AJ250717	Hs.1355	cathepsin E	1.38	8.93
427449	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAI/L	1.38	1.44
427451	AI690916	Hs.178137	transducer of ERBB2, 1	1.38	2.81
440681	AW449696	Hs.166547	ESTs	1.38	2.95
419590	AF005043	Hs.91390	poly (ADP-ribose) glycohydrolase	1.38	2.10
446044	H67567	Hs.13572	calcium modulating ligand	1.37	2.62
400967			Target Exon	1.37	3.12
414506	AF075337	Hs.76293	thymosin, beta 10	1.37	1.18
402599			NM_021186*:Homo sapiens zona pellucida g	1.37	2.68
422932	AI191813	Hs.308220	ESTs	1.37	2.38
433889	AK002082	Hs.3623	hypothetical protein FLJ11220	1.37	2.23
429802	H09548	Hs.5367	ESTs, Weakly similar to I38022 hypotheti	1.37	2.25
443856	AK000574	Hs.9908	nitrogen fixation cluster-like	1.37	1.28
453489	AA300067	Hs.33032	hypothetical protein DKFZp434N185	1.37	2.15
424670	W61215	Hs.116651	epithelial V-like antigen 1	1.37	1.66
428995	AW004975	Hs.194716	MAD (mothers against decapentaplegic, Dr	1.37	1.33
441551	AA318224	Hs.296141	ESTs	1.37	2.95
450528	NM_014072	Hs.25063	PRO0461 protein	1.37	1.19
427605	NM_000997	Hs.337445	ribosomal protein L37	1.37	1.31
459237	AA031675	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	1.37	2.50
413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.37	1.31
404906			NM_025213:Homo sapiens spectrin, beta, n	1.36	3.08
436246	AW450963	Hs.119991	ESTs	1.36	1.00
441478	AA350018	Hs.301342	hypothetical protein MGC4342	1.36	1.43
419715	AF070523	Hs.92384	vitamin A responsive; cytoskeleton relat	1.36	1.28
426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	1.36	2.16
400129			Eos Control	1.36	2.03
450447	AF212223	Hs.25010	hypothetical protein P15-2	1.36	2.13
434697	AL133033	Hs.4084	KIAA1025 protein	1.36	2.01
430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	1.36	2.03
434767	AF153201		C2H2 (Kruppel-type) zinc finger protein	1.36	2.87
459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	1.36	1.27
426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.35	2.20
408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	1.35	2.68
409844	AW502336		gb:UI-HF-BR0p-aka-b-05-0-UI.r1 NIH_MGC_5	1.35	2.29
402517			Target Exon	1.35	2.10
447042	AB035863	Hs.182217	succinate-CoA ligase, ADP-forming, beta	1.35	1.25
405000			Target Exon	1.35	2.32
452065	AK000360	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	1.35	2.36
404666			C9000748:gi|8324209|gb|AAB34384.2| (S775	1.35	2.55
451081	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	1.35	1.70
427979	BE379776	Hs.181309	proteasome (prosome, macropain) subunit,	1.35	2.23
435825	R16702	Hs.91147	ESTs	1.35	2.39
426469	BE297886	Hs.293970	methylmalonate-semialdehyde dehydrogenas	1.35	1.40
447002	BE242866	Hs.16933	HepA-related protein	1.34	2.88
410946	AW811502		gb:QV2-ST0145-061299-015-b04 ST0145 Homo	1.34	2.02
454383	AW500332	Hs.11114	hypothetical protein dJ1181N3.1	1.34	2.13
440512	AA887845	Hs.19673	suppressor of S. cerevisiae gcr2	1.34	2.05
409865	AW502208		gb:UI-HF-BR0p-aju-e-09-0-UI.r1 NIH_MGC_5	1.34	2.63
447390	X95384	Hs.18426	translational inhibitor protein p14.5	1.34	1.00

450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.34	2.45
445831	NM_006055	Hs.13351	LanC (bacterial lantibiotic synthetase c	1.34	1.60
418610	AW245993	Hs.223394	hypothetical protein MGC2742	1.34	1.39
441946	AW298716	Hs.120775	ESTs	1.34	2.30
446192	H49944	Hs.14231	selenoprotein W, 1	1.34	1.17
416285	BE537973	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	1.34	2.22
425590	AI954686	Hs.158321	beaded filament structural protein 2, ph	1.34	2.50
407498	U28131		gb:Human HMGI-C chimeric transcript mRNA	1.34	2.13
441331	AI216764	Hs.149971	ESTs, Moderately similar to ALUB_HUMAN !	1.34	2.05
411789	AF245505	Hs.72157	Adlican	1.34	1.27
420542	NM_000505	Hs.1321	coagulation factor XII (Hageman factor)	1.33	1.25
413892	AI878921	Hs.75607	myristoylated alanine-rich protein kinas	1.33	1.41
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	1.33	1.99
414861	AL119396	Hs.77508	glutamate dehydrogenase 1	1.33	1.66
421687	AL035306	Hs.106823	hypothetical protein MGC14797	1.33	2.18
410846	AW807057		gb:MR4-ST0062-031199-018-b03 ST0062 Homo	1.33	2.07
443937	R66571	Hs.24601	ESTs	1.33	2.02
432360	BE045243	Hs.274416	Target CAT	1.33	1.12
443119	AA312264	Hs.7980	hypothetical protein MGC12966	1.33	2.68
438464	AA669735	Hs.324743	protein phosphatase 4 regulatory subunit	1.33	1.99
401371			ENSP00000198192*:BA438F9.1 (novel protei	1.33	1.10
405443			Target Exon	1.33	2.11
453764	BE008180	Hs.282846	Homo sapiens cDNA FLJ14353 fis, clone Y7	1.33	2.88
424924	AL039103	Hs.153834	pumilio (Drosophila) homolog 1	1.33	1.24
453555	N23574	Hs.123649	ESTs, Moderately similar to ALU7_HUMAN A	1.33	2.23
404343			*C7002191*:gi|5053028|gb|AAD38811.1|AF155*	1.33	1.04
412383	AW947577		gb:RC0-MT0004-140300-031-b09 MT0004 Homo	1.33	2.06
404250			Target Exon	1.33	2.53
413899	AF083892	Hs.75608	tight junction protein 2 (zona occludens	1.33	2.81
422716	AI702835	Hs.124475	ESTs, Weakly similar to YEF4_YEAST HYPOT	1.33	2.30
448862	AI351979	Hs.152717	hypothetical protein FLJ13725	1.33	1.08
409540	AW409569		gb:fh01e09.x1 NIH_MGC_17 Homo sapiens cD	1.33	2.18
431186	NM_012249	Hs.250697	ras-like protein	1.32	1.39
402754			NM_022469*:Homo sapiens hypothetical pro	1.32	1.16
420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	1.32	2.02
459710	AI701596	Hs.121592	ESTs	1.32	2.70
435192	AK000739	Hs.4835	eukaryotic translation initiation factor	1.32	2.22
401383			Target Exon	1.32	2.18
453394	AW960474	Hs.40289	ESTs	1.32	2.20
421820	AW662990	Hs.294133	heme-binding protein	1.32	1.24
444047	AI097452	Hs.135095	ESTs	1.32	2.95
440860	R10482	Hs.132876	ESTs	1.32	2.83
425808	AA364109	Hs.177990	ESTs	1.32	2.11
456558	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	1.32	2.05
447015	AB033029	Hs.16953	KIAA1203 protein	1.32	1.30
414015	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C	1.32	1.39
414843	BE386038	Hs.77492	heterogeneous nuclear ribonucleoprotein	1.32	1.26
424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	1.32	2.01
401196			Target Exon	1.32	2.13
450147	AW373713	Hs.146324	CGI-145 protein	1.32	1.32
422699	BE410590	Hs.119257	ems1 sequence (mammary tumor and squamou	1.32	1.33
405172			Target Exon	1.32	2.11
434087	AF116675	Hs.334476	hypothetical protein PRO1942	1.32	2.30
416720	H05435	Hs.11110	hypothetical protein MGC2508	1.32	2.18
426621	NM_001329	Hs.171391	C-terminal binding protein 2	1.32	1.53
442685	AB033017	Hs.8594	KIAA1191 protein	1.32	1.43
443879	Z28462	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	1.31	2.24
405180	NM_002649		phosphoinositide-3-kinase, catalytic, ga	1.31	1.36
417365	D50683	Hs.82028	transforming growth factor, beta recepto	1.31	0.98
402087			Target Exon	1.31	1.31
429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	1.31	2.05
409935	AW511413	Hs.278025	ESTs	1.31	1.20
430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	1.31	1.31
400172			Eos Control	1.31	1.05
421742	AW970004	Hs.107528	androgen induced protein	1.31	1.79
404273			Target Exon	1.31	2.35
416204	AW972270	Hs.144054	ESTs	1.31	2.15
435076	AW298113	Hs.92909	SON DNA binding protein	1.31	2.05
452497	AA732153	Hs.27865	Homo sapiens cDNA: FLJ21333 fis, clone C	1.30	1.57
404596			Target Exon	1.30	2.23
419080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.30	1.15
427195	W27230	Hs.173912	eukaryotic translation initiation factor	1.30	1.34
438129	AA778647		gb:af87d03.s1 Soares_testis_NHT Homo sap	1.30	2.55
402138			Target Exon	1.30	2.09
404029			NM_018936*:Homo sapiens protocadherin be	1.30	2.83
402731	AL042818		E3 ubiquitin ligase SMURF1	1.30	3.32
458766	AW183618	Hs.55610	solute carrier family 30 (zinc transport	1.30	1.56

434585	AW451715	Hs.184075	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.30	2.73
417219	AW973473	Hs.220936	ESTs	1.30	2.45
428125	AA393071	Hs.182579	leucine aminopeptidase	1.30	2.00
416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.30	1.00
444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	1.30	0.94
406621	X57809	Hs.181125	immunoglobulin lambda locus	1.29	1.02
436663	AW410458	Hs.5258	chromosome 11 open reading frame2	1.29	1.20
417250	N58241	Hs.332115	ESTs	1.29	3.43
434978	AA321238	Hs.4310	eukaryotic translation initiation factor	1.29	1.91
448079	R76981		thyroid hormone receptor-associated prot	1.29	2.01
450626	AW190989	Hs.1508	insulin-degrading enzyme	1.29	2.09
456059	BE543127	Hs.336948	Homo sapiens, clone IMAGE:3530891, mRNA,	1.29	2.23
417809	H75797	Hs.233550	zinc finger protein 208	1.29	2.20
454771	AW819939	Hs.273629	ESTs	1.29	2.10
413895	BE178160		gb:RC3-HT0600-060400-022-h10 HT0600 Homo	1.29	2.08
404649			Target Exon	1.29	1.32
440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like doma	1.29	2.08
405891			Target Exon	1.29	2.00
418965	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	1.29	2.41
412824	AW958075	Hs.11261	small proline-rich protein 2A	1.29	1.27
420037	BE299598	Hs.135569	hypothetical protein FLJ14708	1.29	1.23
459221	BE246522	Hs.306121	leukocyte receptor cluster (LRC) encoded	1.28	2.48
458651	AW612481	Hs.104105	ESTs	1.28	2.35
422984	W28614		chorionic somatomammotropin hormone 1 (p	1.28	1.37
459365	BE067754		gb:MR4-BT0358-140400-006-g10 BT0358 Homo	1.28	1.06
418254	AA732511	Hs.86650	ESTs	1.28	2.38
402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.28	1.99
448456	AI521830	Hs.171050	ESTs	1.28	2.18
450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.28	1.68
405053			Target Exon	1.28	3.23
428915	AI041278	Hs.87908	Snf2-related CBP activator protein	1.28	4.25
443721	AW450451	Hs.266355	ESTs	1.28	1.15
452047	N35953	Hs.43510	ESTs, Weakly similar to BOX B BINDING FA	1.28	2.30
440213	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	1.28	1.19
452900	AA626794		prothymosin, alpha (gene sequence 28)	1.28	1.27
418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	1.28	2.76
458911	AA373131	Hs.24322	ATPase, H transporting, lysosomal (vacuo	1.28	1.21
444250	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	1.28	2.43
431631	AA548906	Hs.122244	ESTs	1.27	1.51
447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	1.27	3.08
430316	NM_000875	Hs.239176	insulin-like growth factor 1 receptor	1.27	1.37
416272	AA178882		gb:zp38b09.r1 Stratagene muscle 937209 H	1.27	2.00
437456	AL047045	Hs.60293	Homo sapiens clone 122482 unknown mRNA	1.27	3.18
456327	H68741	Hs.38774	ESTs	1.27	2.35
403349	NM_001406		ephrin-B3	1.27	2.28
428821	H91282	Hs.286232	Homo sapiens cDNA: FLJ23190 fis, clone L	1.27	2.13
454555	AW807095		gb:MR4-ST0062-040100-024-e02 ST0062 Homo	1.27	2.05
406872	AI760903		gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	1.27	1.44
401720			NM_014587*:Homo sapiens SRY (sex determi	1.27	2.07
400082			Eos Control	1.27	1.26
420183	W92885	Hs.143408	ESTs	1.27	2.24
411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	1.27	1.17
402191			NM_021733*:Homo sapiens testis-specific	1.27	2.44
457118	AI245525	Hs.182469	Homo sapiens mRNA; cDNA DKFZp564K1972 (f	1.27	2.17
408576	NM_003542	Hs.46423	H4 histone family, member G	1.27	2.78
452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	1.27	3.15
414909	R80316	Hs.132569	PP2135 protein	1.27	1.37
416114	AI695549	Hs.183868	glucuronidase, beta	1.26	2.48
455476	AW948172		gb:RC0-MT0013-280300-021-b06 MT0013 Homo	1.26	2.18
445926	AF054284	Hs.334826	splicing factor 3b, subunit 1, 155kD	1.26	1.35
432647	AI807481	Hs.278581	fibroblast growth factor receptor 2 (bac	1.26	1.16
405436			Target Exon	1.26	2.38
406140			Target Exon	1.26	3.20
426201	AW182614	Hs.128499	ESTs	1.26	1.17
433334	AI927208	Hs.231958	matrix metalloproteinase 28	1.26	2.30
423262	NM_005479	Hs.126057	frequently rearranged in advanced T-cell	1.26	2.61
422929	AA356694	Hs.94011	ESTs, Weakly similar to MGB4_HUMAN MELAN	1.26	2.11
445605	AI906088	Hs.87159	hypothetical protein FLJ12577	1.26	3.11
425050	BE391854	Hs.7970	gb:601285394F1 NIH_MGC_44 Homo sapiens c	1.26	2.18
420539	AA282735	Hs.44004	AD031 protein	1.26	2.03
437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.25	1.19
456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.25	1.18
434202	BE382411	Hs.3764	guanylate kinase 1	1.25	1.14
439528	BE613180	Hs.288368	Homo sapiens cDNA: FLJ21314 fis, clone C	1.25	2.12
400178			Eos Control	1.25	2.15
430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	1.25	1.20
412841	AI751157	Hs.101395	hypothetical protein MGC11352	1.25	1.39

425655	BE614551	Hs.738	ribosomal protein L14	1.25	1.22
449636	AI656608	Hs.281328	ESTs, Weakly similar to T00378 KIAA0641	1.25	3.00
418406	X73501	Hs.84905	cytokeratin 20	1.24	2.11
414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.24	1.14
436967	AA761729	Hs.136705	ESTs	1.24	2.53
457216	AA452554	Hs.283697	ESTs, Weakly similar to A41796 neural re	1.24	2.18
418414	J04977	Hs.84981	X-ray repair complementing defective rep	1.24	1.35
423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.24	0.92
421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	1.24	2.71
402329			NM_006505*:Homo sapiens poliovirus recep	1.24	1.13
447525	AF151031	Hs.300631	hypothetical protein	1.24	1.07
445939	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	1.24	2.23
421936	AB040884	Hs.109694	KIAA1451 protein	1.24	2.15
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.24	2.15
426717	N90977	Hs.49690	Homo sapiens mRNA; cDNA DKFZp434D2328 (f	1.24	2.14
404751	T70445		ribosomal protein L9	1.24	1.30
411456	AW847588		gb:IL3-CT0213-161299-038-G09 CT0213 Homo	1.24	2.35
425417	AF098948	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	1.24	2.88
434508	AI648601	Hs.118012	ESTs	1.24	2.03
428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH dehydrogenas	1.24	1.59
418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.24	2.27
414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	1.24	1.53
449210	AI635363	Hs.345517	ESTs	1.24	2.18
439551	W72062	Hs.11112	ESTs	1.24	2.13
426244	AI064808	Hs.168289	succinate dehydrogenase complex, subunit	1.23	1.06
453635	BE148082	Hs.24724	MFH-amplified sequences with leucine-ric	1.23	1.34
429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	1.23	2.27
434943	AI929819	Hs.92909	chromosome 21 open reading frame 50	1.23	2.10
417010	NM_006225	Hs.80776	phospholipase C, delta 1	1.23	1.21
426508	W23184	Hs.170171	glutamate-ammonia ligase (glutamine synt	1.23	1.37
434055	AF168712	Hs.3726	x 003 protein	1.23	1.58
438363	AI886351	Hs.22353	hypothetical protein FLJ21952	1.23	2.44
450937	R49131	Hs.26267	ATP-dependant interferon response protei	1.23	2.28
407018	U49869		NM_018955:Homo sapiens ubiquitin B (UBB)	1.23	1.44
444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	1.23	1.19
440112	AA099014	Hs.231029	Homo sapiens, clone MGC:15961, mRNA, com	1.22	2.07
426672	AW270555	Hs.171774	hypothetical protein	1.22	1.16
404956			C1003210*:gi|6912582|ref|NP_036524.1| pe	1.22	2.18
435088	NM_000481	Hs.102	aminomethyltransferase (glycine cleavage	1.22	1.08
438588	AW274454	Hs.6318	peroxisomal short-chain alcohol dehydrog	1.22	1.02
434454	AF217798	Hs.3850	LIS1-interacting protein NUDEL; endoolig	1.22	1.27
425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	1.22	2.52
428755	D87454	Hs.192966	KIAA0265 protein	1.22	1.16
420685	AA279362		gb:zs84d04.r1 NCI_CGAP_GCB1 Homo sapiens	1.22	2.75
458991	AI743502		gb:wf63h12.x2 Soares_NFL_T_GBC_S1 Homo s	1.22	2.39
414825	X06370	Hs.77432	epidermal growth factor receptor (avian	1.22	1.00
434023	AI277883	Hs.146141	ESTs	1.22	2.12
430801	AI580935	Hs.105698	ESTs	1.22	2.53
414880	AW247305	Hs.119140	eukaryotic translation initiation factor	1.21	1.16
454144	BE280478	Hs.182695	hypothetical protein MGC3243	1.21	1.04
404790			C12001707*:gi|7305215|ref|NP_038599.1| k	1.21	2.05
403943			C5000355:gi|4503225|ref|NP_000765.1| cyt	1.21	2.05
400201			NM_006156*:Homo sapiens neural precursor	1.21	1.35
421005	AW293089	Hs.33263	ESTs	1.21	2.02
414774	X02419	Hs.77274	plasminogen activator, urokinase	1.21	1.11
400789			C11001367*:gi|1076205|pir||S50754 hypoth	1.21	1.06
412853	M34175	Hs.74626	adaptor-related protein complex 2, beta	1.21	1.24
449709	BE410592	Hs.23918	hypothetical protein PP5395	1.20	1.27
413726	AJ278465	Hs.75510	annexin A11	1.20	1.14
428485	NM_002950	Hs.2280	ribophorin I	1.20	1.24
405163			C5000561*:gi|7513700|pir||T14151 Inv pro	1.20	1.11
415887	NM_003375	Hs.78902	voltage-dependent anion channel 2	1.20	1.16
434468	N29309	Hs.39288	ESTs	1.20	3.20
446843	AW135925	Hs.98798	hypothetical protein MGC11332	1.20	2.25
432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1.20	2.18
448242	R60646	Hs.20768	HSPC189 protein	1.20	1.22
415753	U52819	Hs.78781	vascular endothelial growth factor B	1.20	1.05
442156	AI690586	Hs.29403	hypothetical protein FLJ22060	1.20	1.18
408824	L80005	Hs.48375	small nuclear ribonucleoprotein polypept	1.20	1.45
430012	NM_015373	Hs.227637	chromosome 22 open reading frame 2	1.20	1.03
413392	AW021404	Hs.13021	ESTs	1.20	2.07
401286			Target Exon	1.20	2.08
415665	AI097276	Hs.274430	surfeit 6	1.20	2.53
456562	AA306049	Hs.102669	DKFZP434O125 protein	1.20	2.40
408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.20	3.45
427818	AW511222	Hs.193765	ESTs	1.19	2.99
406404			NM_002162*:Homo sapiens intercellular ad	1.19	1.17

400124			Eos Control	1.19	2.12
416023	AA173029		gb:zp05e01.r1 Stratagene ovarian cancer	1.19	2.45
427751	AF000152	Hs.180669	conserved gene amplified in osteosarcoma	1.19	1.07
401204			ENSP00000252232*:Sterol regulatory eleme	1.19	2.40
446771	AA128965	Hs.60679	TATA box binding protein (TBP)-associate	1.19	2.03
429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	1.18	2.36
400130			Eos Control	1.18	2.58
405365			CX001212*:gi|7861932|gb|AAF70445.1| (AF2	1.18	2.38
406181			Target Exon	1.18	2.18
422559	AW247696	Hs.155839	hypothetical protein MGC12934	1.18	2.13
409524	AW402151	Hs.54673	tumor necrosis factor (ligand) superfami	1.18	1.07
438446	AW137476	Hs.135204	Homo sapiens cDNA FLJ13884 fis, clone TH	1.18	2.11
447980	AI703397	Hs.202355	ESTs	1.18	2.02
425503	W92517	Hs.158203	actin binding LIM protein 1	1.18	1.29
411469	T09997	Hs.70327	cysteine-rich protein 2	1.18	0.99
409162	H25530	Hs.50868	solute carrier family 22 (organic cation	1.17	1.04
429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	1.17	1.00
420869	X58964	Hs.123638	regulatory factor X, 1 (influences HLA c	1.17	2.58
425943	H46986	Hs.31861	ESTs	1.17	2.25
415376	R35960	Hs.180711	Homo sapiens, Similar to hypothetical pr	1.17	2.13
420588	AF000982	Hs.147916	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.17	2.38
457205	AI905780	Hs.198272	Target CAT	1.17	1.11
407970	AW403814	Hs.41714	BCL2-associated athanogene	1.16	3.60
440214	AA247118	Hs.7049	hypothetical protein FLJ11305	1.16	2.15
405646			C12000200:gi|4557225|ref|NP_000005.1| al	1.16	1.11
438438	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.16	1.08
431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	1.16	2.08
419885	AA251561	Hs.48689	ESTs	1.16	2.07
427679	AA973904	Hs.176092	ESTs, Moderately similar to MYPH_HUMAN M	1.16	2.15
443865	AW296385	Hs.146139	hypothetical protein FLJ12610	1.15	2.05
415511	AI732617	Hs.182362	ESTs	1.15	3.44
417988	AA210878	Hs.111219	ESTs, Moderately similar to ALU1_HUMAN A	1.15	2.09
405058			Target Exon	1.15	1.16
446623	AF279865	Hs.15711	kinesin family member 13B	1.15	1.21
419754	H52299	Hs.308467	Homo sapiens mRNA; cDNA DKFZp586I0523 (f	1.15	1.15
420003	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	1.15	2.06
422988	AW673847	Hs.97321	ESTs	1.15	1.00
426371	M63967	Hs.169517	aldehyde dehydrogenase 1 family, member	1.15	2.31
422895	NM_015958		CGI-30 protein	1.15	2.08
426295	AW367283	Hs.278270	zinc finger protein 6 (CMPX1)	1.15	2.13
448323	AI492298	Hs.170915	ESTs	1.14	2.54
414244	AA287801	Hs.71711	ESTs, Moderately similar to Z195_HUMAN Z	1.14	2.23
442872	AI471987	Hs.173045	ESTs	1.14	2.09
425318	AU076845	Hs.155596	BCL2/adenovirus E1B 19kD-interacting pro	1.14	2.33
415667	F11582	Hs.78582	developmentally regulated GTP-binding pr	1.14	1.10
401058			Target Exon	1.14	2.20
409838	AW502928		gb:UI-HF-BP0p-aiw-e-10-0-UI.r1 NIH_MGC_5	1.14	2.15
438493	AI130740	Hs.6241	phosphoinositide-3-kinase, regulatory su	1.14	1.00
404392			C7001460:gi|12667420|gb|AAK01436.1|AF332	1.14	2.82
433220	AI076192	Hs.131933	ESTs	1.14	2.78
405166			Target Exon	1.14	2.23
401038			C11000425:gi|4507721|ref|NP_003310.1| ti	1.14	2.71
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	1.14	2.08
442043	BE567620	Hs.99210	ESTs	1.13	2.17
419727	AW160796	Hs.92700	DKFZP564O243 protein	1.13	1.14
425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.13	2.07
414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	1.13	1.47
402712			C1003562*:gi|10047177|dbj|BAB13382.1| (A	1.13	1.18
452289	BE568205	Hs.28827	mitogen-activated protein kinase kinase	1.12	2.16
401496			Target Exon	1.12	1.10
459249	AI970399	Hs.240079	ESTs	1.12	2.67
447495	AW401864	Hs.18720	programmed cell death 8 (apoptosis-induc	1.12	2.03
428422	AI557280	Hs.184270	capping protein (actin filament) muscle	1.11	2.60
421762	AA297546		gb:EST113074 Fetal brain III Homo sapien	1.11	2.15
405855			Target Exon	1.11	1.98
428972	AK001470	Hs.194692	cysteine desulfurase	1.11	2.19
406761	AI241715	Hs.77039	ATP synthase, H transporting, mitochondr	1.10	3.33
432425	AF070619	Hs.274539	Homo sapiens clone 24481 mRNA sequence	1.10	2.30
446241	AI004677	Hs.179260	chromosome 14 open reading frame 4	1.10	2.28
424454	AB011139	Hs.147946	optic atrophy 1 (autosomal dominant)	1.10	2.18
418242	AW976183	Hs.88414	BTB and CNC homology 1, basic leucine zi	1.10	2.07
437407	AI479332	Hs.129031	ESTs	1.10	2.09
447459	AI380255	Hs.159424	ESTs	1.10	2.22
426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	1.09	2.33
403655			NM_003071:Homo sapiens SWI/SNF related,	1.09	2.25
433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	1.09	2.70
403826			Target Exon	1.09	1.10

433333	AI016521	Hs.71816	v-akt murine thymoma viral oncogene homo	1.09	1.06
451382	H86180	Hs.221513	ESTs	1.08	2.75
454717	AW815123		gb:QV4-ST0212-261199-045-b01 ST0212 Homo	1.08	1.98
422743	BE304678	Hs.119598	ribosomal protein L3	1.08	1.00
411672	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.08	1.00
452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	1.08	2.45
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.08	2.15
447703	AI420277		gb:tf06c12.x1 NCI_CGAP_Pr28 *Homo sapiens*	1.08	2.05
452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	1.07	2.03
455234	R41084		gb:Hk763-f Adult heart, Clontech Homo sa	1.07	2.08
413945	NM_000591	Hs.75627	CD14 antigen	1.07	0.91
417333	AL157545	Hs.173179	*bromodomain and PHD finger containing, 3*	*1.07*	1.00
434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.07	1.11
455630	AV655701	Hs.75183	*cytochrome P450, subfamily IIE (ethanol-*	*1.06*	2.14
455424	AW937733		gb:QV3-DT0045-210100-063-d06 DT0045 Homo	1.05	2.03
438324	AI792660	Hs.6162	KIAA0771 *protein*	1.05	2.27
421604	AW293880	Hs.248367	MEGF11 protein	1.05	2.00
422614	AI908006	Hs.295362	*Homo sapiens cDNA FLJ14459 fis, clone HE*	1.04	2.33
404058			Target Exon	1.04	2.10
453085	AW954243		KIAA0251 *protein*	1.04	2.18
417500	H59970		gb:yr16f04.r1 Soares fetal liver spleen	1.04	2.40
408653	AW410189	Hs.98074	*itchy (mouse homolog) E3 ubiquitin prote*	1.04	2.73
440439	N92818	Hs.64754	ESTs, Weakly similar to potential CDS [H	1.04	2.05
409209	AA460160	Hs.73217	ESTs	1.04	2.73
456107	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	1.03	2.18
415403	*F07923*	*Hs.26744*	*ESTs*	*1.02*	2.43
455591	BE008018		gb:QV0-BN0147-290400-214-c01 BN0147 Homo	1.02	2.08
428491	AF091035	Hs.184627	KIAA0118 protein	1.02	2.81
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	1.02	2.11
434540	NM_016045	Hs.3945	CGI-107 protein	1.02	2.78
442174	AI690080	Hs.128907	ESTs, Weakly similar to ARIX homeodomain	1.02	2.05
413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	1.02	1.00
452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	1.02	2.25
454412	AW582568		gb:RC1-ST0278-080100-011-h04 ST0278 Homo	1.00	2.20
426955	AA393669	Hs.238094	ESTs	1.00	2.18
425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	1.00	2.10
405710			CX000682:gi|12741327|ref|XP_008833.2| zi	1.00	2.00
400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1.00	1.00
402001			Target Exon	1.00	1.00
402812			NM_004930*:Homo sapiens capping protein	1.00	1.00
402892			Target Exon	1.00	1.00
403329			Target Exon	1.00	1.00
407202	N58172	Hs.109370	ESTs	1.00	1.00
408684	R61377	Hs.12727	hypothetical protein FLJ21610	1.00	1.00
410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	1.00	1.00
413573	AI733859	Hs.149089	ESTs	1.00	1.00
414343	AL036166	Hs.323378	coated vesicle membrane protein	1.00	1.00
414422	AA147224	Hs.249195	Homeo box A13	1.00	1.00
417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	1.00	1.00
421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	1.00	1.00
423349	AF010258	Hs.127428	homeo box A9	1.00	1.00
424273	W40460	Hs.144442	phospholipase A2, group X	1.00	1.00
424649	BE242035	Hs.151461	embryonic ectoderm development	1.00	1.00
426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	1.00	1.00
427308	D26067	Hs.174905	KIAA0033 protein	1.00	1.00
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.00	1.00
430261	AA305127	Hs.237225	hypothetical protein HT023	1.00	1.00
431078	U82827	Hs.249195	homeo box A13	1.00	1.00
433222	AW514472	Hs.238415	dickkopf (Xenopus laevis) homolog 4	1.00	1.00
434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	1.00
435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	1.00
443054	AI745185	Hs.8939	yes-associated protein 65 kDa	1.00	1.00
443564	AI921685	Hs.199713	ESTs	1.00	1.00
444542	AI161293	Hs.280380	aminopeptidase	1.00	1.00
445413	AA151342	Hs.12677	CGI-147 protein	1.00	1.00
448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	1.00	1.00
448807	AI571940	Hs.7549	ESTs	1.00	1.00
449448	D60730	Hs.57471	ESTs	1.00	1.00
449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	1.00	1.00
450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	1.00
451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00	1.00
452039	AI922988	Hs.172510	ESTs	1.00	1.00
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
453096	AW294631	Hs.11325	ESTs	1.00	1.00
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1.00	1.00
453966	BE148734	Hs.63325	transmembrane protease, serine 4	1.00	1.00
405580			Target Exon	1.00	1.00

430268	AK000737	Hs.237480	hypothetical protein FLJ20730	1.00	1.00
450377	AB033091	Hs.74313	KIAA1265 protein	1.00	1.00
433226	AW503733	Hs.9414	KIAA1488 protein	1.00	1.00
412719	AW016610	Hs.816	ESTs	1.00	1.00
425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	1.00	1.00
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.00	1.00
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	1.00	1.00
438817	AI023799	Hs.163242	ESTs	1.00	1.00
455474	AW948094		gb:RC0-MT0012-290300-031-c10 MT0012 Homo	0.99	2.00
420148	U34227	Hs.95361	myosin VIIA (Usher syndrome 1B (autosoma	0.99	2.33
428466	AF151063	Hs.184456	hypothetical protein	0.98	2.20
421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	0.98	3.09
444654	AV650572	Hs.23440	KIAA1105 protein	0.98	2.00
409759	N40285	Hs.81182	histamine N-methyltransferase	0.97	2.20
401936			Target Exon	0.97	2.39
403463			Target Exon	0.96	2.58
434421	AI915927	Hs.34771	ESTs	0.96	2.15
412636	NM_004415		desmoplakin (DPI, DPII)	0.95	2.01
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	0.93	2.55
421938	AA405951		gb:zu66c01.r1 Soares_testis_NHT Homo sap	0.93	3.10
447470	BE618324	Hs.263561	ESTs, Weakly similar to A53531 oncofetal	0.92	2.08
448369	AW268962	Hs.111335	ESTs	0.91	2.35
421710	AB007930	Hs.107088	KIAA0461 protein	0.91	2.63
406805	AI686003	Hs.296031	ESTs	0.91	2.21
447475	AI380797	Hs.158992	ESTs	0.90	3.25
428892	U82828	Hs.194382	ataxia telangiectasia mutated (includes	0.90	2.02
450222	U75308	Hs.24644	TATA box binding protein (TBP)-associate	0.89	2.73
401572			C15001384*:gi|12737057|ref|XP_012129.1|	0.88	2.00
429226	AA913330	Hs.53542	choreoacanthocytosis gene; KIAA0986 prot	0.88	2.37
421979	AW062518	Hs.233150	hypothetical protein MGC5560	0.87	3.70
407614	NM_001932	Hs.37144	membrane protein, palmitoylated 3 (MAGUK	0.86	2.02
417912	R25269	Hs.50547	ESTs	0.86	2.00
401654			NM_007242:Homo sapiens DEAD/H (Asp-Glu-A	0.86	2.11
403149			NM_001450:Homo sapiens four and a half L	0.86	2.19
413000	BE046280		gb:hn43c09.x2 NCI_CGAP_RDF2 Homo sapiens	0.85	2.40
425166	AK001456	Hs.154919	KIAA0625 protein	0.85	2.18
447371	AA334274	Hs.18368	DKFZP564B0769 protein	0.84	2.13
452801	AI935587	Hs.34447	ESTs	0.84	2.55
400957			Target Exon	0.83	2.15
426420	BE383808	Hs.322430	NDRG family, member 4	0.83	2.14
429354	AA451666	Hs.269363	ESTs	0.80	2.25
417831	H16423	Hs.82685	CD47 antigen (Rh-related antigen, integr	0.78	2.43
443368	BE568891	Hs.199210	ESTs, Moderately similar to bK116F5.2 [H	0.78	2.00
441901	AI914445	Hs.128103	ESTs	0.76	2.06
429462	AI890356	Hs.127804	Homo sapiens, clone IMAGE:3536432, mRNA,	0.76	2.03
403010			C21000152:gi|6226483|sp|Q52118|YMO3_ERWS	0.75	2.43
420344	BE463721	Hs.97101	putative G protein-coupled receptor	0.75	2.42
448332	AW293110	Hs.171068	ESTs	0.74	2.00
421674	T10707	Hs.296355	hypothetical protein FLJ23138	0.71	2.18
450645	AL117441	Hs.301997	hypothetical protein FLJ13033	0.67	2.06
448514	AB020626	Hs.301866	KIAA0819 protein	0.67	2.03
431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.60	2.54
417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	0.60	2.00
425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	0.57	2.15
408077	AL133574	Hs.42458	Homo sapiens mRNA; cDNA DKFZp586C1817 (f	0.53	2.29

TABLE 9B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409345	112147_1	AI949109 AW118631 AI833148 AW117891 R45932 R80970 AA733110 AW269428 T27024 R97693 AI149202 AI475492 H98845 AA609665 AI125598 AW663742 AI140029 AW103164 AA126862 N66829 W65398 H94509 W65300 R07712 R36955 AA812477 AA609576 AI754304 Z41075 AA970004 AW274661 AA923584 AI673108 AA070706 AA541812 T90938
409540	1138613_1	AW409569 BE297044 BE295828
409806	1155259_1	AW500960 AW501280 AW500814
409838	1155987_1	AW502928 AW505606 AW501576 AW501577
409844	1156139_1	AW502336 AW502339 AW501736 AW501839
409855	1156256_1	AW502461 AW503000 AW502207 AW501862
409865	1156518_1	AW502208 AW502366 AW502148
410600	121108_1	AW575742 BE549623 AI335824 BE463447 AA729043 AW408712 AW499616 AA086179 AW499617 AA191322
410846	1223902_1	AW807057 AW807054 AW807189 AW807193 AW807369 AW807429 AW807364 AW807365 AW807078 AW807256 AW807180 AW807331
410946	1227589_1	AW811502 AW811521 AW811548 AW811471 AW811511 AW811508
411456	1246706_1	AW847588 AW847716 AW847664 AW847592

411609	1251530_1	AW993680 AW853769
412210	1283615_1	AW901492 AW947725 AW901448
412383	1292509_1	AW947577 AW947574 AW947576 AW947734 AW947733 AW947732
412560	130601_1	R24601 R23657 AA194467 AI948584 AI678666 AA194383 AI765219 AA702993 AA813511 AA620965 AI990303 AI624882 AI003925 AI338870 AI004689 AI004690 AI127228 Z25302 F29302 BE044308 F32992 AA112966 T30825 F24958 F18071 C00537 T30841 R24502 AI934786 AI770075 AI144132 AA812597 AW203978 H82735 AI813349 AI142908 C04894 AI208243 AI208044 N89963 AI767866 AI290470 AI865963 H83611 BE463806 AI082639 AA507760
412636	13165_1	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674 BE184924 C04715 W39488 AW995615 BE184948 BE159646 AW606653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467 AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975 AI470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI306554 AI686869 AI568892 AW190555 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070 AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA961816 AA283207 AI076962 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861 AW860878
412998	1343218_1	BE046254 BE046673 BE046253
413000	1343239_1	BE046280 BE046763 BE046676
413611	1380017_1	BE153275 BE153189 BE153329 BE153022 BE153030 BE152974
413709	1384144_1	BE158687 BE158688
413804	1390710_1	T64682 BE168190 BE168256
413895	1397743_1	BE178160 BE177986 BE178330 BE178480
415789	1555357_1	H01581 H12850 R65905 H13053
416023	156696_1	AA173029 BE467711 AA176710
416272	158407_1	AA178882 AA179898 AA178897
417500	168443_1	H59970 AA203382 R08822
419555	185884_1	AA244416 AA244401
420685	195591_1	AA279362 AA454496 AA584871
421762	206590_1	AA297546 AA297410 AA297401 AA297465 AA297268 AW966174
421938	209376_1	AA405951 AA300675 AA412243 AA412383
422895	22276_1	NM_015958 AF132964 AA088658 N28882 AI197842 AA338679 AA405666 W16871 AA385447 AI928315 AI928318 AW846613 AW960009 AI860687 AI206534 AI961336 T64873 AI735559 H58826 AA857710 AW337576 BE242131 AA339340 AA371380 AA334618 AA316398 R96579 AW771996 AA366110 W07461 H77948
422984	223488_3	W28614 W27435 AI983043 AA364395 AW572472 AW190386 AI129278 AI913081 AW473549 AA830713 AI982871 AI638647 AI828466 AW572486 N52583 N89687 AW075567 AI571047 AI887479 AI559469 AI685802 AA805256 AI458777 AA974369 AI866929 AI886032 AI823925 AI823566 AW198135 AI287510 AI565910 AA765775 AI866019 AI263697 AI355825 R42668 AA894603 AW105585 AI824555 AW339175 D20479
432638	35173_4	AI017717 AA349996 AA350286 BE501310 R48207 AI372769 AJ003450 AA915976 AI261513 AI033019 AI222825 AW150983 AA420700 AA420670 AW884784 Z40157
433821	374566_1	AW182416 AA918195 AA778707 AA927922 AA868718 AA853991 AA609856 AA634398
434767	39297_1	AF153201 AW888811 AW888810 AW842970 AA383181 F35832 F26805 X78930 AF026094 N83362 AA206766 AW874294 AA284205 AI091885 AA206800 AW370684 AA904608 AA806352 AA894757 AW068376 AA807284 AA311341 AW958314
434809	393566_1	AW974687 AA649656 AA652145
438129	450500_1	AA778647 AW070999 R42302
438713	463722_1	H16902 AA814856 T65225 AI523569 F09869 F04737 AI538427 AI051714 AW172603 F02602 F01437 AI684417 AI801950 F02970 Z39367 F02882 T16704 H14597 AW952332 R52080 H10427 T06175 T31057 AI381431 R60918 R41255 R43059 R39905 H19330 R36968
438924	4669_1	BE535511 M62098 AA306787 AW891766 AA348998 AA338869 AA344013 AW956561 AW389343 AW403607 L40391 AW408435 AA121738 AI568978 H13317 R20373 AW948724 AW948744 AA335023 AA436722 AA448690 C21404 AW884390 AA345454 AA303292 AA174174 BE092290 T90614 AA035104 R76028 AA126924 AA741086 AW022056 AW118940 AA121666 AI832409 AA683475 AI140901 AI623576 AW519064 AW474125 AI953923 AI735349 AW150109 AI436154 AW118130 AW270782 AI804073 N27434 AA876543 AA937815 AI051166 AA505378 AI041975 AI335355 AI089540 AA662243 AI127912 AI925604 AI250880 AI366874 AI564386 AI815196 AI683526 AI435885 AI160934 H79030 AI801493 AA448691 AI673767 AI076042 AI804327 AA813438 AA680002 AI274492 T16177 AI287337 AI935050 AA907805 AA911493 AI589411 AI371358 AW576236 AI078866 AW516168 AA346372 AI560185 AA471009 R75857 AA296025 AA523155 AA853168 AI696593 AI658482 AI566601 AW072797 AA128047 AA035502 AW243274 AA992517 R43760
439004	467743_1	AW979062 AA848000 AA847968 AA829138
441623	52182_1	AA315805 AA376906 BE539395 AW579186 H44349 BE328145 BE041644 AW579187 AW366504 H28241 H25318 W37573 AW600919 AA528775 R75904 AW780125 AA149420 AI672414 AI122760 AA345675 AW172758 AI337912 AI961291 AW090300 AI090244 BE219837 AI623661 BE501576 AI742232 AW887496 BE501734 AI023964 AI288904 AA975373 AA890325 AI458424 AI984583 N32562 AI358102 AW241694 AI038448 AA576391 AI018389 AI672071 AA977874 W37448 AW189392 AA612894 AI373653 H89551 H89365 AI699774 AI277548
442473	543413_1	W27992 AF056988
442506	54405_1	BE566411 AL121194 AW976385 AW366882 AI767324
445182	632151_1	AW189787 AI215430 AW268499 AW205930 AI392907 BE093017 BE093019 BE093010
447703	733191_1	AI420277 AW747989 W26565

448079	74834_1	R76981 AA101801 AA101722 AA122297 AA098802 BE006483 AA343200 AW963375 BE090425 AA213871 BE621402 AA309094 AW960171 AI275045 Z44230 AW243724 AI051487 AI376624 R68631 AW978550 C00116 AI984051 AA122265 AI379941 AW205843 AW205839 AW190219 AW129532 AI954133 AI668869 AI383948 AI537386 AA213788 AI088416 AI360826 AA101802 AI619505 AA101795 AA101723 AW614392 R64287 AA927599 AI251904 AI803003 AI675123 AW023079 AW134959 AI926156 AA831069 AI638324 F29901 R46085 F03383 C17731 R20584 T90131
450936	85190_2	AI033745 AI034133 AA844424 AW166024 AI831699 AI971097 AA011685 H70852 H70851
451844	888230_1	T61430 AI820546 AI821336
452900	93691_1	AA626794 AA626779 AA071274 AA928041 AI954235 N71035 N70230 AW674412 AI871136 AI563955 AI954237 AA649543 AI340231 AI368586 AI868721 W44486 T83736 AA126250 AI343619 H94297 T47633 AI672897 AA496355 R23240 AI814680 AA902119 AA644262 N67040 AW074273 AI357512 AA865354 AI027942 R33837 H95828 N63928 AI418701 AI186469 AA693672 AA778429 AA128352 AW954072 C00015 AA861853 AW022016 AI955845 AI753118 AI755095 AA029523 T70086 AA029458 AW675640 N79606 AI659597 AI417119 AI804089 AI383091 AA128493 T83907 T47632 AA094118 AA496405 H94191 AW887759 N98454 AA512988 AI623761 AW028373 AW249740 AI187029 AA991733 AI683085 AI336036 D60550 D60466 D60009 D60248 AW262673 AI524080 AA205643 AI969141 AW674989 AA093704 R81248 R73069 W01019 R23316 C14688 W44485 AA093663 T70157 H57883 R94790 D81287 D81788 AA364340 AA383533 N41706 BE295144 D60973 D81466 D60551 R33836 D60249 AA354560 W01933 T71478 AA515461 F27984 BE084745 W19084 R81247 AI080252 AI382863 AA205642
453085	94851_1	AW954243 AA829930 AA412478 AA828434 AA814538 AI927418 AI192435 W52897 AA443666 AA031913 AI683306 AA918481 AI183314 D83907 AI206832 AA876122 D83836 D83838 D82533 AI761290 AI191125 AI143749 AW771909 AI241436 AI767267 W56507 AA847787 AA568692 T10502 AI247870 AA715017 AA643304 AA890233 AA811387 AA897470 AA907729 AI708679 AI078010 AA452830 AW419160 AI783713 N80205 W56778 AA676899 AI888718 N69930 AI338935 AI217580 AA639508 AA575836 BE046852 AI312651 AI038406 AA628649 AA643838 AI493761 AA032024 W38849 AA340178 AA447052 AA452969 W19369 AA296364 H44229 W58767 C05751 C05835 AI741989 N98532 AW102617 AA412583 AI922246 W38495 AA355375 AA928571 C06275 AA352500 N93132
454412	1174764_1	AW582568 AW818656 AW818647 AW818655 AW818637 AW818234
454555	1223870_1	AW807095 AW807022 AW845880 AW807096 AW807461 AW846116 AW807070
454717	1230516_1	AW815123 AW815138 AW815259
455234	1265385_1	R41084 AW875856
455424	1289247_1	AW937733 AW937727 AW937883
455474	1292960_1	AW948094 AW948118 AW948070 AW948093 AW948084 AW948088 AW948074 AW948079 AW948117 AW948085 AW948081 AW948096 AW948102 AW948087 AW948080 AW948061 AW948091 AW948098 AW948089 AW948104 AW948119 AW948069 AW948100 AW948112 AW948121 AW948068 AW948109 AW948105 AW948097 AW948120 AW948108 AW948111 AW948114 AW948115 AW948072 AW948083 AW948095 AW948116 AW948078 AW948077 AW948071 AW948067 AW948107 AW948122 AW948065 AW948064 AW948113 AW948063 AW948062
455476	1293055_1	AW948172 AW948178 AW948169 AW948176 AW948191 AW948192 AW948186 AW948184 AW948187 AW948188 AW948189 AW948181 AW948177 AW948171 AW948183 AW948173
455591	1335166_1	BE008018 BE008025 BE008026 BE007959 BE007994 BE008016 BE008019 BE008024 BE008022 BE008027 BE008029 BE008020 BE008015 BE008021 BE008028 BE008023 BE008030 BE008014
455604	1337197_1	BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
455842	1374629_1	BE145837 BE145894
457747	397222_1	AW975000 AA658945 AA661558
458991	850804_1	AI743502 AI807438
459192	923891_1	AW176180 AW176212 AI909464 AW176218 AW176171 AW176203 AW176181 AW176213

TABLE 9C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400634	8567750	Minus	101102-101223,101886-102018
400750	8119067	Plus	198991-199168,199316-199548
400752	7331445	Minus	36215-36461
400772	8131629	Minus	34896-35021,41078-41197
400773	8131629	Minus	44116-44238,48208-48321
400788	7342055	Plus	184369-184715
400789	8307741	Plus	82281-83693
400835	8954121	Plus	89366-89622
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
400845	9188605	Plus	34428-34612
400846	9188605	Plus	39310-39474
400847	9188605	Plus	44643-44835
400957	7705148	Minus	66959-67241
400967	7770682	Minus	32697-32999
401038	7232177	Minus	4277-4469
401041	7232177	Plus	44750-45076
401058	8117654	Minus	45226-45414
401155	9438289	Plus	31381-31526
401177	9438503	Minus	62773-63330
401196	9719673	Plus	33138-33834
401204	9743388	Minus	33694-33872
401286	9801342	Minus	147036-147318
401346	9926605	Minus	12031-13032
401371	9650602	Plus	80901-81283

401383	6721135	Minus	155543-157381
401496	7381769	Minus	82790-83002
401512	7622346	Plus	136399-136557
401563	8247910	Plus	91395-91763
401572	8570271	Minus	78651-78889
401593	7230957	Plus	10368-10572,11293-12356
401600	4388746	Minus	27363-27518,28727-28891,29526-29731
401603	7689963	Minus	116659-116780
401613	4878062	Plus	22461-22831
401654	9097132	Minus	64695-64797
401660	9100664	Minus	173662-174024
401720	6468551	Plus	7783-8468
401784	7249190	Plus	148362-148606,149453-149535,149731-149962
401835	7139700	Plus	142257-142742
401886	7229913	Minus	79215-79393
401936	3808091	Plus	46817-46943
402001	9501818	Plus	68052-68223
402087	8117546	Plus	137069-137213,138678-138828,138969-139050
402138	7704985	Plus	14173-15108
402144	7242326	Plus	115425-115977
402190	8576067	Minus	76488-76959
402191	8576073	Minus	69410-69583
402329	7798735	Plus	15833-16180,18419-18715,22507-22624
402368	9558577	Minus	47218-47330,48052-48203
402371	9558584	Plus	68736-68956
402378	9625333	Minus	41312-41468,48313-48720
402449	9796674	Plus	59867-60039,62588-62828,63465-63623,64923-65108
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402517	9798106	Plus	17569-17721
402599	7239666	Plus	5835-5987
402617	9930797	Minus	69466-69945
402712	8969253	Minus	10941-11138
402731	9211639	Minus	117913-118004,121110-121211,121327-121457,125478-125623,126540-126663
402737	9212184	Minus	13358-13552
402754	9213730	Plus	15345-15852
402760	9213869	Plus	136829-136952,137336-137521
402812	6010110	Plus	25026-25091,25844-25920
402845	9369286	Plus	160451-160617,160788-161009
402869	6434643	Minus	138639-139335
402892	8086844	Minus	194384-194645
403010	3132346	Plus	78385-79052
403149	9799833	Plus	25034-25185
403326	8440025	Minus	110959-111122
403329	8516120	Plus	96450-96598
403342	7233487	Minus	42312-43750
403349	8569773	Minus	167815-168374
403381	9438267	Minus	26009-26178
403463	9929538	Plus	102596-102879
403655	8736093	Plus	65668-65859
403725	7534031	Plus	86737-86843
403728	7534291	Minus	34481-34671
403807	8439933	Minus	162963-165773
403826	9838209	Plus	121197-121358
403885	7710403	Minus	53259-53524
403943	7711864	Plus	100742-100904,101322-101503
403988	8576087	Plus	16251-16462
404029	7671252	Plus	108716-111112
404058	3548785	Plus	99397-101808
404069	3168619	Plus	47310-47450
404178	7630978	Minus	178075-178383
404204	3169112	Minus	79868-80321
404231	8218035	Minus	61077-61322
404250	9187145	Minus	36099-36212,37928-38075
404273	9885189	Plus	97789-98285,99601-99855
404343	9838093	Plus	122664-122931
404349	7630858	Minus	61006-61187
404391	3135305	Minus	26030-26173,27852-27997
404392	3135305	Minus	29738-29857
404397	9558608	Minus	104042-104232
404438	6984205	Plus	63413-63553
404439	7139680	Plus	55316-55585
404530	6479107	Plus	3157-3304
404596	9958262	Minus	104807-105043
404649	9796926	Minus	100027-100399
404666	7272179	Minus	18677-18993
404687	9797554	Minus	128456-128565
404744	9187237	Plus	71776-71852,72885-73019,73700-73822,74692-74850

404751	7630939	Plus	113799-114252,114393-114715
404769	8099713	Minus	175801-176823
404790	7230958	Plus	38611-38761
404906	7331453	Minus	100985-101126
404956	7387343	Plus	55883-56203
404977	3738341	Minus	43081-43229
405000	6957544	Minus	88854-89993
405022	7330304	Plus	217163-217439
405053	7651944	Minus	157134-157430
405058	7655685	Plus	150740-151556
405155	9966228	Plus	130469-130723
405163	9966267	Minus	161171-161299
405165	9966302	Plus	6461-6845
405166	9966302	Plus	40526-40891
405172	9966752	Plus	153027-153262
405180	7139743	Plus	65438-65740
405193	7230072	Plus	128187-128383
405194	7230072	Plus	190465-190645,193346-193610
405245	7249293	Minus	57560-58312
405365	2275192	Minus	119867-120372,120481-120824,121029-121357
405376	1552533	Plus	28875-29099
405418	6997292	Plus	51839-51953
405436	7408068	Minus	55716-55979
405443	7408143	Plus	90716-90887,101420-101577
405474	8439781	Plus	172005-172175
405502	9211311	Minus	50360-50584
405580	4512267	Plus	169232-169647
405595	7159256	Plus	47585-47688
405630	4508116	Minus	103218-103291,105858-105993,110051-110126
405646	4914350	Plus	741-969
405710	5531256	Minus	66203-66832
405806	7274891	Minus	224961-226780
405812	4775630	Minus	29424-29764
405855	7652031	Minus	60377-60795
405879	6758747	Minus	54789-55457
405891	6758795	Plus	41062-41861
405902	6758795	Minus	82322-83110
405932	7767812	Minus	123525-123713
406038	8389537	Plus	37764-37877
406140	9168231	Minus	49887-50219
406181	5923650	Plus	16586-16855
406231	7417725	Plus	17206-17641,17772-17968
406248	7417725	Plus	49711-50227
406274	7543787	Plus	932-1123
406356	7107907	Plus	18761-18973
406404	9256305	Minus	152569-152874
406467	9795551	Plus	182212-182958
406557	7711569	Minus	5446-5574,6170-6352
406575	7711679	Plus	142034-142473

TABLE 10A: Genes preferentially expressed in non-invasive bladder tumors

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1 *80th percentile of Ta tumor AIs divided by the 80th percentile of T2-T4 tumor AIs*

Pkey	ExAccn	UnigeneID	Unigene Title	R1
421110	AJ250717	Hs.1355	cathepsin E	8.23
428651	AF196478	Hs.188401	annexin A10	5.78
451668	Z43948	Hs.326444	cartilage acidic protein 1	5.53
415511	AI732617	Hs.182362	ESTs	4.72
428336	AA503115	Hs.183752	microseminoprotein, beta-	4.66
418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	4.62
400752			NM_003105*:Homo sapiens sortilin-related	3.99
430315	NM_004293	Hs.239147	guanine deaminase	3.82
403010			C21000152:gi|6226483|sp|Q52118|YMO3_ERWS	3.56
404977			Insulin-like growth factor 2 (somatomedi	3.54
426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.51
400409	AF153341		Homo sapiens winged helix/forkhead trans	3.38
400844			NM_003105*:Homo sapiens sortilin-related	3.27
406081			Target Exon	3.22
417275	X63578	Hs.295449	parvalbumin	3.03
402230			Target Exon	2.96
454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.89
403381			ENSP00000231844*:Ecotropic virus integra	2.87
426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	2.86
452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.69
434061	AW024973	Hs.283675	NPD009 protein	2.66
418406	X73501	Hs.84905	cytokeratin 20	2.65
418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	2.59
421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.57
403383			Target Exon	2.56
435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.55
424800	AL035588	Hs.153203	MyoD family inhibitor	2.54
404606			Target Exon	2.53
418205	L21715	Hs.83760	troponin I, skeletal, fast	2.53
431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.52
413786	AW613780	Hs.13500	ESTs	2.51
421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	2.50
416640	BE262478	Hs.79404	neuron-specific protein	2.50
420729	AW964897	Hs.290825	ESTs	2.50
402844			C1000118*:gi|9951913|ref|NP_062832.1| pr	2.48
401093			C12000586*:gi|6330167|dbj|BAA86477.1| (A	2.46
417720	AA205625	Hs.208067	ESTs	2.45
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	2.45
403818			Target Exon	2.44
440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.44
418060	AA211589	Hs.208047	ESTs	2.40
400843			NM_003105*:Homo sapiens sortilin-related	2.38
446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	2.35
401512			NM_014080:Homo sapiens dual oxidase-like	2.34
446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.32
417094	NM_006895	Hs.81182	histamine N-methyltransferase	2.31
436293	AI601188	Hs.120910	ESTs	2.30
436246	AW450963	Hs.119991	ESTs	2.30
447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28/cdc	2.29
417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	2.28
426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	2.27
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	2.26
437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	2.23
415025	AW207091	Hs.72307	ESTs	2.18
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.04
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	2.03
433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	2.01
416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	2.00
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	1.99
452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.89
413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	1.88
432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	1.76
405364			ENSP00000239138*:Guanine nucleotide-bind	1.60
414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.52
401929			C17001690:gi|6005701|ref|NP_009099.1| AT	1.00

TABLE 10B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
411880	1263110_1	AW872477 BE088101 T05990
413804	1390710_1	T64682 BE168190 BE168256

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400752	7331445	Minus	36215-36461
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
401093	8516137	Minus	22335-23166
401512	7622346	Plus	136399-136557
401929	3810670	Minus	3167-3286,4216-4310
402230	9966312	Minus	29782-29932
402844	9369286	Plus	54958-55313
403010	3132346	Plus	78385-79052
403381	9438267	Minus	26009-26178
403383	9438267	Minus	119837-121197
403818	8962065	Minus	138360-138512,144656-144796
404606	9212936	Minus	22310-23269
404977	3738341	Minus	43081-43229
405364	2281075	Minus	48325-48491,49136-49252
406081	9123861	Minus	38115-38691

TABLE 11A: Genes preferentially expressed in muscle-invasive bladder tumors

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1 80th percentile of T2-T4 tumor AIs divided by the 80th percentile of Ta tumor AIs

Pkey	ExAccn	UnigeneID	Unigene Title	R1
423961	D13666	Hs.136348	periostin (OSF-2os)	11.22
421948	L42583	Hs.334309	keratin 6A	10.87
401780			NM_005557*:Homo sapiens keratin 16 (foca	9.16
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	8.40
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	7.88
439926	AW014875	Hs.137007	ESTs	7.73
408243	Y00787	Hs.624	interleukin 8	7.54
414183	AW957446	Hs.301711	ESTs	7.00
411573	AB029000	Hs.70823	KIAA1077 protein	6.52
414522	AW518944	Hs.76325	step II splicing factor SLU7	6.42
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.14
441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.04
427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, r	5.66
420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	5.62
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	5.51
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	5.48
401781			Target Exon	5.46
421116	T19132	Hs.101850	retinol-binding protein 1, cellular	5.41
448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	5.41
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.32
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	5.32
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	5.27
456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	5.22
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.17
406663	U24683	Hs.293441	immunoglobulin heavy constant mu	5.08
425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	4.93
433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.89
425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.74
415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	4.64
412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	4.39
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.30
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	4.29
433470	AW960564		transmembrane 4 superfamily member 1	4.23
417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	4.22
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	4.22
413324	V00571	Hs.75294	corticotropin releasing hormone	4.20
436729	BE621807		transmembrane 4 superfamily member 1	4.18
450455	AL117424	Hs.25035	chloride intracellular channel 4	4.15
413731	BE243845	Hs.75511	connective tissue growth factor	4.09
412429	AV650262	Hs.75765	GRO2 oncogene	4.00
418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	4.00
418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.00
420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	3.97
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	3.95
437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	3.94
413441	AI929374	Hs.75367	Src-like-adapter	3.91
404854			Target Exon	3.81
431319	AA873350	Hs.302232	ESTs	3.77
452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	3.76
429679	NM_006290	Hs.211600	tumor necrosis factor, alpha-induced pro	3.72
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.58
408380	AF123050	Hs.44532	diubiquitin	3.58
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.57
422545	X02761	Hs.287820	fibronectin 1	3.52
418203	X54942	Hs.83758	CDC28 protein kinase 2	3.49
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	3.48
406687	M31126		matrix metalloproteinase 11 (stromelysin	3.41
414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.36
417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	3.32
417497	AW402482	Hs.82212	CD53 antigen	3.30
449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	3.25
445033	AV652402	Hs.72901	mucin 13, epithelial transmembrane	3.23
427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	3.23
427527	AI809057	Hs.293441	immunoglobulin heavy constant mu	3.22
409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.18
453331	AI240665		ESTs	3.15
428036	AW068302		Homo sapiens mRNA for caldesmon, 3' UTR	3.10
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	3.09

414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	3.07
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.02
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	2.77
413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.75
406755	N80129	Hs.94360	metallothionein 1L	2.75
426653	AA530892	Hs.171695	dual specificity phosphatase 1	2.67
443623	AA345519	Hs.9641	complement component 1, q subcomponent,	2.65
443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.64
422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	2.51
410204	AJ243425	Hs.326035	early growth response 1	2.46
438973	AW959503	Hs.60440	ESTs, Weakly similar to serin protease w	2.46
420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	2.44
422626	AA344932	Hs.118786	metallothionein 2A	2.44
442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.43
413902	AU076743	Hs.75613	CD36 antigen (collagen type I receptor,	2.42
434868	R50032	Hs.159263	collagen, type VI, alpha 2	2.42
407207	T03651	Hs.336780	tubulin, beta polypeptide	2.30
438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	2.29
430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20
424909	S78187	Hs.153752	cell division cycle 25B	2.18
419938	AU076772	Hs.1279	complement component 1, r subcomponent	2.17
416819	U77735	Hs.80205	pim-2 oncogene	2.11
422562	AI962060	Hs.118397	AE-binding protein 1	2.07
414081	AW969976	Hs.279009	matrix Gla protein	2.07
426406	AI742501	Hs.169756	complement component 1, s subcomponent	2.03
443950	NM_001425	Hs.9999	epithelial membrane protein 3	2.01
418323	NM_002118	Hs.1162	major histocompatibility complex, class	1.94
414420	AA043424	Hs.76095	immediate early response 3	1.90
415149	X12451	Hs.78056	cathepsin L	1.72
415213	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	1.70
421848	X15880	Hs.108885	collagen, type VI, alpha 1	1.69
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.64
427676	AA394062	Hs.300772	tropomyosin 2 (beta)	1.64
415198	AW009480	Hs.943	natural killer cell transcript 4	1.60
424390	AW815657	Hs.182241	interferon induced transmembrane protein	1.59
426825	AL133415	Hs.297753	vimentin	1.51
452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.46
407694	U77594	Hs.37682	retinoic acid receptor responder (tazaro	1.44

TABLE 11B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
428036	28620_1	AW068302 AI754558 AI750727 AI752631 AA302174 AA327522 M64110 AW859944 AW859989 AI751995 AA769620 AI858829 AI924875 AI888836 AA864291 AI685060 AW088029 AI924908 AW466328 AI093800 AA991651 AI254501 BE004703 AA334442 AW938852 AA194330 AL046953 AA852866 AW391995 W30846 AW662928 W25261 AA042863 R99045 H97060 W03910 H94687 T88984 AL048165 T29632 N31556 N36484 AI798679 AA989355 W23832 AA873789 AI743646 AA363587 AI814748 AW338990 N73740 N83666 AL047816 R24137 R63433 AA524984 AA234043 AA195131 N99903 AA453669 AI240302 AA370271 AI950026 AW771049 AA121476 AA569557 AI752632 AI355594 AI471993 AI159941 N94555 AI753138 N21537 H97881 N25769 AW068044 AA808425 R63380 AA384736 AA384738 AA852352 AI073645 AA527960 AA525036 AA044414 AI752460 AA703064 R01216 AA897183 AI751996 T81078 H95047 AA573642 D58348 N20953 AA437143 N95439 AA579540 AW867056 AA770090 AI085180 AI806799 AA426421 AI572513 R24081 AA853189 AA295620 AA234044 AA371020 AW994984 H20896 AW964438 AA318516 AA318499 AA318727 AA318211 AA318478 AA318444 AA318307 AA318497 AA318448 AA318309 AA318496 AA318213 AA318435 AA318424 AA318217 AA318523 AA318438 AA318487 AA318724 AA593185 AW994985 T69842 AI251813 AA478174 AA447737 T68350 F07712 AA121145 H08973 AA345212 BE000667 AW068210 AW608407 R05674 H16712 N85426 N42354 H85516 BE147991 T28113 R32662 AA384678 AW239275 H82382 AW840700 D58229 C04082 W45394 AW795667 R73973 BE002409 AA042828 AA363555 AJ223812 AA344709 BE149590 R70995 W46881 W90778 N71242 AA534826 AL040676 R23797 H96450 AA062957 D79947 W46960 AW959278 AA295997 AA026215 AW579469 AW365135 AW365134 AW994353 AW972886 AW069166 AA343690 AW888731 AI751527 AA937490 AA937506 AI826715 BE465604 AI925532 AI858109 AW339097 AI858524 AI720571 BE046506 AW384981 AA043908 AA375983 AA525181 AW068366 AW070577 AW891837 N83985 AW182753 AI422979 AI679733 BE006555 AL048166 AI081401 AI888821 AI626043 N37087 AI624140 AI801298 AA600048 AI753947 H89615 N66424 AW069756 AI814880 AI982806 AI754287 AI971816 AW069022 AW069069 AW069454 AA342989 AI077712 AI311467 AI087361 AI801015 W46993 AI281324 AW191963 AI421675 AI300881 AI356670 AA873156 AI004219 AI189685 AA478018 AA076063 AI445222 AI753124 AI521569 AI925026 AI022368 AI475993 H20846 AI223234 AI635123 AA579170 N30442 AW117889 AA807935 AA558975 AI306636 AA888963 AI952591 AI935835 AI445293 H16713 AW139833 AA622122 AA972051 AI280828 H09543 AI453725 AW069613 AI865615 AI753921 AI368782 AI633208 AI446651 W46961 N22201 H82276 C16555 AA291477 AW440535 AW517755 AA669921 AI926777 AW662118 AA553369 N67873 AW023948 C15861 C16601 AI251465 AW079187 BE045090 AI273006 C16390 C16503 AI620823 F13661 N66864 Z21311 C16108 C16089 C16400 AA758273 AI287781 AA864676 AW608074 AW385583 AI589944 AA665817 AW192979 AW469065 AA564048 H84715 C16417 AA731072 AA661674 C16487 N29477 AW189997 AI370492 C16471 AA652809 AA936687 AA506512 C16306 AW028413 AI537935 AA528347 C16255 AW029046 C16202 AI868152 AI524662 T94414 AI567041 AI619654 AW008486 AI075624 AA577434 AA345104 T30105 AA932002 C16585 AI750390 AW294265 AI619552 AA669781 AA026678 AW132002 AW263919 C16562 AA759137 AA693351 Z40779 C16577 AA885045 AW073763 R45484 AI520895 U54708 T49285 AI568126 AW006569 AI093317 AL119781 T61046 AI053563 H51958 AF114144 AA305739 AW950394 AW793928 AW793910 AL047737 AV659047 AV659632 AI750389 AA092053 AA092798 H85367 T61597 R23745 Z20418 T78485 AI751528 AW068121 AA853188 AI752459 AA853711 AW950663 R78964 R36359 R21626 R21522

433470	3672_1	AW960564 AA092457 T55890 D56120 T92525 AI815987 BE182608 BE182595 AW080238 M90657 AA347236 AW961686 AW176446 AA304671 AW583735 T61714 AA316968 AI446615 AA343532 AA083489 AA488005 W52095 W39480 N57402 D82638 W25540 W52847 D82729 D58990 BE619182 AA315188 AA308636 AA112474 W76162 AA088544 H52265 AA301631 H80982 AA113786 BE620997 AW651691 AA343799 BE613669 BE547180 BE546656 F11933 AA376800 AW239185 AA376086 BE544387 BE619041 AA452515 AA001806 AA190873 AA180483 AA159546 F00242 AI940609 AI940602 AI189753 T97663 T66110 AW062896 AW062910 AW062902 AI051622 AI828930 AA102452 AI685095 AI819390 AA557597 AA383220 AI804422 AI633575 AW338147 AW603423 AW606800 AW750567 AW510672 AI250777 AA083510 AW629109 AW513200 AA921353 AI677934 AI148698 AI955858 AA173825 AA453027 AI027865 AW375542 AA454099 AA733014 AI591384 R79300 R80023 AA843108 AA626058 AA844898 AW375550 AA889018 AI474275 AW205937 AI052270 AW388117 AW388111 AA699452 AI242230 N47476 H38178 AA366621 AA113196 AA130023 H39740 T61629 AI885973 AW083671 AA179730 AA305757 AI285455 N83956 AA216013 AA336155 AW999959 T97525 AA345349 T91762 AA771981 AI285092 AI591386 BE392486 BE385852 AA682601 AI682884 AA345840 T85477 AA292949 AA932079 AA098791 D82607 T48574 AW752038 C06300
436729	42585_1	BE621807 AI445461 AI346835 AI453743 AI564644 AI928364 AW984527 BE156214 AI694111 AI591358 C17504 C17476 C17963 C18304 AW071625 AI678712 C17732 D57559 H61762 AI720939 AI262930 H27252 AA479712 AI927769 AA291465 AA155661 AI963432 AI567995 AA421678 AI925607 AA292956 AA192448 AW192593 AI865838 AI696905 AI871950 AI911921 BE619741 BE439796 AI161312 AI597801 AI424384 AI093510 AI240988 AW820230 AI492554 BE044033 AW262737 AW008570 AA043216 AW629505 AA136645 AA037722 AA706057 AA088439 AW806193 AW806183 AA479834 BE501957 AA129574 R38114 AA649494 AA524526 BE327120 AW572531 BE219784 BE349186 AW015724 AA043217 AW772000 AI799814 AI671727 AW779725 AA502832 AI470033 AA129575 W38161 AI972739 AA404570 AA627686 AA723200 AA147228 AA903050 AI990245 AI075878 T32487 C06123 AA157944 AI800106 W60075 AI859160 AA478328 AW673152 AA182640 AI990827 AW275048 AW103470 AI298935 AW471421 R79190 AW085158 W45410 AI333170 AW300456 AA662517 T55840 AI823466 AI692846 AA962397 AW191997 AA136658 AI251817 BE044134 AW339104 AW517762 AA724739 R79933 AA411100 AA191349 AA037696 AA190966 AA757735 AW772283 AA010631 H80983 AI769516 H64985 AI061065 AI950693 AA085492 AI245632 H28594 AW088968 BE156360 AI349390 AI621320 AI738844 AW194272 AA148284 AA953883 C06365 AA487893 AI927217 AI918523 AI453453 AI798502 AI189366 AI261359 AI032569 AW338678 AI972899 AI500576 AI872628 AI693030 Z28771 AI985583 AI363829 AW339301 AA581093 AI650338 W60032 AA603586 AI686240 AW242958 AA719173 AI745717 AW675302 AI582462 AI244845 AI565439 F09579 AI918453 AA035576 AI472527 AW351556 AA191414 AW674145 D57558 AI446740 D57845 AI589264 C05782 AA722206 AI432033 R21752 BE157510 AI829640 AI468237 AW384233 AA989662 AI865912 AW197954 AI344941 X75684 AI344943 AW583310 AA988297 AI334860 AI348877 AI798415 D11921 AI377596 AI983655 AI744233 C06111 AI248307 AA948565 AI224807
453331	96214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R68588 AI350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933

TABLE 11C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
404854	7143420	Plus	14260-14537

TABLE 12A: Genes preferentially expressed in muscle-invasive bladder tumors

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
Seq ID No.: Sequence Identification Number linking information in Table 12A to sequences in Table 13

Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No.
424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. 1 & 2
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	Seq ID No. 3 & 4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. 5 & 6
418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. 7 & 8
406964	M21305		FGENES predicted novel secreted protein	Seq ID No. 9 & 10
429276	AF056085	Hs.198612	G protein-coupled receptor 51	Seq ID No. 11 & 12
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	Seq ID No. 13 & 14
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	Seq ID No. 15 & 16
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. 17 & 18
424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	Seq ID No. 19 & 20
420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	Seq ID No. 21 & 22
415511	AI732617	Hs.182362	ESTs	Seq ID No. 23 - 25
452461	N78223	Hs.108106	transcription factor	Seq ID No. 26 & 27
413324	V00571	Hs.75294	corticotropin releasing hormone	Seq ID No. 28 & 29
443211	AI128388	Hs.143655	ESTs	Seq ID No. 30
439926	AW014875	Hs.137007	ESTs	Seq ID No. 31 & 32
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	Seq ID No. 33
408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. 34 & 35
443171	BE281128	Hs.9030	TONDU	Seq ID No. 36 & 37
432829	W60377	Hs.57772	ESTs	Seq ID No. 38 & 39
410553	AW016824	Hs.272068	hypothetical protein MGC14128	Seq ID No. 40 & 41
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	Seq ID No. 42 & 43
425721	AC002115	Hs.159309	uroplakin 1A	Seq ID No. 44 & 45
420370	Y13645	Hs.97234	uroplakin 2	Seq ID No. 46 & 47
437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	Seq ID No. 48 & 49
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	Seq ID No. 50 & 51
456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	Seq ID No. 52
421110	AJ250717	Hs.1355	cathepsin E	Seq ID No. 53 & 54
451668	Z43948	Hs.326444	cartilage acidic protein 1	Seq ID No. 55 - 60
408243	Y00787	Hs.624	interleukin 8	Seq ID No. 61 & 62
440304	BE159984	Hs.125395	ESTs	Seq ID No. 63 & 64
414918	AI219207	Hs.72222	hypothetical protein FLJ13459	Seq ID No. 65 & 66
418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	Seq ID No. 67 & 68
426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. 69 & 70
405033			C1002652*:gi|544327|sp|Q04799|FMO5_RABIT	Seq ID No. 71 & 72
422282	AF019225	Hs.114309	apolipoprotein L	Seq ID No. 73 & 74
425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	Seq ID No. 75 & 76
400844			NM_003105*:Homo sapiens sortilin-related	Seq ID No. 77 & 78
404875			NM_022819*:Homo sapiens phospholipase A2	Seq ID No. 79 & 80
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	Seq ID No. 81 & 82
431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	Seq ID No. 83 & 84
413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	Seq ID No. 85 & 86
444163	AI126098		FGENESH predicted RNaseH domain-containi	Seq ID No. 87 - 89
444444	AI149332	Hs.14855	ESTs	Seq ID No. 90 & 91
427747	AW411425	Hs.180655	serine/threonine kinase 12	Seq ID No. 92 & 93
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. 94 & 95
420281	AI623693	Hs.323494	Predicted cation efflux pump	Seq ID No. 96 & 97
402305			C19000735*:gi|4508027|ref|NP_003414.1| z	Seq ID No. 98 - 100
436608	AA628980		down syndrome critical region protein DS	Seq ID No. 101 & 102
427239	BE270447		ubiquitin carrier protein	Seq ID No. 103 & 104
413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	Seq ID No. 105 & 106
424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	Seq ID No. 107 & 108
414907	X90725	Hs.77597	polo (Drosophia)-like kinase	Seq ID No. 109 & 110
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. 111 & 112
426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	Seq ID No. 113 & 114
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	Seq ID No. 115 & 116
401093			C12000586*:gi|6330167|dbj|BAA86477.1| (A	Seq ID No. 117 - 119
422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	Seq ID No. 120 & 121
449722	BE280074	Hs.23960	cyclin B1	Seq ID No. 122 & 123
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. 124 & 125
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	Seq ID No. 126 - 133
439606	W79123	Hs.58561	G protein-coupled receptor 87	Seq ID No. 134 & 135
418543	NM_005329	Hs.85962	hyaluronan synthase 3	Seq ID No. 136 & 137
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	Seq ID No. 138 - 141
428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	Seq ID No. 142 & 143
427335	AA448542	Hs.251677	G antigen 7B	Seq ID No. 144 & 145
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	Seq ID No. 146 & 147

404440			NM_021048:Homo sapiens melanoma antigen,	Seq ID No. 148 & 149
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	Seq ID No. 150 & 151
408380	AF123050	Hs.44532	diubiquitin	Seq ID No. 152 & 153
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	Seq ID No. 154 & 155
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	Seq ID No. 156 & 157
438817	AI023799		ESTs	Seq ID No. 158
421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	Seq ID No. 159 & 160
431515	NM_012152	Hs.258583	EDG-7 (endothelial differentiation, lys	Seq ID No. 161 & 162
433159	AB035898	Hs.150587	kinesin-like protein 2	Seq ID No. 163 & 164
432441	AW292425	Hs.163484	ESTs	Seq ID No. 165
425726	AF085808	Hs.159330	uroplakin 3	Seq ID No. 166 & 167
448045	AJ297436	Hs.20166	prostate stem cell antigen	Seq ID No. 168 & 169
431846	BE019924	Hs.271580	uroplakin 1B	Seq ID No. 170 & 171
437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	Seq ID No. 172 & 173
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	Seq ID No. 174 & 175
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	Seq ID No. 176 & 177
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	Seq ID No. 178 & 179
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	Seq ID No. 180 & 181
428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. 182 & 183
429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. 184 & 185
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	Seq ID No. 186 & 187
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	Seq ID No. 188 & 189
423961	D13666	Hs.136348	periostin (OSF-2os)	Seq ID No. 190 & 191
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	Seq ID No. 192 & 193
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein homolog	Seq ID No. 194 & 195
430486	BE062109	Hs.241551	chloride channel, calcium activated, family member 2	Seq ID No. 196 & 197
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	Seq ID No. 198 & 199
409103	AF251237	Hs.112208	XAGE-1 protein	Seq ID No. 200 & 201
129404	AI267700		ESTs	Seq ID No. 202
403047			NM_005656*:Homo sapiens transmembrane protease	Seq ID No. 203 & 204
439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig), transmem	Seq ID No. 205 & 206

TABLE 12B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
413804	1390710_1	T64682 BE168190 BE168256
427239	27647_1	BE270447 AW409921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719 BE268715 BE513876 BE295291 BE297066 AA210923 BE407519 H51344 BE622905 AW248281 AW250313 T19021 AA355115 AA316879 BE269633 BE621936 AA290724 AA380031 AA993616 BE301331 W79220 H73020 AW797850 BE274611 BE314315 BE542407 BE562063 BE312868 BE278817 BE252503 AA426470 M91670 NM_014501 BE264533 AI884863 AI884942 AI678077 AA829937 AI869333 AW273060 AA906924 AI571293 AW172642 AA582906 AW674596 AW300936 AW615753 AW615587 AW665495 AI859296 AA594105 AA928110 AI038859 AI589898 AA828316 AA938955 AA283711 AW170665 BE047759 AW732128 AI015067 AW070748 AW248955 AA975490 AA211097 AI826097 AA826730 AA994072 AI367867 W74508 AI086474 AA827720 AI922589 AW000868 W58033 AA991461 BE048131 M91218 AA876186 AA661759 AI123879 AI089508 AW272915 AI566244 AW245061 AA688299 AW250988 AI953468 AI891144 AW089131 AI471577 AA293354 AA464019 BE044549 T29587 AW956171 BE537716 BE269400 AA918328 AI538087 AA969243 AW075033 BE139361 AI340589 AI250128 AI247038 BE138953 AW075177 AI307208 BE049086 AW302327 AI054335 AI345565 AI334881 AI252075 AI254494 AW075006 AW302733 AW302738 AI054057 AI054217 AI054172 AI054302 AI053722 AI054060 AI054079 AW075181 AI307473 AI312145 AI340734 AI334909 AW071374 BE138502 AW074809 AW301901 AI251662 AI307559 BE139228 AI254764 AW073049 AI251264 AI802837 AW271867 AI307442 AW075100 AW073456 AW072496 AI270787 AW271039 AW071307 AI610913 AW071289 AI251232 AI251262 AW073656 AW072901 AI307493 AI255068 AI251289 AI252160 AI271496 AI252427 AW073469 AW071420 AI270156 AI252926 AI252839 AI252868 AW072520 AW073433 AI340643 AI802854 AI334733 AI583896 AW071311 AI802853 AI289711 AI345036 AW072513 AI348921 AI307478 AI305762 BE139315 AW271034 AI334886 AI340619 AW470478 BE139260 BE138965 AW302085 BE041872 AW268964
432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
436608	42361_3	AA628980 AI126603 BE504035
438817	465592_1	AI023799 AA826307 AI683094 AI307373 AI870547 AW979007
444163	593658_1	AI126098 AI184746 AI148521
456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 12C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400844	9188605	Plus	24746-24872,25035-25204
401093	8516137	Minus	22335-23166

402305	7328724	Plus	40832-41362
404440	7528051	Plus	80430-81581
404875	9801324	Plus	96588-96732,97722-97831
405033	7107731	Minus	142358-142546

Table 13

Seq ID NO: 1 DNA sequence:

Nucleic Acid Accession #: NM_002205

Coding sequence: 24..3173

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1          11         21         31         41         51
|          |          |          |          |          |
CAGGACAGGG AAGAGCGGGC GCTATGGGGA GCCGGACGCC AGAGTCCCCT CTCCACGCCG     60
TGCAGCTGCG CTGGGGCCCC CGGCGCCGAC CCCCGCTCGT GCCGCTGCTG TTGCTGCTCG    120
TGCCGCCGCC ACCCAGGGTC GGGGGCTTCA ACTTAGACGC GGAGGCCCCA GCAGTACTCT    180
CGGGGCCCCC GGGCTCCTTC TTCGGATTCT CAGTGGAGTT TTACCGGCCG GGAACAGACG    240
GGGTCAGTGT GCTGGTGGGA GCACCCAAGG CTAATACCAG CCAGCCAGGA GTGCTGCAGG    300
GTGGTGCTGT CTACCTCTGT CCTTGGGGTG CCAGCCCCAC ACAGTGCACC CCCATTGAAT    360
TTGACAGCAA AGGCTCTCGG CTCCTGGAGT CCTCACTGTC CAGCTCAGAG GGAGAGGAGC    420
CTGTGGAGTA CAAGTCCTTG CAGTGGTTCG GGGCAACAGT TCGAGCCCAT GGCTCCTCCA    480
TCTTGGCATG CGCTCCACTG TACAGCTGGC GCACAGAGAA GGAGCCACTG AGCGACCCCG    540
TGGGCACCTG CTACCTCTCC ACAGATAACT TCACCCGAAT TCTGGAGTAT GCACCCTGCC    600
GCTCAGATTT CAGCTGGGCA GCAGGACAGG GTTACTGCCA AGGAGGCTTC AGTGCCGAGT    660
TCACCAAGAC TGGCCGTGTG GTTTTAGGTG GACCAGGAAG CTATTTCTGG CAAGGCCAGA    720
TCCTGTCTGC CACTCAGGAG CAGATTGCAG AATCTTATTA CCCCGAGTAC CTGATCAACC    780
TGGTTCAGGG GCAGCTGCAG ACTCGCCAGG CCAGTTCCAT CTATGATGAC AGCTACCTAG    840
GATACTCTGT GGCTGTTGGT GAATTCAGTG GTGATGACAC AGAAGACTTT GTTGCTGGTG    900
TGCCCAAAGG GAACCTCACT TACGGCTATG TCACCATCCT TAATGGCTCA GACATTCGAT    960
CCCTCTACAA CTTCTCAGGG GAACAGATGG CCTCCTACTT TGGCTATGCA GTGGCCGCCA   1020
CAGACGTCAA TGGGGACGGG CTGGATGACT TGCTGGTGGG GGCACCCCTG CTCATGGATC   1080
GGACCCCTGA CGGGCGGCCT CAGGAGGTGG GCAGGGTCTA CGTCTACCTG CAGCACCCAG   1140
CCGGCATAGA GCCCACGCCC ACCCTTACCC TCACTGGCCA TGATGAGTTT GGCCGATTTG   1200
GCAGCTCCTT GACCCCCCTG GGGGACCTGG ACCAGGATGG CTACAATGAT GTGGCCATCG   1260
GGGCTCCCTT TGGTGGGGAG ACCCAGCAGG GAGTAGTGTT TGTATTTCCT GGGGGCCCAG   1320
GAGGGCTGGG CTCTAAGCCT TCCCAGGTTC TGCAGCCCCT GTGGGCAGCC AGCCACACCC   1380
CAGACTTCTT TGGCTCTGCC CTTCGAGGAG GCCGAGACCT GGATGGCAAT GGATATCCTG   1440
ATCTGATTGT GGGGTCCTTT GGTGTGGACA AGGCTGTGGT ATACAGGGGC CGCCCCATCG   1500
TGTCCGCTAG TGCCTCCCTC ACCATCTTCC CCGCCATGTT CAACCCAGAG GAGCGGAGCT   1560
GCAGCTTAGA GGGGAACCCT GTGGCCTGCA TCAACCTTAG CTTCTGCCTC AATGCTTCTG   1620
GAAAACACGT TGCTGACTCC ATTGGTTTCA CAGTGGAACT TCAGCTGGAC TGGCAGAAGC   1680
AGAAGGGAGG GGTACGGCGG GCACTGTTCC TGGCCTCCAG GCAGGCAACC CTGACCCAGA   1740
CCCTGCTCAT CCAGAATGGG GCTCGAGAGG ATTGCAGAGA GATGAAGATC TACCTCAGGA   1800
ACGAGTCAGA ATTTCGAGAC AAACTCTCGC CGATTCACAT CGCTCTCAAC TTCTCCTTGG   1860
ACCCCCAAGC CCCAGTGGAC AGCCACGGCC TCAGGCCAGC CCTACATTAT CAGAGCAAGA   1920
GCCGGATAGA GGACAAGGCT CAGATCTTGC TGGACTGTGG AGAAGACAAC ATCTGTGTGC   1980
CTGACCTGCA GCTGGAAGTG TTTGGGGAGC AGAACCATGT GTACCTGGGT GACAAGAATG   2040
CCCTGAACCT CACTTTCCAT GCCCAGAATG TGGGTGAGGG TGGCGCCTAT GAGGCTGAGC   2100
TTCGGGTCAC CGCCCCTCCA GAGGCTGAGT ACTCAGGACT CGTCAGACAC CCAGGGAACT   2160
TCTCCAGCCT GAGCTGTGAC TACTTTGCCG TGAACCAGAG CCGCCTGCTG GTGTGTGACC   2220
TGGGCAACCC CATGAAGGCA GGAGCCAGTC TGTGGGGTGG CCTTCGGTTT ACAGTCCCTC   2280
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GAGACCAGCC TCAGAAGGAG GAGGACCTGG GACCTGCTGT CCACCATGTC TATGAGCTCA   2520
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ACCCCATTAA CCCAAAGGGC CTGGAGTTGG ATCCCGAGGG TTCCCTGCAC CACCAGCAAA   2700
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TAGGTCTACT CATCTACATC CTCTACAAGC TTGGATTCTT CAAACGCTCC CTCCCATATG   3120
GCACCGCCAT GGAAAAAGCT CAGCTCAAGC CTCCAGCCAC CTCTGATGCC TGAGTCCTCC   3180
CAATTTCAGA CTCCCATTCC TGAAGAACCA GTCCCCCCAC CCTCATTCTA CTGAAAAGGA   3240
GGGGTCTGGG TACTTCTTGA AGGTGCTGAC GGCCAGGGAG AAGCTCCTCT CCCCAGCCCA   3300
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GAAAGATAAC TAGGAAATCC ATTCACAGTT CTTTGGGCCA GACATGCCAC AAGGACTTCC   3540
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CACAAGGATA GATGCTGGCC CAGGGCCAGA GCCCAGCTCC AAGGGGAATC AGAACTCAAA   3780
TGGGGCCAGA TCCAGCCTGG GGTCTGGAGT TGATCTGGAA CCCAGACTCA GACATTGGCA   3840
CCAATCCAGG CAGATCCAGG ACTATATTTG GGCCTGCTCC AGACCTGATC CTGGAGGCCC   3900
AGTTCACCCT GATTTAGGAG AAGCCAGGAA TTTCCCAGGA CCTGAAGGGG CCATGATGGC   3960
AACAGATCTG GAACCTCAGC CTGGCCAGAC ACAGGCCCTC CCTGTTCCCC AGAGAAAGGG   4020
GAGCCCACTG TCCTGGGCCT GCAGAATTTG GGTTCTGCCT GCCAGCTGCA CTGATGCTGC   4080
CCCTCATCTC TCTGCCCAAC CCTTCCCTCA CCTTGGCACC AGACACCCAG GACTTATTTA   4140
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Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_002196.1

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1          11         21         31         41         51
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GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCP WGASPTQCTP IEFDSKGSRL   120
LESSLSSSEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCYLST   180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ   240
IAESYYPEYL INLVQGQLQT RQASSIYDDS YLGYSVAVGE FSGDDTEDFV AGVPKGNLTY   300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ   360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET   420
QQGVVFVFPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRDLDGNG YPDLIVGSFG   480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI   540
GFTVELQLDW QKQKGGVRRA LFLASRQATL TQTLLIQNGA REDCREMKIY LRNESEFRDK   600
LSPIHIALNF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF   660
GEQNHVYLGD KNALNLTFHA QNVGEGGAYE AELRVTAPPE AEYSGLVRHP GNFSSLSCDY   720
FAVNQSRLLV CDLGNPMKAG ASLWGGLRFT VPHLRDTKKT IQFDFQILSK NLNNSQSDVV   780
SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPQKEE DLGPAVHHVY ELINQGPSSI   840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGSLHH QQKREAPSRS   900
SASSGPQILK CPEAECFRLR CELGPLHQQE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV   960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IIILAILFGL LLLGLLIYIL  1020
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Seq ID NO: 3 DNA sequence:
Nucleic Acid Accession #: NM_002425
Coding sequence: 23..1453

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TGCCCAGCAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG   180
AAAGGACAGT AATCTCATTG TTAAAAAAAT CCAAGGAATG CAGAAGTTCC TTGGGTTGGA   240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT   300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT   360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT   420
TGAGAAAGCT CTGAAAGTCT GGGAAGAGGT GACTCCACTC ACATTCTCCA GGCTGTATGA   480
AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT   540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA   600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCCT   660
CGTTGCTGCT CATGAACTTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACACTGAAGC   720
TTTGATGTAC CCACTCTACA ACTCATTCAC AGAGCTCGCC CAGTTCCGCC TTTCGCAAGA   780
TGATGTGAAT GGCATTCAGT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT   840
GGTGCCCACA AAATCTGTTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT   900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT   960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTCAT TTGATTTCTG CATTTTGGCC  1020
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CAAGGAAAAG AAGAAAACAT ACTTCTTTGC AGCGGACAAA TACTGGAGAT TTGATGAAAA  1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA  1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC  1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG  1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTTAAT AAATCTAATA  1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCCTGCATG TTCTGTGACT  1560
GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCTTC  1620
ACTTGCTTTT GAATTGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA  1680
ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC  1740
CTT
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Seq ID NO: 4 Protein sequence:
Protein Accession #: NP_002416

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KKIQGMQKFL GLEVTGKLDT DTLEVMRKPR CGVPDVGHFS SFPGMPKWRK THLTYRIVNY   120
TPDLPRDAVD SAIEKALKVW EEVTPLTFSR LYEGEADIMI SFAVKEHGDF YSFDGPGHSL   180
AHAYPPGPGL YGDIHFDDDE KWTEDASGTN LFLVAAHELG HSLGLFHSAN TEALMYPLYN   240
SFTELAQFRL SQDDVNGIQS LYGPPPASTE EPLVPTKSVP SGSEMPAKCD PALSFDAIST   300
LRGEYLFFKD RYFWRRSHWN PEPEFHLISA FWPSLPSYLD AAYEVNSRDT VFIFKGNEFW   360
AIRGNEVQAG YPRGIHTLGF PPTIRKIDAA VSDKEKKKTY FFAADKYWRF DENSQSMEQG   420
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FPRLIADDFP GVEPKVDAVL QAFGFFYFFS GSSQFEFDPN ARMVTHILKS NSWLHC
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Seq ID NO: 5 DNA sequence:
Nucleic Acid Accession #: NM_002421
Coding sequence: 72..1481

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GGGATATTGG AGTAGCAAGA GGCTGGGAAG CCATCACTTA CCTTGCACTG AGAAAGAAGA    60
CAAAGGCCAG TATGCACAGC TTTCCTCCAC TGCTGCTGCT GCTGTTCTGG GGTGTGGTGT   120
CTCACAGCTT CCCAGCGACT CTAGAAACAC AAGAGCAAGA TGTGGACTTA GTCCAGAAAT   180
ACCTGGAAAA ATACTACAAC CTGAAGAATG ATGGGAGGCA AGTTGAAAAG CGGAGAAATA   240
GTGGCCCAGT GGTTGAAAAA TTGAAGCAAA TGCAGGAATT CTTTGGGCTG AAAGTGACTG   300
GGAAACCAGA TGCTGAAACC CTGAAGGTGA TGAAGCAGCC CAGATGTGGA GTGCCTGATG   360
TGGCTCAGTT TGTCCTCACT GAGGGGAACC CTCGCTGGGA GCAAACACAT CTGACCTACA   420
GGATTGAAAA TTACACGCCA GATTTGCCAA GAGCAGATGT GGACCATGCC ATTGAGAAAG   480
CCTTCCAACT CTGGAGTAAT GTCACACCTC TGACATTCAC CAAGGTCTCT GAGGGTCAAG   540
CAGACATCAT GATATCTTTT GTCAGGGGAG ATCATCGGGA CAACTCTCCT TTTGATGGAC   600
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ACCCTAGCTA CACCTTCAGT GGTGATGTTC AGCTAGCTCA GGATGACATT GATGGCATCC   840
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TACACGGATA CCCCAAGGAC ATCTACAGCT CCTTTGGCTT CCCTAGAACT GTGAAGCATA  1200
TCGATGCTGC TCTTTCTGAG GAAAACACTG GAAAAACCTA CTTCTTTGTT GCTAACAAAT  1260
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ATTTCTTTCA TGGAACAAGA CAATACAAAT TTGATCCTAA AACGAAGAGA ATTTTGACTC  1440
TCCAGAAAGC TAATAGCTGG TTCAACTGCA GGAAAAATTG AACATTACTA ATTTGAATGG  1500
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CATTTTTAAC CTCTAGAGTC ACTGATACAC AGAATATAAT CTTATTTATA CCTCAGTTTG  1620
CATATTTTTT TACTATTTAG AATGTAGCCC TTTTTGTACT GATATAATTT AGTTCCACAA  1680
ATGGTGGGTA CAAAAAGTCA AGTTTGTGGC TTATGGATTC ATATAGGCCA GAGTTGCAAA  1740
GATCTTTTCC AGAGTATGCA ACTCTGACGT TGATCCCAGA GAGCAGCTTC AGTGACAAAC  1800
ATATCCTTTC AAGACAGAAA GAGACAGGAG ACATGAGTCT TTGCCGGAGG AAAAGCAGCT  1860
CAAGAACACA TGTGCAGTCA CTGGTGTCAC CCTGGATAGG CAAGGGATAA CTCTTCTAAC  1920
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Seq ID NO: 6 Protein sequence:
Protein Accession #: NP_002412

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1          11         21         31         41         51
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VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN   120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGQADIM ISFVRGDHRD NSPFDGPGGN   180
LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSLGLSHST DIGALMYPSY   240
TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR   300
FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEFADRDEV RFFKGNKYWA VQGQNVLHGY   360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFVANKYWRY DEYKRSMDPG YPKMIAHDFP   420
GIGHKVDAVF MKDGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN
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Seq ID NO: 7 DNA sequence:
Nucleic Acid Accession #: NM_014331
Coding sequence: 1..1506

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GGAATCTTCA TCTCTCCTAA GGGCGTGCTC CAGAACACGG GCAGCGTGGG CATGTCTCTG   240
ACCATCTGGA CGGTGTGTGG GGTCCTGTCA CTATTTGGAG CTTTGTCTTA TGCTGAATTG   300
GGAACAACTA TAAAGAAATC TGGAGGTCAT TACACATATA TTTTGGAAGT CTTTGGTCCA   360
TTACCAGCTT TTGTACGAGT CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT   420
GTGATATCCC TGGCATTTGG ACGCTACATT CTGGAACCAT TTTTTATTCA ATGTGAAATC   480
CCTGAACTTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTGAT GGTCCTAAAT   540
AGCATGAGTG TCAGCTGGAG CGCCCGGATC CAGATTTTCT TAACCTTTTG CAAGCTCACA   600
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TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTTACTGA AGAAGTAGAA   780
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TATGTGCTGA CAAATGTGGC CTACTTTACG ACCATTAATG CTGAGGAGCT GCTGCTTTCA   900
AATGCAGTGG CAGTGACCTT TTCTGAGCGG CTACTGGGAA ATTTCTCATT AGCAGTTCCG   960
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CGCAAGCACA CTCCTCTACC AGCTGTTATT GTTTTGCACC CTTTGACAAT GATAATGCTC  1140
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AGCAAGAGTT AGTTTGGTAT TAAATCCTCA TTAGAACAAC CACCTGTTTC ACTAATAACT  2340
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CTTCAGATGA AACTGTCCAG ATTAATTAGG AAAAGGCATA TATTAACATA AAAATTGCAA  2640
AAGAAATGTC GCTGTAAATA AGATTTACAA CTGATGTTTC TAGAAAATTT CCACTTCTAT  2700
ATCTAGGCTT TGTCAGTAAT TTCCACACCT TAATTATCAT TCAACTTGCA AAAGAGACAA  2760
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GCACTTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTCGG GAGTTCTAGA CCAGCCTGAC  2940
CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCACAT  3000
GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCG  3060
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Seq ID NO: 8 Protein sequence:
Protein Accession #: NP_055146

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GIFISPKGVL QNTGSVGMSL TIWTVCGVLS LFGALSYAEL GTTIKKSGGH YTYILEVFGP   120
LPAFVRVWVE LLIIRPAATA VISLAFGRYI LEPFFIQCEI PELAIKLITA VGITVVMVLN   180
SMSVSWSARI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY   240
YGMYAYAGWF YLNFVTEEVE NPEKTIPLAI CISMAIVTIG YVLTNVAYFT TINAEELLLS   300
NAVAVTFSER LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV   360
RKHTPLPAVI VLHPLTMIML FSGDLDSLLN FLSFARWLFI GLAVAGLIYL RYKCPDMHRP   420
FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM   480
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Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: FGENESH
Coding sequence: 1..546

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CAGCTCGCCG GTGCCCTCGA CCTGCCCGCT GGGTCCTGTG CCTTTGAAGA GAGCACTTGC   240
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CAGTTTGTCA AAGGCCAGAA CTTGGACGTA ACAGTGTACT GCAGGCTCCA GGGCAGTGAG   480
AAACCCTTTG AAACTGGTTC CATGGTTCCA TTCACCTTCA TGTACTGGAT CCACCATGGA   540
AAGTAG
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Seq ID NO: 10 Protein Sequence
Protein Accession #: FGENESH

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1          11         21         31         41         51
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QLAGALDLPA GSCAFEESTC GFDSVLASLP WILNEEGQQP FWSSGDMSDW DYWVGWRKLI   120
HSPLSTPGWS RQVRLQLFQL QFVKGQNLDV TVYCRLQGSE KPFETGSMVP PTFMYWIHHG   180
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Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 461-3286

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ACGCCGGCCC CCCTCTCCGC GTTTGCTCGC TTGCTCCCCG CCTCCCGCAC TCCGCTCGCT    240
CCCACCCCTT CCCGGCGTGA TTGATCCGTC ACGGGCGCCG CCGCTGCCGC CGCCGCCGCC    300
GCGGCCGTTC TGAGCCGAGC CGGAACCCTA GCCCGAGACG GAGCCGGGGC CCGGGCCGGC    360
GCCATTGCGC GGGCGCCGCG GGAAGACCTT GGCGCGGGGC GGCGGGCCGG GCCAGGCCAT    420
GCGGGCCGAG TGAGCCGGCG CCCGCAGCCC GCGGCGCGGC ATGGCTTCCC CGCGGAGCTC    480
CGGGCAGCCC GGGCCGCCGC CGCCGCCGCC ACCGCCGCCC GCGCGCCTGC TACTGCTACT    540
GCTGCTGCCG CTGCTGCTGC CTCTGGCGCC CGGGGCCTGG GGCTGGGCGC GGGGCGCCCC    600
CCGGCCGCCG CCCAGCAGCC CGCCGCTCTC CATCATGGGC CTCATGCCGC TCACCAAGGA    660
GGTGGCCAAG GGCAGCATCG GGCGCGGTGT GCTCCCCGCC GTGGAACTGG CCATCGAGCA    720
GATCCGCAAC GAGTCACTCC TGCGCCCCTA CTTCCTCGAC CTGCGGCTCT ATGACACGGA    780
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CTTGATGGTG TTTGGAGGCG TCTGTCCATC CGTCACATCC ATCATTGCAG AGTCCCTCCA    900
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GAAGTTGCTC AAGCACTACC AGTGGAAGCG CGTGGGCACG CTGACGCAAG ACGTTCAGAG   1080
GTTCTCTGAG GTGCGGAATG ACCTGACTGG AGTTCTGTAT GGCGAGGACA TTGAGATTTC   1140
AGACACCGAG AGCTTCTCCA ACGATCCCTG TACCAGTGTC AAAAAGCTGA AGGGGAATGA   1200
TGTGCGGATC ATCCTTGGCC AGTTTGACCA GAATATGGCA GCAAAAGTGT TCTGTTGTGC   1260
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CCTCACCATC CTCGGGATGA TCATGGCCAG TGCTTTTCTC TTCTTCAACA TCAAGAACCG   1980
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GACCTTTGAA ACACTTTGCA CCGTCAGGAC CTGGATTCTC ACCGTGGGCT ACACGACCGC   2160
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AGATGGAGGA AAGGCCATTT TAAAAAATCA CCTCGATCAA AATCCCCAGC TACAGTGGAA   3060
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AGGCCCCCAG CTGCCAGGCC AGCTGACCCC AGCCTTCCTG GAACAGGGAG TCTGCAGGAG   3840
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CAGACACGCT CTGCAGCATT CACCGACAGT CTGTCATGCA CCCACCACGT TGGCCATGTC  4080
CTTGTGTTCC TATCGGATGC TCCCAGTAAC CAGGGGGACC ACCCGAGCTA ATCATGGAAT  4140
GTCTGTTCCC AGCAAACACG ATAAAGAAAG ATTGTGCACT TTAACCTCTC TCATCAGGGC  4200
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GCAAACACAC CGTCCATTTC TGAAGAGGCT TCGGCCTGAA GGCATTTTCC AATGATGTTA  5640
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Seq ID NO: 12 Protein sequence:
Protein Accession #: EOS sequence

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AVNPAILKLL KHYQWKRVGT LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV   240
KKLKGNDVRI ILGQFDQNMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTEANSS   300
RCLRKNLLAA MEGYIGVDFE PLSSKQIKTI SGKTPQQYER EYNNKRSGVG PSKFHGYAYD   360
GIWVIAKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIIL NAMNETNFFG VTGQVVFRNG   420
ERMGTIKFTQ FQDSREVKVG EYNAVADTLE IINDTIRFQG SEPPKDKTII LEQLRKISLP   480
LYSILSALTI LGMIMASAFL FFNIKNRNQK LIKMSSPYMN NLIILGGMLS YASIFLFGLD   540
GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IFKNVKMKKK IIKDQKLLVI   600
VGGMLLIDLC ILICWQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLGIV   660
YAYKGLLMLF GCFLAWETRN VSIPALNDSK YIGMSVYNVG IMCIIGAAVS FLTRDQPNVQ   720
FCIVALVIIF CSTITLCLVF VPKLITLRTN PDAATQNRRF QFTQNQKKED SKTSTSVTSV   780
NQASTSRLEG LQSENHRLRM KITELDKDLE EVTMQLQDTP EKTTYIKQNH YQELNDILNL   840
GNFTESTDGG KAILKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPILH   900
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Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67-363

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CCTGTTAATC CAAGGTCTTT AGAAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA   240
CGTGTTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA   300
TCGAAGGCCA TCAAGAATTT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT   360
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CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA   480
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GGTTAATGTT CATCATCCTA AGCTATTCAG TAATAACTCT ACCCTGGCAC TATAATGTAA   600
GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTTCTGACC CTGCTTCAAA TATTTCCCTC   660
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TCAGAATCTC AAATAACTAA AAGGTATGCA ATCAAATCTG CTTTTTAAAG AATGCTCTTT   780
ACTTCATGGA CTTCCACTGC CATCCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA   840
CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT   900
CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT   960
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TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA  1020
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Seq ID NO: 14 Protein sequence:
Protein Accession #: NP_001556.1

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EIIATMKKKG EKRCLNPESK AIKNLLKAVS KEMSKRSP
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Seq ID NO: 15 DNA sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 241..1272

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TTGAGGGCCA AGACCAACAC CTACATCAAG ACACCGGTGA GGGGCGAGGA ACCAGTGTTC    240
ATGGTGACAG GGCGACGGGA GGACGTGGCC ACAGCCCGGC GGGAAATCAT CTCAGCAGCG    300
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CTCCCTCTAC CCAATTTACT CTTCTCGCCC CACCTAGGGA CAGATTCCCC CTGCTCTTTT   5460
TGTCCTAGAA ACCCCGCTAG TTTGGGATGG TAGCGTCTGG GGTGGGGAGG GCTTCCCCTT   5520
CCCCACTCGA GGGTGCGGGT GGGGAAGGGG GGGTGGGTGG AGACAGCCCT GGGGCAGGGA   5580
GGATGGTCTC TCCACTGTAG AAAGTAGAGT AGGATTGTGG TCAGACTTAA TTTGAGGCAT   5640
CTAGTGAAGA CACGTACAAA TCCACCAAGG AAAAAGATTT CAAAAGCAAA ATAAAAGCGG   5700
GAAATAAAAC AGACCCAAGA ATAATCAAGT CAAAGTGATG TTGCACAAAA TGCAGAGAAA   5760
CCAAGAAGGG GGAGGGTTAA TGTATTAAAT GTGCTATTAA GAACTTAATT TTATTAAAAG   5820
TACTATTACT TAAGGCTC
```

Seq ID NO: 16 Protein Sequence
Protein Accession #: XP_044166

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1          11         21         31         41         51
|          |          |          |          |          |
MVTGRREDVA TARREIISAA EHFSMIRASR NKSGAAFGVA PALPGQVTIR VRVPYRVVGL   60
VVGPKGATIK RIQQQTNTYI ITPSRDRDPV FEITGAPGNV ERAREEIETH IAVRTGKILE   120
YNNENDFLAG SPDAAIDSRY SDAWRVHQPG CKPLSTFRQN SLGCIGECGV DSGFEAPRLG   180
EQGGDFGYGG YLFPGYGVGK QDVYYGVAET SPPLWAGQEN ATPTSVLFSS ASSSSSSSAK   240
ARAGPPGAHR SPATSAGPEL AGLPRRPPGE PLQGFSKLGG GGLRSPGGGR DCMVCFESEV   300
TAALVPCGHN LFCMECAVRI CERTDPECPV CHITATQAIR IFS                     343
```

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: NM_005940
Coding sequence: 23-1489

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1          11         21         31         41         51
|          |          |          |          |          |
AAGCCCAGCA GCCCCGGGGC GGATGGCTCC GGCCGCCTGG CTCCGCAGCG CGGCCGCGCG     60
CGCCCTCCTG CCCCCGATGC TGCTGCTGCT GCTCCAGCCG CCGCCGCTGC TGGCCCGGGC    120
TCTGCCGCCG GACGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC    180
AGCCCTGCCC AGTAGCCCGG CACCTGCCCC TGCCACGCAG GAAGCCCCCC GGCCTGCCAG    240
CAGCCTCAGG CCTCCCCGCT GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCCGCAA    300
CCGACAGAAG AGGTTCGTGC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG    360
GATCCTTCGG TTCCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC    420
CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCACG AGGGCCGTGC    480
TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGGAC GACCTGCCGT TTGATGGGCC    540
TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT    600
CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAGGGC ACAGACCTGC TGCAGGTGGC    660
AGCCCATGAA TTTGGCCACG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT    720
GTCCGCCTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGGCGT    780
TCAACACCTA TATGGCCAGC CCTGGCCCAC TGTCACCTCC AGGACCCCAG CCCTGGGCCC    840
CCAGGCTGGG ATAGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC CGCCAGATGC    900
CTGTGAGGCC TCCTTTGACG CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC    960
GGGCTTTGTG TGGCGCCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTGGCCTC   1020
TCGCCACTGG CAGGGACTGC CCAGCCCTGT GGACGCTGCC TTCGAGGATG CCCAGGGCCA   1080
CATTTGGTTC TTCCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCCTGGG   1140
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CCCCGCACCC CTCACCGAGC TGGGCCTGGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG  1200
GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCCACCC  1260
CAGCACCCGG CGTGTAGACA GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC  1320
CTCTGAGATC GACGCTGCCT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGCGCGGCCG  1380
CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCCGTCTCGT  1440
GGGTCCTGAC TTCTTTGGCT GTGCCGAGCC TGCCAACACT TTCCTCTGAC CATGGCTTGG  1500
ATGCCCTCAG GGGTGCTGAC CCCTGCCAGG CCACGAATAT CAGGCTAGAG ACCCATGGCC  1560
ATCTTTGTGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGTCTCCTGC AGGGGGATGG  1620
GGTGGGGTAC AACCACCATG ACAACTGCCG GGAGGGCCAC GCAGGTCGTG GTCACCTGCC  1680
AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT  1740
GGGACCCGCT ATGCAGGTCC TGGCAAACCT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG  1800
GTAGCACCAT GGCAGGACTG GGGGAACTGG AGTGTCCTTG CTGTATCCCT GTTGTGAGGT  1860
TCCTTCCAGG GGCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC  1920
TGAGCAACTG GGCTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCCTGC  1980
ATCTGTCTGC CTTCTGGCTG ACAATCCTGG AAATCTGTTC TCCAGAATCC AGGCCAAAAA  2040
GTTCACAGTC AAATGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG  2100
CAACATACCT CAATCCTGTC CCAGGCCGGA TCCTCCTGAA GCCCTTTTCG CAGCACTGCT  2160
ATCCTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT  2220
TTTTTAAACT GAGGATTGTC ATTAAACACA GTTGTTTTCT
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Seq ID NO: 18 Protein sequence:
Protein Accession #: NP_005931.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAPAAWLRSA AARALLPPML LLLLQPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA    60
PAPATQEAPR PASSLRPPRC GVPDPSDGLS ARNRQKRFVL SGGRWEKTDL TYRILRFPWQ   120
LVQEQVRQTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLPF DGPGGILAHA   180
FFPKTHREGD VHFDYDETWT IGDDQGTDLL QVAAHEFGHV LGLQHTTAAK ALMSAFYTFR   240
YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA   300
VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA   360
QYWVYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVDS   420
PVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDP VKVKALEGFP RLVGPDFFGC   480
AEPANTFL
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Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: NM_005794.1
Coding sequence: 434-1276

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1          11         21         31         41         51
|          |          |          |          |          |
GGTTCCCTTC CACGCTGTGA AGCTTTGTTC TTTTGGTCTT CATGATAAAT CTTGCTGCTG    60
CTCACTCGTT GGGTCCGTGC CACCTTTAAG AGCTGTAACA CTCACCGCGA AGGTCTGCAA   120
CTTCACTCCT GGGGCCAGCA AGACCACGAA TGCACCGAGA GGAATGAACA ACTCTGGACA   180
CACCATCTTT AAGAACCGTA ATACTCACCG CAAGGGTCTG CAACTTCATT CTTGAAGTCA   240
GTGAGGCCAA GAACCCATCA ATTCCGTACA CATTTTGGTG ACTTTGAAGA GACTGTCACC   300
TATCACCAAG TGGTGAGACT ATTGCCAAGC AGTGAGACTA TTGCCAAGTG GTGAGACCAT   360
CACCAAGCGG TGAGACTATC ACCTATCGCC AAGTGGCCTG ATTCAGCAGG AAGCATCTCA   420
GACACCAACC ACTATGCTGT CAGCAGTTGC CCGGGGCTAC CAGGGCTGGT TTCATCCCTG   480
TGCTAGGCTT TCTGTGAGGA TGAGCAGCAC CGGGATAGAC AGGAAGGGCG TCCTGGCTAA   540
CCGGGTAGCC GTGGTCACGG GGTCCACCAG TGGGATCGGC TTTGCCATCG CCCGACGTCT   600
GGCCCGGGAC GGGGCCCACG TGGTCATCAG CAGCCGGAAG CAGCAGAACG TGGACCGGGC   660
CATGGCCAAG CTGCAGGGGG AGGGGCTGAG TGTGGCGGGC ATTGTGTGCC ACGTGGGGAA   720
GGCTGAGGAC CGGGAGCAGC TGGTGGCCAA GGCCCTGGAG CACTGTGGGG GCGTCGACTT   780
CCTGGTGTGC AGCGCAGGGG TCAACCCTCT GGTAGGGAGC ACTCTGGGGA CCAGTGAGCA   840
GATCTGGGAC AAGATCCTAA GTGTGAACGT GAAGTCCCCA GCCCTGCTGC TGAGCCAGTT   900
GCTGCCCTAC ATGGAGAACA GGAGGGGTGC TGTCATCCTG GTCTCTTCCA TTGCAGCTTA   960
TAATCCAGTA GTGGCGCTGG GTGTCTACAA TGTCAGCAAG ACAGCGCTGC TGGGTCTCAC  1020
TAGAACACTG GCATTGGAGC TGGCCCCCAA GGACATCCGG GTAAACTGCG TGGTTCCAGG  1080
AATTATAAAA ACTGACTTCA GCAAAGTGTT TCATGGGAAT GAGTCTCTCT GGAAGAACTT  1140
CAAGGAACAT CATCAGCTGC AGAGGATTGG GGAGTCAGAG GACTGTGCAG GAATCGTGTC  1200
CTTCCTGTGC TCTCCAGATG CCAGCTACGT CAACGGGGAG AACATTGCGG TGGCAGGCTA  1260
CTCCACTCGG CTCTGAGAGG AGTGGGGGCG GCTGCGTAGC TGTGGTCCCA GCCCAGGAGC  1320
CTGAGGGGGT GTCTAGGTGA TCATTTGGAT CTGGAGCAGA GTCTGCCATT CTGCCAGACT  1380
AGCAATTTGG GGGCTTACTC ATGCTAGGCT TGAGGAAGAA GAAAAACGCT TCGGCATTCT  1440
CC
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Seq ID NO: 20 Protein sequence:
Protein Accession #: NP_005785.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MLSAVARGYQ GWFHPCARLS VRMSSTGIDR KGVLANRVAV VTGSTSGIGF AIARRLARDG    60
AHVVISSRKQ QNVDRAMAKL QGEGLSVAGI VCHVGKAEDR EQLVAKALEH CGGVDFLVCS   120
AGVNPLVGST LGTSEQIWDK ILSVNVKSPA LLLSQLLPYM ENRRGAVILV SSIAAYNPVV   180
ALGVYNVSKT ALLGLTRTLA LELAPKDIRV NCVVPGIIKT DFSKVFHGNE SLWKNFKEHH   240
QLQRIGESED CAGIVSFLCS PDASYVNGEN IAVAGYSTRL
```

Seq ID NO: 21 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 77-904

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1          11         21         31         41         51
|          |          |          |          |          |
GCCGCGTTTT GCCTCCGCAG CAGCTCTGGG CTCTTCTCAG CTGCGCGAGC AGCTGCTCCA     60
ATGCCCCGGA GTGGCCATGG GCGCCCCGCA CTGGTGGGAC CAGCTGCAGG CTGGTAGCTC    120
GGAGGTGGAC TGGTGCGAGG ACAACTACAC CATCGTGCCT GCTATCGCCG AGTTCTACAA    180
CACGATCAGC AATGTCTTAT TTTTCATTTT ACCGCCCATC TGCATGTGCT TGTTTCGTCA    240
GTATGCAACA TGCTTCAACA GTGGCATCTA CTTAATCTGG ACTCTTTTGG TTGTAGTGGG    300
AATTGGATCC GTCTACTTCC ATGCAACCCT TAGTTTCTTG GGTCAGATGC TTGATGAACT    360
TGCAGTCCTT TGGGTTCTGA TGTGTGCTTT GGCCATGTGG TTCCCCAGAA GGTATCTACC    420
AAAGATCTTT CGGAATGACC GGGGTAGGTT CAAGGTGGTG GTCAGTGTCC TGTCTGCGGT    480
TACGACGTGC CTGGCATTTG TCAAGCCTGC CATCAACAAC ATCTCTCTGA TGACCCTGGG    540
AGTTCCTTGC ACTGCACTGC TCATCGCAGA GCTAAAGAGG TGTGACAACA TGCGTGTGTT    600
TAAGCTGGGC CTCTTCTCGG GCCTCTGGTG GACCCTGGCC CTGTTCTGCT GGATCAGTGA    660
CCGAGCTTTC TGCGAGCTGC TGTCATCCTT CAACTTCCCC TACCTGCACT GCATGTGGCA    720
CATCCTCATC TGCCTTGCTG CCTACCTGGG CTGTGTATGC TTTGCCTACT TTGATGCTGC    780
CTCAGAGATT CCTGAGCAAG GCCCTGTCAT CAAGTTCTGG CCCAATGAGA AATGGGCCTT    840
CATTGGTGTC CCCTATGTGT CCCTCCTGTG TGCCAACAAG AAATCATCAG TCAAGATCAC    900
GTGATGGCAA GATGGTGGCT GGCTTCTCTG CTTATCGCCC CTCATGCAGT GGGCTTCCTT    960
TGCTAGGAAG ACAGCCAAGG GAGTTCGAAT AGTTGGGGTG TGGGCTATCT TTTCAAAAAT   1020
CTATTTGCTG GGGCTCTTAA TTTCTTTAGT GTTCTTTGTA TGTAGGGATT TAAACTTTGT   1080
CATATGGTAC AAATATTCCC TGCCCCCCTG CAGTTTCCCA TTTGTCTTTC AGTATGTTAA   1140
TATTTTTGTG CCATACTGGT TTTAAACTTT CATGTTGTCA CATCTGTTAA TCTTTTCTTT   1200
AGGATTTCTG GATTTTGTGT AATTTTTAAA AAGGTCCCCT CCTCCTCCCT AATGTGTCTG   1260
TGGACCACCT GGATTCCACT GTACAAGGGG AAAAGTGTCT ATTCCTTTCC CAAAGATGGA   1320
AAATGGAGGG CTTAGGGACA CTAGATGCAT CTTTCTCAGC ATCACTTCCA GATGCAGTGA   1380
CTTGTTGGGC TGCGTCCTTA ATGGCCATGG CAGAGCAGTC CCTTGGGGGA TCCAGCCCTG   1440
TACAATGCAT CTCTTCCTGG AGAAAGCTGG CCTGCTCCAG ACCCCACCAT TCCCAGGCGC   1500
CCTTGGAGTG GACTCTACTG ATGACAGACA GACCCTCTGA GAGACAAGAC CCTCTGACTC   1560
TGTGATGGAA GATGCCAGAG ATTTTCCTTT GGGGTAATTG TCCTTAAACA AAACCAAACA   1620
GATGAAACAC ACACAGGACT TGTGGCTAAA AAGGCTAGTT TTTCACTTGC ATTTCTCAAC   1680
TAACCCAGGT TTTACATGCA TCTGTGAATC CTTTTACTAC TACCTCTGTG GAGAGATGGA   1740
GAGACTTCAG ATAAACGTGA AGCTAATGAG TAAAACCCTC TCTGCCAAAA CCTACACTCC   1800
ACTTTAGGCC CTTCTTGAAG ATGAGCACAA TTTTTAAATA CTGAGCACAA TTTTTAAATA   1860
CTGACATCAC TTCCTCTTCC CCCTCCCACC CCAGCTCAGC AGCCTCAAAT CTACAGAGAA   1920
GAAGAATTAT GGCATGAACA TTCCCACAGA CCCACCATCT TTAAGACTTG ACCTCTGTAA   1980
GTTTACCAAA GGGCTCCTCA CAATTGTGGT GGGGGTTCTG GTTCAAAATT TGGAGCAAAC   2040
ATGAAGTTTT TGGAAACGTT TTCTCATTTG AAGCCTCCAG TATGCTGTAC TATTCTGGAA   2100
ATTACCTTCA AGAGTCTCAC TTCTTGTTTC TGTTGTGTTT TCTGTGGGCA TCATGTTCTT   2160
CACGCTTGCA GTAGAAGGTG CTTTCTCGGT TTCCCAGAGT ATCCAACGGC TCACCTTTCT   2220
CAAGTGCTGG CAGTAGCTAT GCACTCACGG GCTGGTTTGG GTCGCTGGTG CAGCAGCGCA   2280
AATCTGTTGC CTTCTGAATT TTTCTCACCT AATGTGACAC TGGCTACAAT GAATCTTCTC   2340
TTCATCGGGC TGAATGAAAG ATTCAAGAAC CATCTTCAAG GTGCATGGTG GGAATTATCA   2400
ACCTCAGGGA TACTCATTTT AACTCAGGCG TGTCCTGCTT TGTAACATTC CATTGTTGGG   2460
AGAGGGCAGG ACAGGTGTGT TCTTCTGTGG GCAGGAGTCA TGTCACTGTC CTACATATGT   2520
AAGAGTTGGG AAGGTGACGA TTTTTGACAC ATCCAGGAAC TCTTACTCTA GTTAGAATTT   2580
GTACCAGATC CAAGGTGAAA ACCCCAATAA GCAACTGAAT TTAGAGTTTA AAAATGAATG   2640
ACTTTATGCT ACATCTGTGG TTATCAAATT ATATAGGTTG TTGAGAAGCA GAACGCTGTT   2700
TGTAGTAAGA AATCTTTGTG GAACCCCAGT GTGTGAAGTA AATTGTATGT TATTAAATTT   2760
ATTTAAGGTT AAATTTATGG CATTTACTTA ATAATATATG AGGTGGTGAA AATGCAAATT   2820
AACAAATTGG TAATTTCCAA GGTAGAAAAA TTAGGTGTTG AATGAATGTA TATGTTGGTT   2880
TATTATAGTT TTATATATAT ATAGAGAGAG TGTTTTGTTT TTGAGTCAGG GTCTTGCTCT   2940
ATTACCCAGG CTGGAGTGCA GTGGTGCAGT CATGACTCAC TGTAGCCTCT GTCTCCCAGG   3000
CTCAAGTGAT CCTCTCACCT CAGCCTCCCC AGGAGCTGGG AGTACTGGTG CGTGCCTCCA   3060
CTCCCAGCTA ATTTTTGTAT TTTTTCATAG AGATGGGGTT TCACCATTTT GCCCAGGCTG   3120
GTCTCAAACT TCTGGGCTCA AGAGATTCGC CCGCCTCGGC CTCCCAAAGT GCTGGGAATA   3180
GGCATGAGCC GTCACGCCTG GCCTAAAAAA TATTTTTAAA ATGATCTTTG AATTAAATAT   3240
TCGTAGAATT TCTAATGTAT CTCTTTGAGA CCTAGGAGGT TGATGGAACA GAACTGCTGT   3300
TAAGTCCTTT GGGTTTCAAG TCTAGAATTT TTTAAAGGCA AATATCAGCT CATTCTTATT   3360
TTAGATTGAC CTTATCAGGC ATGGATTCTG GTCTCATCTA CTTTATGGTA TAAATGCTCC   3420
AAGGTAGGGG GTTTGGTATA TATTTTAAGC CCGGCTTTTT TTTTTTTTTT TTTTTTTTTT   3480
TTTTTAATGT GAGAAGCAGA ATGTGCTTCT AGAAACTGGT TTTAAAGAGA TGAGCTGAGA   3540
AAGAAATGTG GAATGGAGTA TATTTGAGGA GGACAAAACA TAACTTCACT TTTGAACAGA   3600
AATCACTCTA GCTTGCCAGC ATGGGATGTA AACCAAGAGA GTAGAAATAT ACCCATCTTA   3660
TTTTAAGTTG GGTTTATGGC ATCGCTCATA TATGTAAAAG CACTACAAAC TCTTTAAAGA   3720
AAATTGGGAA ACTACAGAGA AGTCAAAGAA AAAAAAAAGT AACCCATATT TCTATTGCCC   3780
AGGTATAATC CTTGTTAATA TTTTGGTTTG GTCTCCTCTT TTTTTCCCCC AATATAGTTG   3840
TAAATAAATG ATGTCTTTCA GAGTTGACAT TTATCCTGTA GCTTGAATGG CATGTAAATG   3900
CCAGTTGTAT ATTTTTTCAT GAAGTGTAGG TTTGGAATAC ACTAGAGTTA GCTATATGCT   3960
TGAATGCTGA TCACTGGATT CTGAGACTGA CTACTGAGTC TACCTTTTTA ATCAAGCCTA   4020
ACATGAATGG GCTCCAAAAA GTAATGAATG TAATTGTACT TTTTGATGTG CCTCTGCACT   4080
TGGCTTGGTG AGTCATCATA AATAGCTGTT AAATATGTGA CTTTACAGAT TTTGATATGT   4140
TCAGATTGTA AAAAATGAAT AGTTTATTTC ATTAATTGAT GGGCAGTCAA GAATCTCCCT   4200
CC
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Seq ID NO: 22 Protein sequence:
Protein Accession #: EOS sequence

1          11         21         31         41         51
|          |          |          |          |          |
MGAPHWWDQL QAGSSEVDWC EDNYTIVPAI AEFYNTISNV LFFILPPICM CLFRQYATCF    60
NSGIYLIWTL LVVVGIGSVY FHATLSFLGQ MLDELAVLWV LMCALAMWFP RRYLPKIFRN   120
DRGRFKVVVS VLSAVTTCLA FVKPAINNIS LMTLGVPCTA LLIAELKRCD NMRVFKLGLF   180
SGLWWTLALF CWISDRAFCE LLSSFNFPYL HCMWHILICL AAYLGCVCFA YFDAASEIPE   240
QGPVIKFWPN EKWAFIGVPY VSLLCANKKS SVKIT
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Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: CAT cluster

1          11         21         31         41         51
|          |          |          |          |          |
TGAAGTATCT CTGTTTAATG TCATATATCT GAGATGTTCT GTGGAGCCAG AATTCAAAAC    60
CCAGATACGC AGGAGGACAC ATTCTTGATC GGTATTTTAT TCTATTATTT TTATTAGTTC   120
CAATCCTTAT GACTCTGTTT AAAATGAGTA TCTGCATTAT TGTGCAAACA CTTCTGAGAT   180
CTCATCACAT ACCTGATCCC ATTTAACTTC AGTCTATCCC TCCATTACTT TTTGTGGAAA   240
GTGCTATCTA AGTTGGAGGT TCTGCTTGAG TATTCTTAAT TTTTCTTCTT TTTAATGCAT   300
ACGGTGGTCA AAGTAAATAG CTAACATATT GGCATCAAAC CATTGCCTAT TGAAGCAAGC   360
TTTGAATGAA ATTGGTTTGT CATTGACCAC TGTAAGAAAC TCATTTGTAA AGATAATACT   420
GAAAAACATC CTGACTCTTA TGTATGCTTG CCTGTCTCTG AACTCCACCT CTATCAGCAT   480
ACTCAATACA TTGCCTCTTT CCAACATTTA TCTCCTATTT CAGGAGAAAG TTTTGTGGGA   540
GCGTCTACCA CGTTGCAAAG ATTCAACATT TCTCTTAAAA ATAGGAGTTT CTTTTAGATA   600
TAAGCAATGA AATTTCAAGC AACAATATTA CTTCTCTCAT GTCCTTTGCT TTTTTAAGAT   660
CTGAACCTCA AGATTCAAAT GGATTTTCAT TGAAATTCAC CACGATCCCC TCTGCAGCTG   720
TGGTCTGAAA GTACCATTTC TGCATTTATT TTAGCCCATG GAATAACTGT GCTGAGAAAC   780
CACAGAGTCA ATCAGATTCA AAATGTTAAA ATCCTTCCTG CTTGGAGTTT TCCGTCTTCA   840
CATCAAAGCA TTTCATGCCC GTCAGCAACT TTTTAATGCA TTTGCTCATG GTTTGCAGAA   900
TTTCCATTTA AAGACTTTCC TTGGCTGACT TCTCTGATGA GGTTTCCTGC TTGCCTC
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Seq ID NO: 24 DNA sequence
Nucleic Acid Accession #: Eos sequence

1          11         21         31         41         51
|          |          |          |          |          |
GTGTGTAGTC GGGTATGAGA ACGATTGCAA GCAAAAGCAG CTGAGGGACG CTGTCCAAGG    60
AGTAGGCTCA GTAGCACGAA CTGCAAATAC TTGAGAAGGG AAAAGTTCAG CCTTGTGCTG   120
GAAAGTGGTT TAGCATGCTG GAGCTGGTTT TCTGCTTGGT AGCCCTACAA CTTTGGCCCA   180
ACTACTTGGC CTCTGGGACT CAGATTCCTC CTCTTTAAAA TGGTGCTAAT AATAGCACCC   240
ACCCTCTGTG AGGAGGATGC TGTGAGGACA AAATGAGATC ATCCACATAA GCCGTGAACC   300
CTGTTCCTGG TAAGCTCCTG GAAAGAAGTC TATGGATTAT ACTCAACCTA CACTCCAGTT   360
AAAGGAACAT CTACACACAG AGGAAATGAA TAACATGAAG TGAAGTCTTC ATCTCCATTC   420
CCAACAGTCC CCATTCTACT TGCAGAAAGG TTGCTTACAC TGAAAATCAG TTTATTTTCC   480
CCTGGTGCAA AGAACAGTCG TTTCTCCAAA ACTGAAGCTG GAAATTATCT GAAATATCAG   540
GTCCTCCGGA AAAGGGACGT GAAGCCCCCT TTGTAATTTC TGCATTAGCG TGCTCTCCTG   600
GCAAGCAGGA AACCTCATCA GAGAAGTCAG CCAAGGAAAG TCTTTAAATG GAAATTGTGC   660
AAACGAGGAG CAAATGCATT AAAAAGTTGC TGACGGGCAT GAAATGCTTT GATGTGAAGA   720
CGGAAAACTC CAAGCAGGAA GGATTTTAAC ATTTTGAATC TGATTGACTC TGTGGTTTCT   780
CAGCACAGTT ATTCCATGGG CTAAAATAAA TGCAGAAATG GTACTTTCAG ACCACAGCTG   840
CAGAGGGGAT CGTGGTGAAT TTCAATGAAA ATCCATTTGA ATCTTGAGGT TCAGATCTTA   900
AAAAAGCAAA GGACATGAGA GAAGTAATAT TGTTGCTTGA AATTTCATTG CTTATATCTA   960
AAAGAAACTC CTATTTTTAA GAGAAATGTT GAATCTTTGC AACGTGGTAG ACGCTCCCAC  1020
AAAACTTTCT CCTGAAATAG GAGATAAATG TTGGAAAGAG GCAATGTATT GAGTATGCTG  1080
ATAGAGGTGG AGTTCAGAGA CAGGCAAGCA TACATAAGAG TCAGGATGTT TTTCAGTATT  1140
ATCTTTACAA ATGAGTTTCT TACAGTGGTC AATGACAAAC CAATTTCATT CAAAGCTTGC  1200
TTCAATAGGC AATGGTTTGA TGCCAATATG TTAGCTATTT ACTTTGACCA CCGTATGCAT  1260
TAAAAAGAAG AAAAATTAAG AATACTCAAG CAGAACCTCC AACTTAGATA GCACTTTCCA  1320
CAAAAAGTAA TGGAGGGATA GACTGAAGTT AAATGGGATC AGGTATGTGA TGAGATCTCA  1380
GAAGTGTTTG CACAATAATG CAGATACTCA TTTTAAACAG AGTCATAAGG ATTGGAACTA  1440
ATAAAAATAA TAGAATAAAA TACCGATCAA GAATGTGTCC TCCTGCGTAT CTGGGTTTTG  1500
AATTCTGGCT CCACAGAACT TGTCAGATAT ATGACATTAA AC
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Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: Eos sequence

1          11         21         31         41         51
|          |          |          |          |          |
GTGTGTAGTC GGGTATGAGA ACGATTGCAA GCAAAAGCAG CTGAGGGACG CTGTCCAAGG    60
AGTAGGCTCA GTAGCACGAA CTGCAAATAC TTGAGAAGGG AAAAGTTCAG CCTTGTGCTG   120
GAAAGTGGTT TAGCATGCTG GAGCTGGTTT TCTGCTTGGT AGCCCTACAA CTTTGGCCCA   180
ACTACTTGGC CTCTGGGACT CAGATTCCTC CTCTTTAAAA TGGTGCTAAT AATAGCACCC   240
ACCCTCTGTG AGGAGGATGC TGTGAGGACA AAATGAGATC ATCCACATAA GCCGTGAACC   300
CTGTTCCTGG TAAGGAAATG AATAACATGA AGTGAAGTCT TCATCTCCAT TCCCAACAGT   360
CCCCATTCTA CTTGCAGAAA GGTTGCTTAC ACTGAAAATC AGTTTATTTT CCCCTGGTGC   420
AAAGAACAGT CGTTTCTCCA AAACTGAAGC TGGAAATTAT CTGAAATATC AGGTCCTCCG   480
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GAAAAGGGAC GTGAAGCCCC CTTTGTAATT TCTGCATTAG CGTGCTCTCC TGGCAAGCAG   540
GAAACCTCAT CAGAGAAGTC AGCCAAGGAA AGTCTTTAAA TGGAAATTGT GCAAACGAGG   600
AGCAAATGCA TTAAAAAGTT GCTGACGGGC ATGAAATGCT TTGATGTGAA GACGGAAAAC   660
TCCAAGCAGG AAGGATTTTA ACATTTTGAA TCTGATTGAC TCTGTGGTTT CTCAGCACAG   720
TTATTCCATG GGCTAAAATA AATGCAGAAA TGGTACTTTC AGACCACAGC TGCAGAGGGG   780
ATCGTGGTGA ATTTCAATGA AAATCCATTT GAATCTTGAG GTTCAGATCT TAAAAAAGCA   840
AAGGACATGA GAGAAGTAAT ATTGTTGCTT GAAATTTCAT TGCTTATATC TAAAAGAAAC   900
TCCTATTTTT AAGAGAAATG TTGAATCTTT GCAACGTGGT AGACGCTCCC ACAAAACTTT   960
CTCCTGAAAT AGGAGATAAA TGTTGGAAAG AGGCAATGTA TTGAGTATGC TGATAGAGGT   1020
GGAGTTCAGA GACAGGCAAG CATACATAAG AGTCAGGATG TTTTTCAGTA TTATCTTTAC   1080
AAATGAGTTT CTTACAGTGG TCAATGACAA ACCAATTTCA TTCAAAGCTT GCTTCAATAG   1140
GCAATGGTTT GATGCCAATA TGTTAGCTAT TTACTTTGAC CACCGTATGC ATTAAAAAGA   1200
AGAAAAATTA AGAATACTCA AGCAGAACCT CCAACTTAGA TAGCACTTTC CACAAAAAGT   1260
AATGGAGGGA TAGACTGAAG TTAAATGGGA TCAGGTATGT GATGAGATCT CAGAAGTGTT   1320
TGCACAATAA TGCAGATACT CATTTTAAAC AGAGTCATAA GGATTGGAAC TAATAAAAAT   1380
AATAGAATAA AATACCGATC AAGAATGTGT CCTCCTGCGT ATCTGGGTTT TGAATTCTGG   1440
CTCCACAGAA CTTGTCAGAT ATATGACATT AAAC
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Seq ID NO: 26 DNA sequence
Nucleic Acid Accession #: NM_013282.2
Coding sequence: 85..2466

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1          11         21         31         41         51
|          |          |          |          |          |
CGACTCCTTA GAGCATGGCA TGGCTCAGAG GTGCTGGTAA AACTGATGGG GGTTTTTGCT   60
GTCCCTCCCC TCAGCGCCGA CACCATGTGG ATCCAGGTTC GGACCATGGA CGGGAGGCAG   120
ACCCACACGG TGGACTCGCT GTCCAGGCTG ACCAAGGTGG AGGAGCTGAG GCGGAAGATC   180
CAGGAGCTGT TCCACGTGGA GCCAGGCCTG CAGAGGCTGT TCTACAGGGG CAAACAGATG   240
GAGGACGGCC ATACCCTCTT CGACTACGAG GTCCGCCTGA ATGACACCAT CCAGCTCCTG   300
GTCCGCCAGA GCCTCGTGCT CCCCCACAGC ACCAAGGAGC GGGACTCCGA GCTCTCCGAC   360
ACCGACTCCG GCTGCTGCCT GGGCCAGAGT GAGTCAGACA AGTCCTCCAC CCACGGCGAG   420
GCGGCCGCCG AGACTGACAG CAGGCCAGCC GATGAGGACA TGTGGGATGA GACGGAATTG   480
GGGCTGTACA AGGTCAATGA GTACGTCGAT GCTCGGGACA CGAACATGGG GGCGTGGTTT   540
GAGGCGCAGG TGGTCAGGGT GACGCGGAAG GCCCCCTCCC GGGACGAGCC CTGCAGCTCC   600
ACGTCCAGGC CGGCGCTGGA GGAGGACGTC ATTTACCACG TGAAATACGA CGACTACCCG   660
GAGAACGGCG TGGTCCAGAT GAACTCCAGG GACGTCCGAG CGCGCGCCCG CACCATCATC   720
AAGTGGCAGG ACCTGGAGGT GGGCCAGGTG GTCATGCTCA ACTACAACCC CGACAACCCC   780
AAGGAGCGGG GCTTCTGGTA CGACGCGGAG ATCTCCAGGA AGCGCGAGAC CAGGACGGCG   840
CGGGAACTCT ACGCCAACGT GGTGCTGGGG GATGATTCTC TGAACGACTG TCGGATCATC   900
TTCGTGGACG AAGTCTTCAA GATTGAGCGG CCGGGTGAAG GGAGCCCCAT GGTTGACAAC   960
CCCATGAGAC GGAAGAGCGG GCCGTCCTGC AAGCACTGCA AGGACGACGT GAACAGACTC   1020
TGCCGGGTCT GCGCCTGCCA CCTGTGCGGG GGCCGGCAGG ACCCCGACAA GCAGCTCATG   1080
TGCGATGAGT GCGACATGGC CTTCCACATC TACTGCCTGG ACCCGCCCCT CAGCAGTGTT   1140
CCCAGCGAGG ACGAGTGGTA CTGCCCTGAG TGCCGGAATG ATGCCAGCGA GGTGGTACTG   1200
GCGGGAGAGC GGCTGAGAGA GAGCAAGAAG AAGGCGAAGA TGGCCTCGGC CACATCGTCC   1260
TCACAGCGGG ACTGGGGCAA GGGCATGGCC TGTGTGGGCC GCACCAAGGA ATGTACCATC   1320
GTCCCGTCCA ACCACTACGG ACCCATCCCG GGGATCCCCG TGGGCACCAT GTGGCGGTTC   1380
CGAGTCCAGG TCAGCGAGTC GGGTGTCCAT CGGCCCCACG TGGCTGGCAT ACACGGCCGG   1440
AGCAACGACG GAGCGTACTC CCTAGTCCTG GCGGGGGGCT ATGAGGATGA CGTGGACCAT   1500
GGGAATTTTT TCACATACAC GGGTAGTGGT GGTCGAGATC TTTCCGGCAA CAAGAGGACC   1560
GCGGAACAGT CTTGTGATCA GAAACTCACC AACACCAACA GGGCGCTGGC TCTCAACTGC   1620
TTTGCTCCCA TCAATGACCA AGAAGGGGCC GAGGCCAAGG ACTGGCGGTC GGGGAAGCCG   1680
GTCAGGGTGG TGCGCAATGT CAAGGGTGGC AAGAATAGCA AGTACGCCCC CGCTGAGGGC   1740
AACCGCTACG ATGGCATCTA CAAGGTTGTG AAATACTGGC CCGAGAAGGG GAAGTCCGGG   1800
TTTCTCGTGT GGCGCTACCT TCTGCGGAGG GACGATGATG AGCCTGGCCC TTGGACGAAG   1860
GAGGGGAAGG ACCGGATCAA GAAGCTGGGG CTGACCATGC AGTATCCAGA AGGCTACCTG   1920
GAAGCCCTGG CCAACCGAGA GCGAGAGAAG GAGAACAGCA AGAGGGAGGA GGAGGAGCAG   1980
CAGGAGGGGG GCTTCGCGTC CCCCAGGACG GGCAAGGGCA AGTGGAAGCG GAAGTCGGCA   2040
GGAGGTGGCC CGAGCAGGGC CGGGTCCCCG CGCCGGACAT CCAAGAAAAC CAAGGTGGAG   2100
CCCTACAGTC TCACGGCCCA GCAGAGCAGC CTCATCAGAG AGGACAAGAG CAACGCCAAG   2160
CTGTGGAATG AGGTCCTGGC GTCACTCAAG GACCGGCCGG CGAGCGGCAG CCCGTTCCAG   2220
TTGTTCCTGA GTAAAGTGGA GGAGACGTTC CAGTGTATCT GCTGTCAGGA GCTGGTGTTC   2280
CGGCCCATCA CGACCGTGTG CCAGCACAAC GTGTGCAAGG ACTGCCTGGA CAGATCCTTT   2340
CGGGCACAGG TGTTCAGCTG CCCTGCCTGC CGCTACGACC TGGGCCGCAG CTATGCCATG   2400
CAGGTGAACC AGCCTCTGCA GACCGTCCTC AACCAGCTCT TCCCCGGCTA CGGCAATGGC   2460
CGGTGATCTC CAAGCACTTC TCGACAGGCG TTTTGCTGAA AACGTGTCGG AGGGCTCGTT   2520
CATCGGCACT GATTTTGTTC TTAGTGGGCT TAACTTAAAC AGGTAGTGTT TCCTCCGTTC   2580
CCTAAAAAGG TTTGTCTTCC TTTTTTTTTA TTTTTATTTT TCAAATCTAT ACATTTTCAG   2640
GAATTTATGT ATTCTGGCTA AAAGTTGGAC TTCTCAGTAT TGTGTTTAGT TCTTTGAAAA   2700
CATAAAAGCC TGCAATTTCT CGACAAAACA ACACAAGATT TTTTAAAGAT GGAATCAGAA   2760
ACTACGTGGT GTGGAGGCTG TTGATGTTTC TGGTGTCAAG TTCTCAGAAG TTGCTGCCAC   2820
CAACTCTTTA AGAAGGCGAC AGGATCAGTC CTTCTCTAGG GTTCTGGCCC CCAAGGTCAG   2880
AGCAAGCATC TTCCTGACAG CATTTTGTCA TCTAAAGTCC AGTGACATGG TTCCCCGTGG   2940
TGGCCCGTGG CAGCCCGTGG CATGGCGTGG CTCAGCTGTC TGTTGAAGTT GTTGCAAGGA   3000
AAAGAGGAAA CATCTCGGGC CTAGTTCAAA CCTTTGCCTC AAAGCCATCC CCCACCAGAC   3060
TGCTTAGCGT CTGAGATCCG CGTGAAAAGT CCTCTGCCCA CGAGAGCAGG GAGTTGGGGC   3120
CACGCAGAAA TGGCCTCAAG GGGACTCTGC TCCACGTGGG GCCAGGCGTG TGACTGACGC   3180
TGTCCGACGA AGGCGGCCAC GGACGGACGC CAGCACACGA AGTCACGTGC AAGTGCCTTT   3240
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GATTCGTTCC TTCTTTCTAA AGACGACAGT CTTTGTTGTT AGCACTGAAT TATTGAAAAT   3300
GTCAACCAGA TTCTAGAAAC TGCGGTCATC CAGTTCTTCC TGACACCGGA TGGGTGCTTG   3360
GGAACCGTTT GAGCCTTATA GATCATTTAC ATTCAATTTT TTTAACTCAG CAAGTGAGAA   3420
CTTACAAGAG GGTTTTTTTT TAATTTTTTT TTCTCTTAAT GAACACATTT TCTAAATGAA   3480
TTTTTTTTGT AGTTACTGTA TATGTACCAA GAAAGATATA ACGTTAGGGT TTGGTTGTTT   3540
TTGTTTTTGT ATTTTTTTTC TTTTGAAAGG GTTTGTTAAT TTTTCTAATT TTACCAAAGT   3600
TTGCAGCCTA TACCTCAATA AAACAGGGAT ATTTTAAATC ACATACCTGC AGACAAACTG   3660
GAGCAATGTT ATTTTTAAAG GGTTTTTTTC ACCTCCTTAT TCTTAGATTA TTAATGTATT   3720
AGGGAAGAAT GAGACAATTT TGTGTAGGCT TTTTCTAAAG TCCAGTACTT TGTCCAGATT   3780
TTAGATTCTC AGAATAAATG TTTTTCACAG ATTGAAAAAA AAAAAAAA                3828
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Seq ID NO: 27 Protein Sequence
Protein Accession #: NP_037414.2

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1          11         21         31         41         51
|          |          |          |          |          |
MWIQVRTMDG RQTHTVDSLS RLTKVEELRR KIQELPHVEP GLQRLFYRGK QMEDGHTLFD   60
YEVRLNDTIQ LLVRQSLVLP HSTKERDSEL SDTDSGCCLG QSESDKSSTH GEAAAETDSR   120
PADEDMWDET ELGLYKVNEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTSRPALEE   180
DVIYHVKYDD YPENGVVQMN SRDVRARART IIKWQDLEVG QVVMLNYNPD NPKERGFWYD   240
AEISRKRETR TARELYANVV LGDDSLNDCR IIFVDEVFKI ERPGEGSPMV DNPMRRKSGP   300
SCKHCKDDVN RLCRVCACHL CGGRQDPDKQ LMCDECDMAF HIYCLDPPLS SVPSEDEWYC   360
PECRNDASEV VLAGERLRES KKKAKMASAT SSSQRDWGKG MACVGRTKEC TIVPSNHYGP   420
IPGIPVGTMW RFRVQVSESG VHRPHVAGIH GRSNDGAYSL VLAGGYEDDV DHGNFFTYTG   480
SGGRDLSGNK RTAEQSCDQK LTNTNRALAL NCFAPINDQE GAEAKDWRSG KPVRVVRNVK   540
GGKNSKYAPA EGNRYDGIYK VVKYWPEKGK SGFLVWRYLL RRDDDEPGPW TKEGKDRIKK   600
LGLTMQYPEG YLEALANRER EKENSKREEE EQQEGGFASP RTGKGKWKRK SAGGGPSRAG   660
SPRRTSKKTK VEPYSLTAQQ SSLIREDKSN AKLWNEVLAS LKDRPASGSP FQLFLSKVEE   720
TFQCICCQEL VFRPITTVCQ HNVCKDCLDR SFRAQVFSCP ACRYDLGRSY AMQVNQPLQT   780
VLNQLFPGYG NGR
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Seq ID NO: 28 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence:186..776

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1          11         21         31         41         51
|          |          |          |          |          |
AGAAACTCAG AGACCAAGTC CATTGAGAGA CTGAGGGGAA AGAGAGGAGA GAAAGAAAAA   60
GAGAGTGGGA ACAGTAAAGA GAAAGGAAGA CAACCTCCAG AGAAAGCCCC CGGAGACGTC   120
TCTCTGCAGA GAGGCGGCAG CACCCGGCTC ACCTGCGAAG CGCCTGGGAA GCGAGTGCCC   180
CTAACATGCG GCTGCCGCTG CTTGTGTCCG CGGGAGTCCT GCTGGTGGCT CTCCTGCCCT   240
GCCCGCCATG CAGGGCGCTC CTGAGCCGCG GGCCGGTCCC GGGAGCTCGG CAGGCGCCGC   300
AGCACCCTCA GCCCTTGGAT TTCTTCCAGC CGCCGCCGCA GTCCGAGCAG CCCCAGCAGC   360
CGCAGGCTCG GCCGGTCCTG CTCCGCATGG GAGAGGAGTA CTTCCTCCGC CTGGGGAACC   420
TCAACAAGAG CCCGGCCGCT CCCCTTTCGC CCGCCTCCTC GCTCCTCGCC GGAGGCAGCG   480
GCAGCCGCCC TTCGCCGGAA CAGGCGACCG CCAACTTTTT CCGCGTGTTG CTGCAGCAGC   540
TGCTGCTGCC TCGGCGCTCG CTCGACAGCC CCGCGGCTCT CGCGGAGCGC GGCGCTAGGA   600
ATGCCCTCGG CGGCCACCAG GAGGCACCGG AGAGAGAAAG GCGGTCCGAG GAGCCTCCCA   660
TCTCCCTGGA TCTCACCTTC CACCTCCTCC GGGAAGTCTT GGAAATGGCC AGGGCCGAGC   720
AGTTAGCACA GCAAGCTCAC AGCAACAGGA AACTCATGGA GATTATTGGG AAATAAAACG   780
GTGCGTTTGG CCAAAAAGAA TCTGCATTTA GCACAAAAAA AATTTAAAAA AATACAGTAT   840
TCTGTACCAT AGCGCTGCTC TTATGCCATT TGTTTATTTT TATATAGCTT GAAACATAGA   900
GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAAGTGTA TTCACGTGCA   960
GCAGCAACAC AATGTTATTC GTTTTGTCTA CGTTTAGTTT CCGTTTCCAG GTGTTTATAG   1020
TGGTGTTTTA AAGAGAATGT AGACCTGTGA GAAAACGTTT TGTTTGAAAA AGCAGACAGA   1080
AGTCACTCAA TTGTTTTTGT TGTGGTCTGA GCCAAAGAGA ATGCCATTCT CTTGGGTGGG   1140
TAAGACTAAA TCTGTAAGCT CTTTGAAACA ACTTTCTCTT GTAAACGTTT CAGTAATAAA   1200
ACATCTTTCC AGTCCTTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT   1260
TAATAAAAGT TGCAAAGGT
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Seq ID NO: 29 Protein Sequence
Protein Accession #: NP_000747.1

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1          11         21         31         41         51
|          |          |          |          |          |
MRLPLLVSAG VLLVALLPCP PCRALLSRGP VPGARQAPQH PQPLDFFQPP PQSEQPQQPQ   60
ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SSLLAGGSGS RPSPEQATAN FFRVLLQQLL   120
LPRRSLDSPA ALAERGARNA LGGHQEAPER ERRSEEPPIS LDLTFHLLRE VLEMARAEQL   180
AQQAHSNRKL MEIIGK
```

Seq ID NO: 30 DNA sequence
Nucleic Acid Accession #: CAT cluster

```
1          11         21         31         41         51
|          |          |          |          |          |
ATTTCTTGAG ATGGCTCCTC TTGGAACTAT GCATCTCTCC TGATACTTGG ATGCTTTTCC   60
TCTGACTGAT GAAGATCCTG AATACCAAAG AGGGCCGCTG AAAGGGCTCT AGGAGTACAC   120
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CTTCTAGGAA CCCTAAGCCA GAGAGAGGCT TCACTACATC ATGCTTCCTG ACATCTCTCC   180
CTTTGAAGAG CAGTCAGACT CCTGCTTTGC TCTTCAGACT TAATTTGGGG GTTTAACAGG   240
TGAGGTTGCT GGGGGAACTC TTTTACAACA TCTCTCTGAA AGAATCCGGG CTGCCAGTTT   300
CATTTGGTTT GGGTGTCAGT AGCATGATGG AAAGACAAAA AAACACAACT TGACATCTGC   360
AGAAATGGGT TCAAATTTTA CCTGCAACTC ACCAATTCTG TGGCCTTGGT TCAGCAATTA   420
AACTCCCTAA AATTCAGTTT TTTCTTTGTA AAATGGGGTT ATGAACAGTA CCTACTTCAA   480
AATGTGTTTG TGAAGATTAA AAAAGTTAAC ATAAAGAGTT TAGAAGAGTG TCTGGCATAT   540
TGTGCTCAAT AAGTGTTTAT TTATTTATTG CTGAATAAAC CAGTAATTTA ATTAGTAT
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Seq ID NO: 31 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 134..1917

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1          11         21         31         41         51
|          |          |          |          |          |
CACCTCAGCC CCAACCCCAA CCCCAGCCGC ATCCCCTGCC CCAGCTGACG GGTCAAAGCC   60
TCAGGAGAGT GTGGCTCTCC CCAGGCGCTA CCAGGAGGGG CAGGTCTCAG CCAGCTGGGG   120
AAACCTTATT GCCATGGTTC TTAGAAGCCA CCCCTTCCCC AGGCAAGACA GGCCCCAAGG   180
GAGTGTCCCG AGGGCGGTTC CCGGGAGCCC CGTGGGTCCC AGCACTTCCA CACACTCTGA   240
GGACAGACAC GGCCCCTCTT CTTCAGTGGG GACAGTCATA GGGACAGGTA CAGGGGGCCT   300
GGTTGAGGCT GGAGGTCAGC CACAGCCAAG AAGCTCCGAG ACCAACGGAT CGCCCAGCCC   360
AGACCCTCCC CCAGGCCTAA GAGGAGAGGG AACCAGGGAG AAAAGTCTAG ACCCGCTGCC   420
CCAAGCCGCG ATGCCCAGGG GCCCCGCACA GCCCCCCGCG CAGAGGCCGC CTGGCCCCGC   480
GGCCTCCTCC TCTGCGAGGC GCTCACAGCC GGTACCCCAG CTACGGAAAC GCAGCAGGTG   540
CGAAATCGCC CCGAGCTCGG AGCAGGAGGT CAGGCCGGCC GCCTCGGGGG ACCCTCAAGG   600
GGAGGCGCCG GGGGAGGGGG GCAGCCCTGC CGGCCGCAGC GGGGCGCTCA CGGAAAAGCA   660
GGAGGAGGCC CGGAAGCTCA TGGTGTTTCT GCAGAGGCCC GGGGGTTGGG GGGTGGTGGA   720
GGGGCCCCGG AAGCCCAGCT CCCGGGCCCT GGAGCCCGCC ACGGCGGCAG CCCTGCGGCG   780
GCGGCTGGAC CTGGGCAGTT GCCTGGACGT GCTGGCCTTT GCCCAGCAGC ACGGAGAGCC   840
CGGCCTGGCG CAGGAGACCT ACGCGCTGAT GAGCGACAAC CTGCTGCGAG TGCTGGGAGA   900
CCCGTGCCTC TACCGCCGGC TGAGCGCGGC CGACCGCGAG CGCATCCTCA GCCTGCGGAC   960
CGGCCGGGGC CGGGCGGTGC TGGGCGTCCT CGTACTGCCC AGCCTCTACC AGGGGGGCCG   1020
CTCAGGGCTC CCCAGGGGCC CTCGTGGCGA GGAGCCTCCT GCGGCGGCCC CTGTGTCCCT   1080
GCCTCTACCT GCGCACCTGC ATGTGTTCAA CCCCCGGGAG AACACCTGGC GGCCCCTGAC   1140
CCAGGTGCCC GAGGAGGCCC CGCTTCGGGG CTGCGGTCTC TGCACCATGC ACAACTACCT   1200
GTTTCTGGCG GGGGGCATCC GTGGCTCCGG TGCCAAGGCC GTCTGCTCCA ACGAGGTCTT   1260
CTGCTACAAC CCTCTGACCA ACATCTGGAG CCAGGTTCGG CCCATGCAGC AGGCCCGAGC   1320
CCAGCTCAAG CTGGTGGCCC TGGACGGGCT GCTCTATGCC ATCGGTGGCG AATGCCTGTA   1380
CAGCATGGAG TGCTACGACC CGCGAACAGA CGCCTGGACC CCACGCGCGC CACTCCCCGC   1440
AGGCACCTTC CCTGTGGCCC ACGAGGCTGT GGCCTGCCGT GGGGACATCT ACGTCACCGG   1500
GGGTCACCTC TTCTACCGCC TGCTCAGGTA CAGCCCCGTG AAGGATGCTT GGGACGAGTG   1560
CCCATACAGT GCCAGCCACC GGCGTTCCAG CGACATCGTG GCACTGGGGG GCTTCCTGTA   1620
CCGCTTCGAC CTGCTGCGGG GCGTGGGCGC CGCCGTGATG CGCTACAACA CAGTGACCGG   1680
CTCCTGGAGC AGGGCTGCCT CCCTGCCCCT GCCCGCCCCC GCCCCACTGC ACTGCACCAC   1740
CCTGGGCAAC ACCATTTACT GCCTCAACCC CCAGGTCACT GCCACCTTCA CGGTCTCTGG   1800
GGGGACTGCC CAGTTCCAGG CCAAGGAGCT GCAGCCCTTC CCCTTGGGGA GCACCGGGGT   1860
CCTCAGTCCA TTCATCCTGA CTCTGCCCCC TGAGGACCGG CTGCAGACCT CACTCTGAGT   1920
GGCAGGCAGA GAACCAAAGC TGCTTCGCTG CTCTCCAGGG AGACCCTCCT GGGATGGGCC   1980
TGAGAGGCCG GGGCTCAGGG AAGGGGCTGG GATCGGAACT TCCTGCTCTT GTTTCTGGAC   2040
AACTTTCCCC TTCTGCTTTA AAGGTTGTCG ATTATTTTGA AGCCCAGACT CCCTCAGCCT   2100
CTTTCTGCCC CTCACTCCAC ACCCAGACTG TTTCCTGACT CAATTCCGTA CCTACTTACA   2160
GACCCTCTCA GCTTGCTGAC ACCCCCCTGT CTGTGGGACT CCCTATTCCC TAGAGCCAGG   2220
GACTGATGCG TCTCCACAGA CAAGGACTTG GCTCGCTGGA GCTCTGCTGA GCCGAGAGAG   2280
GAGGGGGTAG AAAACATTCA CACTTCCTAT GCTCTGTCAG CAGGACAGGG AGCAAAAACG   2340
TCCCCAGGCA ACGCCCTCGC CTCTGGGACT TTCTGCCTGT CCTAAGGCCT CCCCAGGTAC   2400
CAACCCCGTA GCTATCTGGG TCTGTTTGGC ACTGTGGATT CTCAAGGGCC TAGAACCCTT   2460
GCCTCTGAAA CTGGTCCGCT GGTGCAGCCC TGCTGTCTGC AGCTCCTGCC CATACCCCCA   2520
GCCCACACCA GGCCAGGCCC ACTCCGGGCT CACCACCCTC TGCAGCCTTG TGGGGCTCTC   2580
CCAGCCCCTC CAGAAGCCCA CCCCACTTCT CGCCAACCCC CGATCTCTAA ATGAGGCCTG   2640
AGCGTCACCC TAGTTCTGCC CCTTTTTAGC TGTGTAGACT TGGACGAGAC ATTTGACTTC   2700
CCTTTCTCCT TGTCTATAAA ATGTGGACAG TGGACGTCTG TCACCCAAGA GAGTTGTGGG   2760
AGACAAGATC ACAGCTATGA GCACCTCGCA CGGTGTCCAG GATGCACAGC ACAATCCATG   2820
ATGCGTTTTC TCCCCTTACG CACTTTGAAA CCCATGCTAG AAAAGTGAAT ACATCTGACT   2880
GTGCTCCACT CCAACCTCCA GCCTGGATGT CCCTGTCTGG GCCCTTTTTC TGTTTTTTAT   2940
TCTATGTTCA GCACCACTGG CACCAAATAC ATTTTAATTC ACCGAAAGCA
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Seq ID NO: 32 Protein Sequence
Protein Accession #: XP_054631.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPRGPAQPPA QRPPGPAASS SARRSQPVPQ LRKRSRCEIA PSSEQEVRPA ASGDPQGEAP   60
GEGGSPAGRS GALTEKQEEA RKLMVFLQRP GGWGVVEGPR KPSSRALEPA TAAALRRRLD   120
LGSCLDVLAF AQQHGEPGLA QETYALMSDN LLRVLGDPCL YRRLSAADRE RILSLRTGRG   180
RAVLGVLVLP SLYQGGRSGL PRGPRGEEPP AAAPVSLPLP AHLHVFNPRE NTWRPLTQVP   240
EEAPLRGCGL CTMHNYLFLA GGIRGSGAKA VCSNEVFCYN PLTNIWSQVR PMQQARAQLK   300
LVALDGLLYA IGGECLYSME CYDPRTDAWT PRAPLPAGTF PVAHEAVACR GDIYVTGGHL   360
FYRLLRYSPV KDAWDECPYS ASHRRSSDIV ALGGFLYRFD LLRGVGAAVM RYNTVTGSWS   420
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RAASLPLPAP APLHCTTLGN TIYCLNPQVT ATFTVSGGTA QFQAKELQPF PLGSTGVLSP   480
FILTLPPEDR LQTSL
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Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
CCTCTGTCTA ACCTTACATG AAAAAACCCG TTTCCAACGA AGGCCTCTAA AAGGCCAAGA   60
AATCCCCTTG CAGACTTTAC AAACAGAGTG TTTCCTAACT GCTCTATGAA CAGAAAGGTT   120
AAACTCTGTG AGTTGAACCA ACACATCACA ACGCAGTTTG TGGGAATGAT TCTGTCTAGT   180
TTTGAAACGA AGATATTTCC TTTTCTGCCG TTGACCTTAA AGCGCTTGAA ATCTACACTT   240
GCAAATTGCA CAAATAGAGT GTTTCAAATC TGCTCTGTCT AAGGGAACGT TCAACTCTGT   300
GAGTTGAATG CACACAACAC AAGGAAGTTA CTGGGAATTC TTCTGTCTAG CCTTACATGA   360
AAGAAAACCC GTTTCCAACG AAGGCCTCTA AGTGGTCAAA ATATCCACGT GCAGACTTTA   420
CAAACAGAGT GTTTCCAAAC TGCTGAATGA AAAGAAAAGT AAACTCTGAG AGTTGAACGC   480
ACACATCGCA GAGCAGTTTC TGAGAATGAT TCTGTCTAGT TTTTATACGA AGATATTTCC   540
TTTTCTGCCT TTGGCCTCAA AGCGCTTGAA ATCTCCACTT GCAAATTCCA CAAAAAGAGT   600
GTTTCAAATC TGCTCTGTCT AAAGGAAGGT TCAACTCTGT GAGTTGAATA CACACAACAC   660
AAAGAAGTTA CTGAGAATTC TTCTGTCTAG CATTATATGA AGAAATCCCG TTTCCAACGA   720
AGGCATCTAA GAGGTCCAAA TATCCACTTG CAGACTTTAC AAACAGAGGG TTTCCAGAAT   780
GGCTGTATGA AAAGAAAGGT TAAACTCTGT GAGTTAAACA CACA
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Seq ID NO: 34 DNA sequence
Nucleic Acid Accession #: AF011468.1
Coding sequence: 257..1468

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1          11         21         31         41         51
|          |          |          |          |          |
GGAAGACTTG GGTCCTTGGG TCGCAGGTGG GAGCCGACGG GTGGGTAGAC CGTGGGGGAT   60
ATCTCAGTGG CGGACGAGGA CGGCGGGGAC AAGGGGCGGC TGGTCGGAGT GGCGGAGCGT   120
CAAGTCCCCT GTCGGTTCCT CCGTCCCTGA GTGTCCTTGG CGCTGCCTTG TGCCCGCCCA   180
GCGCCTTTGC ATCCGCTCCT GGGCACCGAG GCGCCCTGTA GGATACTGCT TGTTACTTAT   240
TACAGCTAGA GGCATCATGG ACCGATCTAA AGAAAACTGC ATTTCAGGAC CTGTTAAGGC   300
TACAGCTCCA GTTGGAGGTC CAAAACGTGT TCTCGTGACT CAGCAAATTC CTTGTCAGAA   360
TCCATTACCT GTAAATAGTG GCCAGGCTCA GCGGGTCTTG TGTCCTTCAA ATTCTTCCCA   420
GCGCGTTCCT TTGCAAGCAC AAAAGCTTGT CTCCAGTCAC AAGCCGGTTC AGAATCAGAA   480
GCAGAAGCAA TTGCAGGCAA CCAGTGTACC TCATCCTGTC TCCAGGCCAC TGAATAACAC   540
CCAAAAGAGC AAGCAGCCCC TGCCATCGGC ACCTGAAAAT AATCCTGAGG AGGAACTGGC   600
ATCAAAACAG AAAAATGAAG AATCAAAAAA GAGGCAGTGG GCTTTGGAAG ACTTTGAAAT   660
TGGTCGCCCT CTGGGTAAAG GAAAGTTTGG TAATGTTTAT TTGGCAAGAG AAAAGCAAAG   720
CAAGTTTATT CTGGCTCTTA AAGTGTTATT TAAAGCTCAG CTGGAGAAAG CCGGAGTGGA   780
GCATCAGCTC AGAAGAGAAG TAGAAATACA GTCCCACCTT CGGCATCCTA ATATTCTTAG   840
ACTGTATGGT TATTTCCATG ATGCTACCAG AGTCTACCTA ATTCTGGAAT ATGCACCACT   900
TGGAACAGTT TATAGAGAAC TTCAGAAACT TTCAAAGTTT GATGAGCAGA GAACTGCTAC   960
TTATATAACA GAATTGGCAA ATGCCCTGTC TTACTGTCAT TCGAAGAGAG TTATTCATAG   1020
AGACATTAAG CCAGAGAACT TACTTCTTGG ATCAGCTGGA GAGCTTAAAA TTGCAGATTT   1080
TGGGTGGTCA GTACATGCTC CATCTTCCAG GAGGACCACT CTCTGTGGCA CCCTGGACTA   1140
CCTGCCCCCT GAAATGATTG AAGGTCGGAT GCATGATGAG AAGGTGGATC TCTGGAGCCT   1200
TGGAGTTCTT TGCTATGAAT TTTTAGTTGG GAAGCCTCCT TTTGAGGCAA ACACATACCA   1260
AGAGACCTAC AAAAGAATAT CACGGGTTGA ATTCACATTC CCTGACTTTG TAACAGAGGG   1320
AGCCAGGGAC CTCATTTCAA GACTGTTGAA GCATAATCCC AGCCAGAGGC CAATGCTCAG   1380
AGAAGTACTT GAACACCCCT GGATCACAGC AAATTCATCA AAACCATCAA ATTGCCAAAA   1440
CAAAGAATCA GCTAGCAAAC AGTCTTAGGA ATCGTGCAGG GGGAGAAATC CTTGAGCCAG   1500
GGCTGCCATA TAACCTGACA GGAACATGCT ACTGAAGTTT ATTTTACCAT TGACTGCTGC   1560
CCTCAATCTA GAACGCTACA CAAGAAATAT TTGTTTTACT CAGCAGGTGT GCCTTAACCT   1620
CCCTATTCAG AAAGCTCCAC ATCAATAAAC ATGACACTCT GAAGTGAAAG TAGCCACGAG   1680
AATTGTGCTA CTTATACTGG TTCATAATCT GGAGGCAAGG TTCGACTGCA GCCGCCCCGT   1740
CAGCCTGTGC TAGGCATGGT GTCTTCACAG GAGGCAAATC CAGAGCCTGG CTGTGGGGAA   1800
AGTGACCACT CTGCCCTGAC CCCGATCAGT TAAGGAGCTG TGCAATAACC TTCCTAGTAC   1860
CTGAGTGAGT GTGTAACTTA TTGGGTTGGC GAAGCCTGGT AAAGCTGTTG GAATGAGTAT   1920
GTGATTCTTT TTAAGTATGA AAATAAAGAT ATATGTACAG ACTTGTATTT TTTCTCTGGT   1980
GGCATTCCTT TAGGAATGCT GTGTGTCTGT CCGGCACCCC GGTAGGCCTG ATTGGGTTTC   2040
TAGTCCTCCT TAACCACTTA TCTCCCATAT GAGAGTGTGA AAAATAGGAA CACGTGCTCT   2100
ACCTCCATTT AGGGATTTGC TTGGGATACA GAAGAGGCCA TGTGTCTCAG AGCTGTTAAG   2160
GGCTTATTTT TTTAAAACAT TGGAGTCATA GCATGTGTGT AAACTTTAAA TATGCAAATA   2220
AATAAGTATC TATGTCTAAA AAAAAAAAAA AAA
```

Seq ID NO: 35 Protein Sequence
Protein Accession #: AAC63902.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDRSKENCIS GPVKATAPVG GPKRVLVTQQ IPCQNPLPVN SGQAQRVLCP SNSSQRVPLQ   60
AQKLVSSHKP VQNQKQKQLQ ATSVPHPVSR PLNNTQKSKQ PLPSAPENNP EEELASKQKN   120
EESKKRQWAL EDFEIGRPLG KGKFGNVYLA REKQSKFILA LKVLFKAQLE KAGVEHQLRR   180
EVEIQSHLRH PNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQKLSKFDE QRTATYITEL   240
ANALSYCHSK RVIHRDIKPE NLLLGSAGEL KIADFGWSVH APSSRRTTLC GTLDYLPPEM   300
```

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IEGRMHDEKV DLWSLGVLCY EFLVGKPPFE ANTYQETYKR ISRVEFTFPD FVTEGARDLI   360
SRLLKHNPSQ RPMLREVLEH PWITANSSKP SNCQNKESAS KQS
```

Seq ID NO: 36 DNA sequence
Nucleic Acid Accession #: NM_016267
Coding sequence: 67..843

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGCACGAGG ACAGAATCAG GTGATGGTCC AGAATTAAGA GCTGTCACCT GTGTCATTCA   60
CTCACAATGG AAGAAATGAA GAAGACTGCC ATCCGGCTGC CCAAAGGCAA ACAGAAGCCT   120
ATAAAGACGG AATGGAATTC CCGGTGTGTC CTTTTCACCT ACTTCCAAGG GGACATCAGC   180
AGCGTAGTGG ATGAACACTT CTCCAGAGCT CTGAGCAATA TCAAGAGCCC CCAGGAATTG   240
ACCCCCTCGA GTCAGAGTGA AGGTGTGATG CTGAAAAACG ATGATAGCAT GTCTCCAAAT   300
CAGTGGCGTT ACTCGTCTCC ATGGACAAAG CCACAACCAG AAGTACCTGT CACAAACCGT   360
GCCGCCAACT GCAACTTGCA TGTGCCTGGT CCCATGGCTG TGAATCAGTT CTCACCGTCC   420
CTGGCTAGGA GGGCCTCTGT TCGGCCTGGG GAGCTGTGGC ATTTCTCCTC CCTGGCGGGC   480
ACCAGCTCCT TAGAGCCTGG CTACTCTCAT CCCTTCCCCG CTCGGCACCT GGTTCCAGAG   540
CCCCAGCCTG ATGGGAAACG TGAGCCTCTC CTAAGTCTCC TCCAGCAAGA CAGATGCCTA   600
GCCCGTCCTC AGGAATCTGC CGCCAGGGAG AATGGCAACC CTGGCCAGAT AGCTGGAAGC   660
ACAGGGTTGC TCTTCAACCT GCCTCCCGGC TCAGTTCACT ATAAGAAACT ATATGTATCT   720
CGTGGATCTG CCAGTACCAG CCTTCCAAAT GAAACTCTTT CAGAGTTAGA GACACCTGGG   780
AAATACTCAC TTACACCACC AAACCACTGG GGCCACCCAC ATCGATACCT GCAGCATCTT   840
TAGTCAAGTT GGAGGAGAAA GACAACACTT GGTCTAAGAC ACGGCAGCAA GACATCCCTG   900
CATATTGTTC CAGATAAAAA TGAAAGCTGC TCACACCCAC TTGCCTCCCC AATCTGTTAA   960
ACAGCTTCGT GTCTAGTATG AGCTCAGTAC TTGCCCTGTG AAAATCCCAG AAGCCCCCGC   1020
TGTCAATGTT CCCCATCCAC ACCCTGCTTG CTCCTGTGTA ACAGCTCAGA TGATGAATAA   1080
TAATAAAACT GTACTTTTTT GGAAAAAAAA AAAAAAAAAA AAAAAA
```

Seq ID NO: 37 Protein Sequence
Protein Accession #: NP_057351.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEEMKKTAIR LPKGKQKPIK TEWNSRCVLF TYFQGDISSV VDEHFSRALS NIKSPQELTP   60
PSSQSEGVML KNDDSMSPNQ WRYSSPWTKP QPEVPVTNRA ANCNLHVPGP MAVNQFSPSL   120
AARRASVRPG ELWHFSSLAG TSSLEPGYSH PFPARHLVPE PQPDGKREPL LSLLQQDRCL   180
ARRPQESAAR ENGNPGQIAG STGLLFNLPP GSVHYKKLYV SRGSASTSLP NETLSELETP   240
GKYYSLTPPN HWGHPHRYLQ HL
```

Seq ID NO: 38 DNA sequence
Nucleic Acid Accession #: AK058088.1
Coding sequence: 252..1772

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1          11         21         31         41         51
|          |          |          |          |          |
AGGAAACCAA GGCAAGCTCC CCCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA   60
GCCCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGGCGCCCCC AGCTCTCCTG   120
TAACTCAGAG GCCAGTGTGA TGGGAGTTCC TCCACTCAGC ACACTTCCCC TGTAAACACG   180
CCTGTGGTGG GCAAAAGGGC TTTGGAACGG TTGCTTGTCT TTTCTCTCCT GCGTAATTTC   240
CACTTTCATT CATGATAATG TCGAACACGC ACAAAGCTCG GCTGGAACGC CGGGTCACTG   300
GCTCAACCAA CCGGTGGCGT TTGCCCAAAC AGCCTTTCTC TGGGGACCTG CTCTCACTTT   360
CCCAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT   420
TATGCATTTC ACAAATCCAG AAGTTTTTCT TTGAGAATTT CAAGAACAAG GACATCCAAA   480
GTGGGGAAGC AGATGTGATT CTCGAGTGCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC   540
GGCTTTTTCA GTCTGAGACC TTGGCCAAGC TCTACCTGAA AGCCCTGGCG CAGGGCACCA   600
CACACCCCCT GAGGGAGCTG GAGGAGCTTC TGCGAGCTCA ATCACCTAAG AAGACCAAAG   660
AAAAATCCCC TGCAAAGAGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGGTCACTA   720
AAGTCGCCTT CGCCACGGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACTTGG   780
AAGACCTACT GGGAGTGCTG GCTTCCGCCC ACATCCTCCA GTTCAGTGGC CTGTTTCAAA   840
GGTGCGTGGA TGTGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG   900
CCGGCTGCAA GTACAAGGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAAATGA   960
ACTTGGTTCC TCTAGGGGGG ACGCAGATCC ACCTCCACAA AATCCCACAG GACCTGCTCC   1020
ACAAAGTGCT GAAGTCCCCC AGGTTATTTA CCTTTAGTGA ATTCCATCTT CTGAAAACAA   1080
TGCTTTTGTG GGTCTTCTTG CAACTGAACT ACAAGATTCA GGCAATTCCG ACTTATGAAA   1140
CCGTGATGAC ATTTTTTAAG AGCTTTCCTG AGAACTGTTG CTTTCTGGAC CGGGACATAG   1200
GACGGAGCTT GAGGCCGCTC TTCCTCTGCT TGCGTCTGCA CGGCATCACC AAAGGCAAGG   1260
ATCTGGAGGT GCTGCGGCAC CTTAACTTCT TCCCAGAGTC ATGGCTCGAC CAGGTTACAG   1320
TCAACCATTA CCACGCACTG GAGAATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA   1380
CCCAGGCTGT GAGATTTGGG CTGCTCTTTA ACCAGGAGAA TACAACTTAT TCGAAAACGA   1440
TTGCTCTATA TGGATTCTTC TTTAAGATAA AGGGACTCAA ACATGATACT ACCTCTTATA   1500
GTTTTTACAT GCAGAGAATA AAGCACACAG ACCTGGAATC TCCCTCTGCG GTCTACGAGC   1560
ACAACCACGT CAGCCTGCGA GCGGCACGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCCC   1620
TGGTTGACGG CAAGTGGCAG GAGTTCAGGA CAAACCAGAT CAAGCAGAAG TTTGGGTTGA   1680
CCACGTCATC CTGCAAAAGC CATACCTTGA AAATCCAAAC TGTGGGCATC CCAATCTATG   1740
TAAGTTTTGC ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAATCT ATGGGATTTT   1800
CCCCCCACTG GTCTGCATAA AAGAAAATAA AATGACATAA AAGGGAGC
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Seq ID NO: 39 Protein Sequence
Protein Accession #: BAB71658.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MIMSNTHKAR LERRVTGSTN RWRLPKQPFS GDLLSLSQMC KALSIDFEEA LRNPDRLCIS   60
QIQKFFPENF KNKDIQSGEA DVILECLGFK WELHQPRLFQ SETLAKLYLK ALAQGTTHPL   120
RELEELLRAQ SPKKTKEKSP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL   180
GVLASAHILQ FSGLFQRCVD VMIARLKPST IKKFYEAGCK YKEEQLTTGC EKWLEMNLVP   240
LGGTQIHLHK IPQDLLHKVL KSPRLFTFSE FHLLKTMLLW VFLQLNYKIQ AIPTYETVMT   300
FFKSFPENCC FLDRDIGRSL RPLFLCLRLH GITKGKDLEV LRHLNFFPES WLDQVTVNHY   360
HALENGGDMV HLKDLNTQAV RFGLLFNQEN TTYSKTIALY GFFFKIKGLK HDTTSYSFYM   420
QRIKHTDLES PSAVYEHNHV SLRAARLVKY EIRAEALVDG KWQEFRTNQI KQKFGLTTSS   480
CKSHTLKIQT VGIPIYVSFA FIFPAS
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Seq ID NO: 40 DNA sequence
Nucleic Acid Accession #: NM_032899.1
Coding sequence: 186..1070

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGA TTGCTCAGGA CAGCGGTAAA TCACTTCTTG GAGGTGCCCT GCACGCCGGT   60
CCTGGGAGCA GGCGGCCTCC CGGGGGTGCG GGAGCCCCAC TCCTCCGTGG TGTGTTCCAT   120
TTGCTTCCCA CATCTGGAGG AGCTGACGTG CCAGCCTCCC CCAGCACCAC CCAGGGACGG   180
GAGGCATGAG CCGGTCAAGG CACCTGGGCA AAATCCGGAA GCGTCTGGAA GATGTCAAGA   240
GCCAGTGGGT CCGGCCAGCC AGGGCTGACT TTAGTGACAA CGAGAGTGCC CGGCTGGCCA   300
CGGACGCCCT CTTGGATGGG GGTTCTGAAG CCTACTGGCG GGTGCTCAGC CAGGAAGGCG   360
AGGTGGACTT CTTGTCCTCG GTGGAGGCCC AGTACATCCA GGCCCAGGCC AGGGAGCCCC   420
CGTGTCCCCC AGACACCCTG GGAGGGGCGG AAGCAGGCCC TAAGGGACTG GACTCCAGCT   480
CCCTACAGTC CGGCACCTAC TTCCCTGTGG CCTCAGAGGG CAGCGAGCCG GCCCTACTGC   540
ACAGCTGGGC CTCAGCTGAG AAGCCCTACC TGAAGGAAAA ATCCAGCGCC ACTGTGTACT   600
TCCAGACCGT CAAGCACAAC AACATCAGAG ACCTCGTCCG CCGCTGCATC ACCCGGACTA   660
GCCAGAACAT TTCCATCCGG AGTGTGGAAG GAGAGATATA CTGTGCCAAG TCAGGCAGGA   720
AATTCACTGG CCAAATCCGG GAGAAGTTCA TCATCTCGGA CTGGAGATTT GTCCTGTCTG   780
GATCTTACAG CTTCACCTGG CTCTGCGGAC ACGTGCACCG GAACATCCTC TCCAAGTTCA   840
CAGGCCAGGC GGTGGAGCTG TTTGACGAGG AGTTCCGCCA CCTCTACGCC TCCTCCAAGC   900
CTGTGATGGG CCTGAAGTCC CCGCGGCTGG TCGCCCCCGT CCCGCCCGGA GCAGCCCCGG   960
CCAATGGCCG CCTTAGCAGC AGCAGTGGCT CCGCCAGTGA CCGCACGTCC TCCAACCCCT   1020
TCAGCGGCCG CTCGGCAGGC AGCCACCCCG GTACCCGAAC TGACGGCTGA GATGAGGTTA   1080
GAATGACTGG GCCCGGCTGA ACATTCCAAA TTGGATTTCA CCATCTGCTG AGAAAGTTTA   1140
AGGAAGGCAA AGCTTGCCAG GTCACAGAAG CTCCCAAGCC CAGCTTTCCA AAGGCCTCAG   1200
CCTGTGCCTG TGTCGAGCTC AGTCCTGGGA GATAGGGGAG AACCTGCAGG CAGGAACAAG   1260
CCCCCCTACT CCTGACCACC CTCCATCAGC AGTCTCCCCT CCGTGGTCGT CTTTGTTGAC   1320
AAAGGTGCAG TTTCTCCTCT CCTGGGCACC TGTAACATGT GATGCGCTGC CTGCTGGGAG   1380
GTTAGGTCGG GGCTGCCCCG GCGAGTGGAG CATGAGCAGA ACCGCCGAGG GTCACTTCTG   1440
GGCAGAAGCT TTGAGAGCCT GGGTCCAGGT TGCCACATAG AAGCAGCTCT CCAGTTGAAA   1500
CCCTCCTCTG CCAGCCTGGG GTCCTAAGCG ATGAGCAGAA TCCCCCACTC CCACCCCACC   1560
AACCCACAAT GGATATGTAG TGAGCAAGAA ATAAACCTTT GTTGTTTAAA AAAAAAAAAA   1620
AAAAAAAA
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Seq ID NO: 41 Protein Sequence
Protein Accession #: NP_116288.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSRSRHLGKI RKRLEDVKSQ WVRPARADFS DNESARLATD ALLDGGSEAY WRVLSQEGEV   60
DFLSSVEAQY IQAQAREPPC PPDTLGGAEA GPKGLDSSSL QSGTYFPVAS EGSEPALLHS   120
WASAEKPYLK EKSSATVYFQ TVKHNNIRDL VRRCITRTSQ NISIRSVEGE IYCAKSGRKF   180
TGQIREKFII SDWRFVLSGS YSFTWLCGHV HRNILSKFTG QAVELFDEEF RHLYASSKPV   240
MGLKSPRLVA PVPPGAAPAN GRLSSSSGSA SDRTSSNPFS GRSAGSHPGT RTDG
```

Seq ID NO: 42 DNA sequence
Nucleic Acid Accession #: NM_000782.2
Coding sequence: 405..1946

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1          11         21         31         41         51
|          |          |          |          |          |
TGGAGAGGGA CAGGAGGAAA CGCAGCGCCA GCAGCATCTC ATCTACCCTC CTTGACACCT   60
CCCCGTGGCT CCAGCAAGCC CTAGAGGTCA GCCTTGCGGA CCAACAGGAG GACTCCCAGC   120
TTTCCCTTTT CAAGAGGTAC CCCAGACACC GGCCACCCTC TTCCAGCCCC TGCGGCCAGT   180
GCAAGGAGGC ACCAATGCTC TGAGGCTGTC GCGTGGTGCA GCGTCGAGCA TCCTCGCCGA   240
GTCCTTCTGC TGCCTGTCCC GCCTCACCCC GCTCCATCAC ACCAGCTGGC CCTCTTTGCT   300
TCCTTTTCCC AGAATCGTTA AGCCCCGACT CCCACTAGCA CCTCGTACCA ACCTCGCCCC   360
ACCCCATCCT CCTGCCTTCC CGCGCTCCGG TGTCCCCCGC TGCCATGAGC TCCCCCATCA   420
GCAAGAGCCG CTCGCTTGCC GCCTTCCTGC AGCAGCTGCG CAGTCCGAGG CAGCCCCCGA   480
GACTGGTGAC ATCTACGGCG TACACGTCCC CTCAGCCGCG AGAGGTGCCA GTCTGCCCGC   540
TGACAGCTGG TGGCGAGACT CAGAACGCGG CCGCCCTGCC GGGCCCCACC AGCTGGCCAC   600
TGCTGGCGAG CCTGCTGCAG ATTCTCTGGA AAGGGGGTCT CAAGAAACAG CACGACACCC   660
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TGGTGGAGTA CCACAAGAAG TATGGCAAGA TTTTCCGCAT GAAGTTGGGT TCCTTTGAGT   720
CGGTGCACCT GGGCTCGCCA TGCCTGCTGG AAGCGCTGTA CCGCACCGAG AGCGTACCCC   780
AGCGGCTGGA GATCAAACCG TGGAAGGCCT ATCGCGACTA CCGCAAAGAA GGCTACGGGC   840
TGCTGATCCT GGAAGGGGAA GACTGGCAGC GGGTCCGGAG TGCCTTTCAA AAGAAACTAA   900
TGAAACCAGG GGAAGTGATG AAGCTGGACA ACAAAATCAA TGAGGTCTTG GCCGATTTTA   960
TGGGCAGAAT AGATGAGCTC TGTGATGAAA GAGGCCACGT CGAAGACTTG TACAGCGAAC  1020
TGAACAAATG GTCGTTTGAA AGTATCTGCC TCGTGTTGTA TGAGAAGAGA TTTGGGCTTC  1080
TCCAGAAGAA TGCAGGGGAT GAAGCTGTGA ACTTCATCAT GGCCATCAAA ACAATGATGA  1140
GCACGTTTGG GAGGATGATG GTCACTCCAG TCGAGCTGCA CAAGAGCCTC AACACCAAGG  1200
TCTGGCAGGG ACACACTCTG GCCTGGGACA CCATTTTCAA ATCAGTCAAA GCTTGTATCG  1260
ACAACCGGTT AGAGAAGTAT TCTCAGCAGC CTAGTGCAGA TTTCCTTTGT GACATTTATC  1320
ACCAGAATCG GCTTTCAAAG AAAGAATTGT ATGCTGCTGT CACAGAGCTC CAGCTGGCTG  1380
CGGTGGAAAC GACAGCAAAC AGTCTAATGT GGATTCTCTA CAATTTATCC CGTAATCCCC  1440
AAGTGCAACA AAAGCTTCTT AAGGAAATTC AAAGTGTATT ACCTGAGAAT CAGAGGCCAC  1500
GGGAGGAAGA TTTGAGGAAT ATGCCGTATT TAAAAGCCTG TCTGAAAGAA TCTATGAGGC  1560
TTACCCCGGG TGTACCATTT ACAACTCGGA CTCTTGACAA GGCAACAGTT CTGGGTGAAT  1620
ATGCTTTACC CAAAGGAACA GTGCTCATGC TAAATACCCA GGTGTTGGGA TCCAGTGAAG  1680
ACAATTTTGA AGATTCAAGT CAGTTTAGAC CTGAACGTTG GCTTCAGGAG AAGGAAAAAA  1740
TTAATCCTTT TGCGCATCTT CCATTTGGCG TTGGAAAAAG AATGTGCATT GGTCGCCGAT  1800
TAGCAGAGCT TCAACTGCAT TTGGCTCTTT GTTGGATTGT CCGCAAATAC GACATCCAGG  1860
CCACAGACAA TGAGCCTGTT GAGATGCTAC ACTCAGGCAC CCTGGTGCCC AGCCGGGAAC  1920
TCCCCATCGC GTTTTGCCAG CGATAATACG CCTCAGATGG TGGTATTTGC TAACATCATA  1980
TCCAACTCAG GGAAGCGGAC TGAGTGCTGG GATCCAAGGC ATTCTACAGG GTTCACTGCT  2040
GGTTTACACT TCACCTGTGT CAGCACCATC TTCAGGTGCT TAGAATGGCC TGGGAGCCTG  2100
TTCTGTCTTG CATCTTCCAT GACATGAAAG GGAGGCTGGC ACTTGTCAGT CAGGTAGAGG  2160
TTACAAACCG TTTCAGGCCC TGCTACCACA TTCACTGTTT GAATCTTTAA TTCCCAAGAA  2220
TAAGTTTACA TTTCACAATG AATGACCTAC AACAGCTAAA TTTTCTGGGG CTGGGAGTAA  2280
TACTGACAAT CCATTTACTG TAGCTCTGCT TAATGTACTA CTTAGGAAAA TGTCCCTGCT  2340
TAATAATGTA AGCCAAGCTA AATGATGGTT AAAGTTATCA GGCCTCCCAT GAAATTGCGT  2400
TCTTCCTGCA TTGAAATAAA AACATTATTG GGAAACTAGA GAACACCTCT ATTTTTAAAA  2460
GGACTTTAAC GAAGTCAAAC AACTTCTAAG ACTAGTGATT CACTGGGGCA TTATTTGTTA  2520
GAGGACCTTA AAATTGTTTA TTTTTTAAAT GTGATTCCTT TATGGCATTA GGGTAAAGAT  2580
GAAGCAATAA TTTTTAAATT GTGTATGTGC ATATGAAGCA CAGACATGCA TGTGTGTGTG  2640
TGTCTGTGTG TGTGTGTCCG TGTATGTGTG TGTGGGTTCT AATGGTAATT TGCCTCAGTC  2700
ATTTTTTTAA TATTTGCAGT ACTTGATTTA GGATCTGTGG TGCAGGGCAT GTTTCAAAGT  2760
TTAGTCACAG CTTAAAAACA TTCAGTGTGA CTTTAATATT ATAAAATGAT TTCCCATGCC  2820
ATAATTTTTC TGTCTATTAA ATGGGACAAG TGTAAAGCAT GCAAAAGTTA GAGATCTGTT  2880
ATATAACATT TGTTTTGTGA TTTGAACTCC TAGGAAAAAT ATGATTTCAT AAATGTAAAA  2940
TGCACAGAAA TGCATGCAAT ACTTATAAGA CTTAAAAATT GTGTTTACAG ATGGTTTATT  3000
TGTGCATATT TTTACTACTG CTTTTCCTAA ATGCATACTG TATATAATTC TGTGTATTTG  3060
ATAAATATTT CTTCCTACAT TATATTTTTA GAATATTTCA GAAATATACA TTTATGTCTT  3120
TATATTGTAA TAAATATGTA CATATCTAGG TATATGCTTT CTCTCTGCTG TGAAATTATT  3180
TTTAGAATTA TAATTCACGT CTTGTCATAT TTCATCTGTA TACCTTCAAA TTCTCTGAAA  3240
GTAAAAATAA AAGTTTTTAA ATATT
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Seq ID NO: 43 Protein Sequence
Protein Accession #: NP_000773.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSSPISKSRS LAAFLQQLRS PRQPPRLVTS TAYTSPQPRE VPVCPLTAGG ETQNAAALPG   60
PTSWPLLASL LQILWKGGLK KQHDTLVEYH KKYGKIFRMK LGSFESVHLG SPCLLEALYR  120
TESVPQRLEI KPWKAYRDYR KEGYGLLILE GEDWQRVRSA FQKKLMKPGE VMKLDNKINE  180
VLADFMGRID ELCDERGHVE DLYSELNKWS FESICLVLYE KRFGLLQKNA GDEAVNFIMA  240
IKTMMSTFGR MMVTPVELHK SLNTKVWQGH TLAWDTIFKS VKACIDNRLE KYSQQPSADF  300
LCDIYHQNRL SKKELYAAVT ELQLAAVETT ANSLMWILYN LSRNPQVQQK LLKEIQSVLP  360
ENQRPREEDL RNMPYLKACL KESMRLTPGV PFTTRTLDKA TVLGEYALPK GTVLMLNTQV  420
LGSSEDNFED SSQFRPERWL QEKEKINPFA HLPFGVGKRM CIGRRLAELQ LHLALCWIVR  480
KYDIQATDNE PVEMLHSGTL VPSRELPIAF CQR
```

Seq ID NO: 44 DNA sequence
Nucleic Acid Accession #: NM_007000.2
Coding sequence: 1-777

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGCGTCTG CGGCAGCAGC GGAGGCCGAG AAGGGATCTC CAGTTGTGGT GGGCCTGCTA   60
GTTGTGGGCA ATATCATTAT TCTGCTGTCA GGCCTGTCCC TGTTTGCTGA GACCATATGG  120
GTGACAGCCG ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATGACGTC  180
TTCGCTGGTG CCTGGATTGC CATCTTCTGC GGCTTCTCCT TCTTCATGGT AGCCAGTTTT  240
GGTGTGGGTG CCGCACTCTG CCGCCGCCGG TCCATGGTCC TCACGTACCT GGTGCTCATG  300
CTCATCGTCT ACATCTTCGA GTGCGCCTCC TGCATCACGT CCTACACCCA CCGTGACTAC  360
ATGGTGTCCA ACCCATCCCT GATCACCAAG CAGATGCTGA CCTTCTACAG CGCGGACACC  420
GACCAGGGCC AGGAGCTGAC CCGCCTCTGG GACCGCGTCA TGATTGAGCA AGAATGCTGT  480
GGCACATCTG GTCCCATGGA CTGGGTGAAC TTCACGTCAG CCTTCCGGGC GGCCACTCCG  540
GAGGTGGTGT TCCCCTGGCC CCCACTGTGC TGTCGCCGGA CGGGAAACTT CATCCCCCTC  600
AACGAGGAGG GCTGCCGCCT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA  660
CACATCGGCC ACGCCATCGA CAGCTACACG TGGGGTATCT CGTGGTTTGG GTTTGCCATC  720
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CTGATGTGGA CGCTCCCGGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGAGGG   780
ACAGGAGGGG AAGGCAACAT ACACACCCCG GACTCCTCCG CATCCTCCTC CTGCTTCCTC   840
CGCTGGGCCT GGATGGCTGC CTCACCTCTC ACCTCCCAAC GTCCCTAGCC CTTACGTCCT   900
TCCACTTCCA AGATCTTTTT CCAGGTTCCT GAGCCCTACT GTGTCTCAGG TGTGCCCTGA   960
AACCCCAGGG CTTGTGTGCA CATATCCTTA GCCCATCTTT CAAGGGACCT CTCCATGATC  1020
CCACCTCCCA TTCACAGATA CCTCTCTTGT AGCTCTCTGA CCTCCTCCTT CATGGCAGGC  1080
ATCGCCATTC TTGCTGAACC GTTTGTGATT GCCATTTGAG CTCTGGAAGC CTCTATTGCC  1140
ATGAGAGTTC TGTCACGGTC ACTTTACTGT CCCCATCATC ACCCAGCACG GGGCTAAGCA  1200
TATACTAGAT AGTCAATAAA TAA
```

Seq ID NO: 45 Protein sequence:
Protein Accession #: NP_008931.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MASAAAAEAE KGSPVVVGLL VVGNIIILLS GLSLFAETIW VTADQYRVYP LMGVSGKDDV    60
FAGAWIAIFC GFSFFMVASF GVGAALCRRR SMVLTYLVLM LIVYIFECAS CITSYTHRDY   120
MVSNPSLITK QMLTFYSADT DQGQELTRLW DRVMIEQECC GTSGPMDWVN FTSAFRAATP   180
EVVFPWPPLC CRRTGNFIPL NEEGCRLGHM DYLFTKGCFE HIGHAIDSYT WGISWFGFAI   240
LMWTLPVMLI AMYFYTML
```

Seq ID NO: 46 DNA sequence
Nucleic Acid Accession #: NM_006760.1
Coding sequence: 39..593

```
1          11         21         31         41         51
|          |          |          |          |          |
GAAAGCCTGC CAGCACCTAT TCCACCTCCC AGCCCAGCAT GGCACCCCTG CTGCCCATCC    60
GGACCTTGCC CTTGATCCTG ATTCTGCTGG CTCTGCTGTC CCCAGGGGCT GCAGACTTCA   120
ACATCTCAAG CCTCTCTGGT CTGCTGTCCC CGGCGCTAAC GGAGAGCCTG CTGGTTGCCT   180
TGCCCCCCTG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGGAGA GCCAATGACA   240
GCAAAGTGGT GACGTCCAGC TTTGTGGTGC CTCCGTGCCG TGGGCGCAGG GAACTGGTGA   300
GTGTGGTGGA CAGTGGTGCT GGCTTCACAG TCACTCGGCT CAGTGCATAC CAGGTGACAA   360
ACCTCGTGCC AGGAACCAAA TTCTACATTT CCTACCTAGT GAAGAAGGGG ACAGCCACTG   420
AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGAA TCCATTGGGC   480
TGGGTATGGC CCGCACAGGG GGCATGGTGG TCATCACGGT GCTGCTCTCT GTCGCCATGT   540
TCCTGCTGGT GCTGGGCTTC ATCATTGCCC TGGCACTGGG CTCCCGCAAG TAAGGAGGTC   600
TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGGCACCA TCCAGCTCCC CAGCCCACCT   660
GCTCCCAGGC CCCAGGCCTG TGGCTCCCTT GGTGCCCTCG CCTCCTCCTC CTGCCCTCCT   720
CTCCCCTAGA GCCCTCTCCT CCCTCTGTCC CTCTCCTTGC CCCCAGTGCC TCACCTTCCA   780
ACACTCCATT ATTCCTCTCA CCCCACTCCT GTCAGAGTTG ACTTTCCTCC CATTTTACCA   840
CTTTAAACAC CCCCATAACA ATTCCCCCAT CCTTCAGTGA ACTAAGTCCC TATAATAAAG   900
GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA
```

Seq ID NO: 47 Protein Sequence
Protein Accession #: NP_006751.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAPLLPIRTL PLILILLALL SPGAADFNIS SLSGLLSPAL TESLLVALPP CHLTGGNATL    60
MVRRANDSKV VTSSFVVPPC RGRRELVSVV DSGAGFTVTR LSAYQVTNLV PGTKFYISYL   120
VKKGTATESS REIPMSTLPR RNMESIGLGM ARTGGMVVIT VLLSVAMFLL VLGFIIALAL   180
GSRK
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Seq ID NO: 48 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 200-2932

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1          11         21         31         41         51
|          |          |          |          |          |
ATTGCTGATG GATCAGTGAG CCTGTGTTCA TGCCAGTGAG CTGCTGTGGC TCAGATACTG    60
ATACTTTCTT TCCAAACAGC ATAAGAAGTG ATTGAGCCAC AAGTATACTG AAGGAAGGGC   120
TCCCTCGAGT TCTGGTGTGA AGAGATAAAT CACCAGTCAC AGACTATGCA CCCGACTGCT   180
GCTGTTCAGT CCAGGGAAAA TGAAAGTTGG AGTGCTGTGG CTCATTTCTT TCTTCACCTT   240
CACTGACGGC CACGGTGGCT TCCTGGGGAA AAATGATGGC ATCAAAACAA AAAAAGAACT   300
CATTGTGAAT AAGAAAAAAC ATCTAGGCCC AGTCGAAGAA TATCAGCTGC TGCTTCAGGT   360
GACCTATAGA GATTCCAAGG AGAAAAGAGA TTTGAGAAAT TTTCTGAAGC TCTTGAAGCC   420
TCCATTATTA TGGTCACATG GGCTAATTAG AATTATCAGA GCAAAGGCTA CCACAGACTG   480
CAACAGCCTG AATGGAGTCC TGCAGTGTAC CTGTGAAGAC AGCTACACCT GGTTTCCTCC   540
CTCATGCCTT GATCCCCAGA ACTGCTACCT TCACACGGCT GGAGCACTCC CAAGCTGTGA   600
ATGTCATCTC AACAACCTCA GCCAGAGTGT CAATTTCTGT GAGAGAACAA AGATTTGGGG   660
CACTTTCAAA ATTAATGAAA GGTTTACAAA TGACCTTTTG AATTCATCTT CTGCTATATA   720
CTCCAAATAT GCAAATGGAA TTGAAATTCA ACTTAAAAAA GCATATGAAA GAATTCAAGG   780
TTTTGAGTCG GTTCAGGTCA CCCAATTTCG AAATGGAAGC ATCGTTGCTG GGTATGAAGT   840
TGTTGGCTCC AGCAGTGCAT CTGAACTGCT GTCAGCCATT GAACATGTTG CCGAGAAGGC   900
TAAGACAGCC CTTCACAAGC TGTTTCCATT AGAAGACGGC TCTTTCAGAG TGTTCGGAAA   960
AGCCCAGTGT AATGACATTG TCTTTGGATT TGGGTCCAAG GATGATGAAT ATACCCTGCC  1020
CTGCAGCAGT GGCTACAGGG GAAACATCAC AGCCAAGTGT GAGTCCTCTG GGTGGCAGGT  1080
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CATCAGGGAG ACTTGTGTGC TCTCTCTGCT TGAAGAACTG AACAAGAATT TCAGTATGAT  1140
TGTAGGCAAT GCCACTGAGG CAGCTGTGTC ATCCTTCGTG CAAAATCTTT CTGTCATCAT  1200
TCGGCAAAAC CCATCAACCA CAGTGGGGAA TCTGGCTTCG GTGGTGTCGA TTCTGAGCAA  1260
TATTTCATCT CTGTCACTGG CCAGCCATTT CAGGGTGTCC AATTCAACAA TGGAGGATGT  1320
CATCAGTATA GCTGACAATA TCCTTAATTC AGCCTCAGTA ACCAACTGGA CAGTCTTACT  1380
GCGGGAAGAA AAGTATGCCA GCTCACGGTT ACTAGAGACA TTAGAAAACA TCAGCACTCT  1440
GGTGCCTCCG ACAGCTCTTC CTCTGAATTT TTCTCGGAAA TTCATTGACT GGAAAGGGAT  1500
TCCAGTGAAC AAAAGCCAAC TCAAAAGGGG TTACAGCTAT CAGATTAAAA TGTGTCCCCA  1560
AAATACATCT ATTCCCATCA GAGGCCGTGT GTTAATTGGG TCAGACCAAT TCCAGAGATC  1620
CCTTCCAGAA ACTATTATCA GCATGGCCTC GTTGACTCTG GGGAACATTC TACCCGTTTC  1680
CAAAAATGGA AATGCTCAGG TCAATGGACC TGTGATATCC ACGGTTATTC AAAACTATTC  1740
CATAAATGAA GTTTTCCTAT TTTTTTCCAA GATAGAGTCA AACCTGAGCC AGCCTCATTG  1800
TGTGTTTTGG GATTTCAGTC ATTTGCAGTG GAACGATGCA GGCTGCCACC TAGTGAATGA  1860
AACTCAAGAC ATCGTGACGT GCCAATGTAC TCACTTGACC TCCTTCTCCA TATTGATGTC  1920
ACCTTTTGTC CCCTCTACAA TCTTCCCCGT TGTAAAATGG ATCACCTATG TGGGACTGGG  1980
TATCTCCATT GGAAGTCTCA TTTTATGCCT GATCATCGAG GCTTTGTTTT GGAAGCAGAT  2040
TAAAAAAAGC CAAACCTCTC ACACACGTCG TATTTGCATG GTGAACATAG CCCTGTCCCT  2100
CTTGATTGCT GATGTCTGGT TTATTGTTGG TGCCACAGTG GACACCACGG TGAACCCTTC  2160
TGGAGTCTGC ACAGCTGCTG TGTTCTTTAC ACACTTCTTC TACCTCTCTT TGTTCTTCTG  2220
GATGCTCATG CTTGGCATCC TGCTGGCTTA CCGGATCATC CTCGTGTTCC ATCACATGGC  2280
CCAGCATTTG ATGATGGCTG TTGGATTTTG CCTGGGTTAT GGGTGCCCTC TCATTATATC  2340
TGTCATTACC ATTGCTGTCA CGCAACCTAG CAATACCTAC AAAAGGAAAG ATGTGTGTTG  2400
GCTTAACTGG TCCAATGGAA GCAAACCACT CCTGGCTTTT GTTGTCCCTG CACTGGCTAT  2460
TGTGGCTGTG AACTTCGTTG TGGTGCTGCT AGTTCTCACA AAGCTCTGGA GGCCGACTGT  2520
TGGGGAAAGA CTGAGTCGGG ATGACAAGGC CACCATCATC CGCGTGGGGA AGAGCCTCCT  2580
CATTCTGACC CCTCTGCTAG GGCTCACCTG GGGCTTTGGA ATAGGAACAA TAGTGGACAG  2640
CCAGAATCTG GCTTGGCATG TTATTTTTGC TTTACTCAAT GCATTCCAGG GATTTTTTAT  2700
CTTATGCTTT GGAATACTCT TGGACAGTAA GCTGCGACAA CTTCTGTTCA ACAAGTTGTC  2760
TGCCTTAAGT TCTTGGAAGC AAACAGAAAA GCAAAACTCA TCAGATTTAT CTGCCAAACC  2820
CAAATTCTCA AAGCCTTTCA ACCCACTGCA AAACAAAGGC CATTATGCAT TTTCTCATAC  2880
TGGAGATTCC TCCGACAACA TCATGCTAAC TCAGTTTGTC TCAAATGAAT AAGGCAAGGA  2940
ATCATAAAAT CAAGAAAAAA TTTCCAGAAC AACTTGACAT TTAGAGACAA ATGTCAATGA  3000
AGAAATTATG CTCAGTATTC GATCGGGTTT TCTGATTTAG GGGTCTGGGA ATAAAACAAG  3060
AATGTCTCAG TGGCTTCA
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Seq ID NO: 49 Protein sequence:
Protein Accession #: EOS sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MKVGVLWLIS PFTFTDGHGG FLGKNDGIKT KKELIVNKKK HLGPVEEYQL LLQVTYRDSK    60
EKRDLRNFLK LLKPPLLWSH GLIRIIRAKA TTDCNSLNGV LQCTCEDSYT WFPPSCLDPQ   120
NCYLHTAGAL PSCECHLNNL SQSVNFCERT KIWGTFKINE RFTNDLLNSS SAIYSKYANG   180
IEIQLKKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK   240
LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV   300
LSLLEELNKN FSMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNISSLSL   360
ASHFRVSNST MEDVISIADN ILNSASVTNW TVLLREEKYA SSRLLETLEN ISTLVPPTAL   420
PLNFSRKFID WKGIPVNKSQ LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FQRSLPETII   480
SMASLTLGNI LPVSKNGNAQ VNGPVISTVI QNYSINEVFL FFSKIESNLS QPHCVFWDFS   540
HLQWNDAGCH LVNETQDIVT CQCTHLTSFS ILMSPFVPST IFPVVKWITY VGLGISIGSL   600
ILCLIIEALF WKQIKKSQTS HTRRICMVNI ALSLLIADVW FIVGATVDTT VNPSGVCTAA   660
VFFTHFFYLS LFFWMLMLGI LLAYRIILVF HHMAQHLMMA VGFCLGYGCP LIISVITIAV   720
TQPSNTYKRK DVCWLNWSNG SKPLLAFVVP ALAIVAVNFV VVLLVLTKLW RPTVGERLSR   780
DDKATIIRVG KSLLILTPLL GLTWGFGIGT IVDSQNLAWH VIFALLNAFQ GFFILCFGIL   840
LDSKLRQLLF NKLSALSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKGHYA FSHTGDSSDN   900
IMLTQFVSNE
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Seq ID NO: 50 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 63-3224

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1          11         21         31         41         51
|          |          |          |          |          |
CAGGAATTTG TGGCGGAGAG GGCAAATAAC TGCGGCTCTC CCGGCGCCCC GATGCTCGCA    60
CCATGTCGAG GCGCAAGCAG GCGAAACCCC AGCACATCAA CTCGGAGGAG GACCAGGGCG   120
AGCAGCAGCC GCAGCAGCAG ACCCCGGAGT TTGCAGATGC GGCCCCAGCG GCGCCCGCGG   180
CGGGGGAGCT GGGTGCTCCA GTGAACCACC CAGGGAATGA CGAGGTGGCG AGTGAGGATG   240
AAGCCACAGT AAAGCGGCTT CGTCGGGAGG AGACGCACGT CTGTGAGAAA TGCTGTGCGG   300
AGTTCTTCAG CATCTCTGAG TTCCTGGAAC ATAAGAAAAA TTGCACTAAA AATCCACCTG   360
TCCTCATCAT GAATGACAGC GAGGGGCCTG TGCCTTCAGA AGACTTCTCC GGAGCTGTAC   420
TGAGCCACCA GCCCACCAGT CCCGGCAGTA AGGACTGTCA CAGGGAGAAT GGCGGCAGCT   480
CAGAGGACAT GAAGGAGAAG CCGGATGCGG AGTCTGTGGT GTACCTAAAG ACAGAGACAG   540
CCCTGCCACC CACCCCCCAG GACATAAGCT ATTTAGCCAA AGGCAAAGTG GCCAACACTA   600
ATGTGACCTT GCAGGCACTA CGGGGCACCA AGGTGGCGGT GAATCAGCGG AGCGCGGATG   660
CACTCCCTGC CCCCGTGCCT GGTGCCAACA GCATCCCGTG GGTCCTCGAG CAGATCTTGT   720
GTCTGCAGCA GCAGCAGCTA CAGCAGATCC AGCTCACCGA GCAGATCCGC ATCCAGGTGA   780
ACATGTGGGC CTCCCACGCC CTCCACTCAA GCGGGGCAGG GGCCGACACT CTGAAGACCT   840
TGGGCAGCCA CATGTCTCAG CAGGTTTCTG CAGCTGTGGC TTTGCTCAGC CAGAAAGCTG   900
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GAAGCCAAGG TCTGTCTCTG GATGCCTTGA AACAAGCCAA GCTACCTCAC GCCAACATCC    960
CTTCTGCCAC CAGCTCCCTG TCCCCAGGGC TGGCACCCTT CACTCTGAAG CCGGATGGGA   1020
CCCGGGTGCT CCCGAACGTC ATGTCCCGCC TCCCGAGCGC TTTGCTTCCT CAGGCCCCGG   1080
GCTCGGTGCT CTTCCAGAGC CCTTTCTCCA CTGTGGCGCT AGACACATCC AAGAAAGGGA   1140
AGGGGAAGCC ACCGAACATC TCCGCGGTGG ATGTCAAACC CAAAGACGAG GCGGCCCTCT   1200
ACAAGCACAA GTGTAAGTAC TGTAGCAAGG TTTTTGGGAC TGATAGCTCC TTGCAGATCC   1260
ACCTCCGCTC CCACACTGGA GAGAGACCCT TCGTGTGCTC TGTCTGTGGT CATCGCTTCA   1320
CCACCAAGGG CAACCTCAAG GTGCACTTTC ACCGACATCC CCAGGTGAAG GCAAACCCCC   1380
AGCTGTTTGC CGAGTTCCAG GACAAAGTGG CGGCCGGCAA TGGCATCCCC TATGCACTCT   1440
CTGTACCTGA CCCCATAGAT GAACCGAGTC TTTCTTTAGA CAGCAAACCT GTCCTTGTAA   1500
CCACCTCTGT AGGGCTACCT CAGAATCTTT CTTCGGGGAC TAATCCCAAG GACCTCACGG   1560
GTGGCTCCTT GCCCGGTGAC CTGCAGCCTG GGCCTTCTCC AGAAAGTGAG GGTGGACCCA   1620
CACTCCCTGG GGTGGGACCA AACTATAATT CCCCAAGGGC TGGTGGCTTC CAAGGGAGTG   1680
GGACCCCTGA GCCAGGGTCA GAGACCCTGA AATTGCAGCA GTTGGTGGAG AACATTGACA   1740
AGGCCACCAC TGATCCCAAC GAATGTCTCA TTTGCCACCG AGTCTTAAGC TGTCAGAGCT   1800
CCCTCAAGAT GCATTATCGC ACCCACACCG GGGAGAGACC GTTCCAGTGT AAGATCTGTG   1860
GCCGAGCCTT TTCTACCAAA GGTAACCTGA AGACACACCT TGGGGTTCAC CGAACCAACA   1920
CATCCATTAA GACGCAGCAT TCGTGCCCCA TCTGCCAGAA GAAGTTCACT AATGCCGTGA   1980
TGCTGCAGCA ACATATTCGG ATGCACATGG GCGGTCAGAT TCCCAACACG CCCCTGCCAG   2040
AGAATCCCTG TGACTTTACG GGTTCTGAGC CAATGACCGT GGGTGAGAAC GGCAGCACCG   2100
GCGCTATCTG CCATGATGAT GTCATCGAAA GCATCGATGT AGAGGAAGTC AGCTCCCAGG   2160
AGGCTCCCAG CAGCTCCTCC AAGGTCCCCA CGCCTCTTCC CAGCATCCAC TCGGCATCAC   2220
CCACGCTAGG GTTTGCCATG ATGGCTTCCT TAGATGCCCC AGGGAAAGTG GGTCCTGCCC   2280
CTTTTAACCT GCAGCGCCAG GGCAGCAGAG AAAACGGTTC CGTGGAGAGC GATGGCTTGA   2340
CCAACGACTC ATCCTCGCTG ATGGGAGACC AGGAGTATCA GAGCCGAAGC CCAGATATCC   2400
TGGAAACCAC ATCCTTCCAG GCACTCTCCC CGGCCAATAG TCAAGCCGAA AGCATCAAGT   2460
CAAAGTCTCC CGATGCTGGG AGCAAAGCAG AGAGCTCCGA GAACAGCCGC ACTGAGATGG   2520
AAGGTCGGAG CAGTCTCCCT TCCACGTTTA TCCGAGCCCC GCCGACCTAT GTCAAGGTTG   2580
AAGTTCCTGG CACATTTGTG GGACCCTCGA CATTGTCCCC AGGGATGACC CCTTTGTTAG   2640
CAGCCCAGCC ACGCCGACAG GCCAAGCAAC ATGGCTGCAC ACGGTGTGGG AAGAACTTCT   2700
CGTCTGCTAG CGCTCTTCAG ATCCACGAGC GGACTCACAC TGGAGAGAAG CCTTTTGTGT   2760
GCAACATTTG TGGGCGAGCT TTTACCACCA AAGGCAACTT AAAGGTTCAC TACATGACAC   2820
ACGGGGCGAA CAATAACTCA GCCCGCCGTG GAAGGAAGTT GGCCATCGAG AACACCATGG   2880
CTCTGTTAGG TACGGACGGA AAAAGAGTCT CAGAAATCTT TCCCAAGGAA ATCCTGGCCC   2940
CTTCAGTGAA TGTGGACCCT GTTGTGTGGA ACCAGTACAC CAGCATGCTC AATGGCGGTC   3000
TGGCCGTGAA GACCAATGAG ATCTCTGTGA TCCAGAGTGG GGGGGTTCCT ACCCTCCCGG   3060
TTTCCTTGGG GGCCACCTCC GTTGTGAATA ACGCCACTGT CTCCAAGATG GATGGCTCCC   3120
AGTCGGGTAT CAGTGCAGAT GTGGAAAAAC CAAGTGCTAC TGACGGCGTT CCCAAACACC   3180
AGTTTCCTCA CTTCCTGGAA GAAAACAAGA TTGCGGTCAG CTAAGGGAGA ACTTGCGTGG   3240
AAGGAGCAAT GCAGACACAG TGAAATCTCT AGAATCTGCT TTGTTTTGTA AGAACTCATC   3300
TCCTCCTGTT TTCTTTTTCT TACTGATATG CAAATGATGT TTACTACGTT GGTTGTGACC   3360
ACAACCTCAG GCAAGTGCTA CAATCACGAT TGTTGCTATG CTGCTTTGCA AAAAGTTG
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Seq ID NO: 51 Protein sequence:
Protein Accession #: NP_065169.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSRRKQAKPQ HINSEEDQGE QQPQQQTPEF ADAAPAAPAA GELGAPVNHP GNDEVASEDE     60
ATVKRLRREE THVCEKCCAE FFSISEFLEH KKNCTKNPPV LIMNDSEGPV PSEDFSGAVL    120
SHQPTSPGSK DCHRENGGSS EDMKEKPDAE SVVYLKTETA LPPTPQDISY LAKGKVANTN    180
VTLQALRGTK VAVNQRSADA LPAPVPGANS IPWVLEQILC LQQQQLQQIQ LTEQIRIQVN    240
MWASHALHSS GAGADTLKTL GSHMSQQVSA AVALLSQKAG SQGLSLDALK QAKLPHANIP    300
SATSSLSPGL APFTLKPDGT RVLPNVMSRL PSALLPQAPG SVLFQSPFST VALDTSKKGK    360
GKPPNISAVD VKPKDEAALY KHKCKYCSKV FGTDSSLQIH LRSHTGERPF VCSVCGHRFT    420
TKGNLKVHFH RHPQVKANPQ LFAEFQDKVA AGNGIPYALS VPDPIDEPSL SLDSKPVLVT    480
TSVGLPQNLS SGTNPKDLTG GSLPGDLQPG PSPESEGGPT LPGVGPNYNS PRAGGFQGSG    540
TPEPGSETLK LQQLVENIDK ATTDPNECLI CHRVLSCQSS LKMHYRTHTG ERPFQCKICG    600
RAFSTKGNLK THLGVHRTNT SIKTQHSCPI CQKKFTNAVM LQQHIRMHMG GQIPNTPLPE    660
NPCDFTGSEP MTVGENGSTG AICHDDVIES IDVEEVSSQE APSSSSKVPT PLPSIHSASP    720
TLGFAMMASL DAPGKVGPAP FNLQRQGSRE NGSVESDGLT NDSSSLMGDQ EYQSRSPDIL    780
ETTSFQALSP ANSQAESIKS KSPDAGSKAE SSENSRTEME GRSSLPSTFI RAPPTYVKVE    840
VPGTFVGPST LSPGMTPLLA AQPRRQAKQH GCTRCGKNFS SASALQIHER THTGEKPFVC    900
NICGRAFTTK GNLKVHYMTH GANNNSARRG RKLAIENTMA LLGTDGKRVS EIFPKEILAP    960
SVNVDPVVWN QYTSMLNGGL AVKTNEISVI QSGGVPTLPV SLGATSVVNN ATVSKMDGSQ   1020
SGISADVEKP SATDGVPKHQ FPHFLEENKI AVS
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Seq ID NO: 52 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
TCTAGCATTA AAGGAAGAAA CCCCGTCTTG CAACGAAGGC CTCAAAGAGG TCCAAATATC     60
AACTTGCAGA CATAACAAGC AGAGTGTTTC TAAACTGCTC TAAGAAAAGA AAGGTTAAAC    120
TCTGTGAGTT GAAGGCACAC ATCACAAAGT AGTTTCTGAG AATGATTCTG TCTAGTTTTT    180
ATTTGAAGAT ATTTCCTTTT CTACTGTTGG CATCAAATCG CTTGAAATCT CCACTTGCAA    240
ATTCCACAAA AAGAGTGTTT CAAATCTGCT CTGTGTAAAG GGACGTTCCA CTCTGTGAGT    300
TGAATACACA CAACACAAGG AAGTTACTGA GAATTCTTCT GTCTAGCATG ATATGAAGAA    360
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ATCCCGTTTC CAACGAAGGC CTCAATGAGG TCTATATATC CACTTGCAGA CTTTACAAAC   420
AGAGTGTTTC CTAACTGCTC TATGAAAAGA AAGGTTAAAC TCTGTGGAGT TGAACGCACA   480
CATCACAAAA GGAGTTTCTG AGAATCATTC TGTCTAGTTT TTTTAGGAAG ATATTTCCTT   540
TTCTACCGTT GACTTCAAAG CGGCTGAAAT
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Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_001910.1
Coding sequence: 50..1240

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1          11         21         31         41         51
|          |          |          |          |          |
GGAGAGAAGA AAGGAGGGGG CAAGGGAGAA GCTGCTGGTC GGACTCACAA TGAAAACGCT   60
CCTTCTTTTG CTGCTGGTGC TCCTGGAGCT GGGAGAGGCC CAAGGATCCC TTCACAGGGT   120
GCCCCTCAGG AGGCATCCGT CCCTCAAGAA GAAGCTGCGG GCACGGAGCC AGCTCTCTGA   180
GTTCTGGAAA TCCCATAATT TGGACATGAT CCAGTTCACC GAGTCCTGCT CAATGGACCA   240
GAGTGCCAAG GAACCCCTCA TCAACTACTT GGATATGGAA TACTTCGGCA CTATCTCCAT   300
TGGCTCCCCA CCACAGAACT TCACTGTCAT CTTCGACACT GGCTCCTCCA ACCTCTGGGT   360
CCCCTCTGTG TACTGCACTA GCCCAGCCTG CAAGACGCAC AGCAGGTTCC AGCCTTCCCA   420
GTCCAGCACA TACAGCCAGC CAGGTCAATC TTTCTCCATT CAGTATGGAA CCGGGAGCTT   480
GTCCGGGATC ATTGGAGCCG ACCAAGTCTC TGTGGAAGGA CTAACCGTGG TTGGCCAGCA   540
GTTTGGAGAA AGTGTCACAG AGCCAGGCCA GACCTTTGTG GATGCAGAGT TTGATGGAAT   600
TCTGGGCCTG GGATACCCCT CCTTGGCTGT GGGAGGAGTG ACTCCAGTAT TTGACAACAT   660
GATGGCTCAG AACCTGGTGG ACTTGCCGAT GTTTTCTGTC TACATGAGCA GTAACCCAGA   720
AGGTGGTGCG GGGAGCGAGC TGATTTTTGG AGGCTACGAC CACTCCCATT TCTCTGGGAG   780
CCTGAATTGG GTCCCAGTCA CCAAGCAAGC TTACTGGCAG ATTGCACTGG ATAACATCCA   840
GGTGGGAGGC ACTGTTATGT TCTGCTCCGA GGGCTGCCAG GCCATTGTGG ACACAGGGAC   900
TTCCCTCATC ACTGGCCCTT CCGACAAGAT TAAGCAGCTG CAAAACGCCA TTGGGGCAGC   960
CCCCGTGGAT GGAGAATATG CTGTGGAGTG TGCCAACCTT AACGTCATGC CGGATGTCAC   1020
CTTCACCATT AACGGAGTCC CCTATACCCT CAGCCCAACT GCCTACACCC TACTGGACTT   1080
CGTGGATGGA ATGCAGTTCT GCAGCAGTGG CTTTCAAGGA CTTGACATCC ACCCTCCAGC   1140
TGGGCCCCTC TGGATCCTGG GGGATGTCTT CATTCGACAG TTTTACTCAG TCTTTGACCG   1200
TGGGAATAAC CGTGTGGGAC TGGCCCCAGC AGTCCCCTAA GGAGGGGCCT TGTGTCTGTG   1260
CCTGCCTGTC TGACAGACCT TGAATATGTT AGGCTGGGGC ATTCTTTACA CCTACAAAAA   1320
GTTATTTTCC AGAGAATGTA GCTGTTTCCA GGGTTGCAAC TTGAATTAAG ACCAAACAGA   1380
ACATGAGAAT ACACACACAC ACACACATAT ACACACACAC ACACTTCACA CATACACACC   1440
ACTCCCACCA CCGTCATGAT GGAGGAATTA CGTTATACAT TCATATTTTG TATTGATTTT   1500
TGATTATGAA AATCAAAAAT TTTCACATTT GATTATGAAA ATCTCCAAAC ATATGCACAA   1560
GCAGAGATCA TGGTATAATA AATCCCTTTG CAACTCCACT CAGCCCTGAC AACCCATCCA   1620
CACACGGCCA GGCCTGTTTA TCTACACTGC TGCCCACTCC TCTCTCCAGC TCCACATGCT   1680
GTACCTGGAT CATTCTGAAG CAAATTCCGA GCATTACATC ATTTGTCCA TAAATATTTC   1740
TAACATCCTT AAATATACAA TCGGAATTCA AGCATCTCCC ATTGTCCCAC AAATGTTTGG   1800
CTGTTTTTGT AGTTGGATTG TTTGTATTAG GATTCAAGCA AGGCCCATAT ATTGCATTTA   1860
TTTGAAATGT CTGTAAGTCT CTTTCCATCT ACAGAGTTTA GCACATTTGA ACGTTGCTGG   1920
TTGAAATCCC GAGGTGTCAT TTGACATGGT TCTCTGAACT TATCTTTCCT ATAAAATGGT   1980
AGTTAGATCT GGAGGTCTGA TTTTGTGGCA AAAATACTTC CTAGGTGGTG CTGGGTACTT   2040
CTTGTTGCAT CCTGTCAGGA GGCAGATAAT GCTGGTGCCT CTCTATTGGT AATGTTAAGA   2100
CTGCTGGGTG GGTTTGGAGT TCTTGGCTTT AATCATTCAT TACAAAGTTC AGCATTTT
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Seq ID NO: 54 Protein Sequence
Protein Accession #: NP_001901.1

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MKTLLLLLLV LLELGEAQGS LHRVPLRRHP SLKKKLRARS QLSEFWKSHN LDMIQFTESC   60
SMDQSAKEPL INYLDMEYFG TISIGSPPQN FTVIFDTGSS NLWVPSVYCT SPACKTHSRF   120
QPSQSSTYSQ PGQSFSIQYG TGSLSGIIGA DQVSVEGLTV VGQQFGESVT EPGQTFVDAE   180
FDGILGLGYP SLAVGGVTPV FDNMMAQNLV DLPMFSVYMS SNPEGGAGSE LIFGGYDHSH   240
FSGSLNWVPV TKQAYWQIAL DNIQVGGTVM FCSEGCQAIV DTGTSLITGP SDKIKQLQNA   300
IGAAPVDGEY AVECANLNVM PDVTFTINGV PYTLSPTAYT LLDFVDGMQF CSSGFQGLDI   360
HPPAGPLWIL GDVFIRQFYS VFDRGNNRVG LAPAVP
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Seq ID NO: 55 DNA sequence
Nucleic Acid Accession #: NM_018058.1
Coding sequence: 319..1575

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GACGGCCGGG AGGAGATCTA CTTCCTCAAC ACCAATAATG CCTTCTCGGG GGTGGCCACG   120
TACACCGACA AGTTGTTCAA GTTCCGCAAT AACCGGTGGG AAGACATCCT GAGCGATGAG   180
GTCAACGTGG CCCGTGGTGT GGCCAGCCTC TTTGCCGGAC GCTCTGTGGC CTGTGTGGAC   240
AGAAAGGGCT CTGGACGCTA CTCTATCTAC ATTGCCAATT ACGCCTACGG TAATGTGGGC . 300
CCTGATGCCC TCATTGAAAT GGACCCTGAG GCCAGTGACC TCTCCCGGGG CATTCTGGCG   360
CTCAGAGATG TGGCTGCTGA GGCTGGGGTC AGCAAATATA CAGGGGGCCG AGGCGTCAGC   420
GTGGGCCCCA TCCTCAGCAG CAGTGCCTCG GATATCTTCT GCGACAATGA GAATGGGCCT   480
AACTTCCTTT TCCACAACCG GGGCGATGGC ACCTTTGTGG ACGCTGCGGC CAGTGCTGGT   540
GTGGACGACC CCCACCAGCA TGGGCGAGGT GTCGCCCTGG CTGACTTCAA CCGTGATGGC   600
AAAGTGGACA TCGTCTATGG CAACTGGAAT GGCCCCCACC GCCTCTATCT GCAAATGAGC   660
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ACCCATGGGA AGGTCCGCTT CCGGGACATC GCCTCACCCA AGTTCTCCAT GCCCTCCCCT   720
GTCCGCACGG TCATCACCGC CGACTTTGAC AATGACCAGG AGCTGGAGAT CTTCTTCAAC   780
AACATTGCCT ACCGCAGCTC CTCAGCCAAC CGCCTCTTCC GCGTCATCCG TAGAGAGCAC   840
GGAGACCCCC TCATCGAGGA GCTCAATCCC GGCGACGCCT TGGAGCCTGA GGGCCGGGGC   900
ACAGGGGGTG TGGTGACCGA CTTCGACGGA GACGGGATGC TGGACCTCAT CTTGTCCCAT   960
GGAGAGTCCA TGGCTCAGCC GCTGTCCGTC TTCCGGGGCA ATCAGGGCTT CAACAACAAC   1020
TGGCTGCGAG TGGTGCCACG CACCCGGGTT GGGGCCTTTG CCAGGGGAGC TAAGGTCGTG   1080
CTCTACACCA AGAAGAGTGG GGCCCACCTG AGGATCATCG ACGGGGGCTC AGGCTACCTG   1140
TGTGAGATGG AGCCCGTGGC ACACTTTGGC CTGGGGAAGG ATGAAGCCAG CAGTGTGGAG   1200
GTGACGTGGC CAGATGGCAA GATGGTGAGC CGGAACGTGG CCAGCGGGGA GATGAACTCA   1260
GTGCTGGAGA TCCTCTACCC CCGGGATGAG GACACACTTC AGGACCCAGC CCCACTGGAG   1320
ACACCAATGA ATGCATCCAG TTCCCATTCG TGTGCCCTCG AGACAAGCCC GTATGTGTCA   1380
ACACCTATGG AAGCTACAGG TGCCGGACCA ACAAGAAGTG CAGTCGGGGC TACGAGCCCA   1440
ACGAGGATGG CACAGCCTGC GTGGGGACTC TCGGCCAGTC ACCGGGCCCC CGCCCCACCA   1500
CCCCCACCGC TGCTGCTGCC ACTGCCGCTG CTGCTGCCGC TGCTGGAGCT GCCACTGCTG   1560
CACCGGTCCT CGTAGATGGA GATCTCAATC TGGGGTCGGT GGTTAAGGAG AGCTGCGAGC   1620
CCAGCTGCTG AGCAGGGGTG GGACATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA   1680
AAGTGGGCTT GTGCTGCTGC CTAGACAGTA GGGATGTAAA GGCCTGGGAG CTAGACCCTC   1740
CCCAAGCCCA TCCATGCACA TTACTTAGCT AACAATTAGG GAGACTCGTA AGGCCAGGCC   1800
CTGTGCTGGG CACATAGCTG TGATCACAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC   1860
ATTCCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCCAGGGA GGTGGTGTCA   1920
CTGCACAGGA AGTATGAGGA CTTTAGTGTC CTGAGTTCAA ATCCTGATTC AGGAACTCAC   1980
AAAGCTATGT GACCTTACAC CAGTCACTTA ACTTGTTAGC CATCCATTAT CGCATCTGCA   2040
AAATGGGGAT TAAGAATAGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA   2100
GACACTTGGC ACAAAACCTG GCACATAGTA AAGGCTCAAT AAAAACAAGT GCCTCTCACT   2160
GGGCTTTGTC AACACGTG
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Seq ID NO: 56 Protein Sequence
Protein Accession #: NP_060528.1

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MDPEASDLSR GILALRDVAA EAGVSKYTGG RGVSVGPILS SSASDIFCDN ENGPNFLFHN   60
RGDGTFVDAA ASAGVDDPHQ HGRGVALADF NRDGKVDIVY GNWNGPHRLY LQMSTHGKVR   120
FRDIASPKFS MPSPVRTVIT ADFDNDQELE IFFNNIAYRS SSANRLFRVI RREHGDPLIE   180
ELNPGDALEP EGRGTGGVVT DFDGDGMLDL ILSHGESMAQ PLSVFRGNQG FNNNWLRVVP   240
RTRVGAFARG AKVVLYTKKS GAHLRIIDGG SGYLCEMEPV AHFGLGKDEA SSVEVTWPDG   300
KMVSRNVASG EMNSVLEILY PRDEDTLQDP APLETPMNAS SSHSCALETS PYVSTPMEAT   360
GAGPTRSAVG ATSPTRMAQP AWGLSASHRA PAPPPPPLLL PLPLLLPLLE LPLLHRSS
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Seq ID NO: 57 DNA sequence
Nucleic Acid Accession #: AJ279016.1
Coding sequence: 1..1962

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AGTAATCCCA CCCAGCTCAA CTATGGTGTG GCAGTTACTG ATGTGGACCA TGATGGGGAC   180
TTTGAGATCG TCGTGGCGGG GTACAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC   240
CAGAAGCGGC TGGTGAACAT CGCGGTCGAT GAGCGCAGCT CACCCTACTA CGCGCTGCGG   300
GACCGGCAGG GGAACGCCAT CGGGGTCACA GCCTGCGACA TCGACGGGGA CGGCCGGGAG   360
GAGATCTACT TCCTCAACAC CAATAATGCC TTCTCGGGGG TGGCCACGTA CACCGACAAG   420
TTGTTCAAGT TCCGCAATAA CCGGTGGGAA GACATCCTGA GCGATGAGGT CAACGTGGCC   480
CGTGGTGTGG CCAGCCTCTT TGCCGGACGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT   540
GGACGCTACT CTATCTACAT TGCCAATTAC GCCTACGGTA ATGTGGGCCC TGATGCCCTC   600
ATTGAAATGG ACCCTGAGGC CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG   660
GCTGCTGAGG CTGGGGTCAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCCATC   720
CTCAGCAGCA GTGCCTCGGA TATCTTCTGC GACAATGAGA ATGGGCCTAA CTTCCTTTTC   780
CACAACCGGG GCGATGGCAC CTTTGTGGAC GCTGCGGCCA GTGCTGGTGT GGACGACCCC   840
CACCAGCATG GGCGAGGTGT CGCCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC   900
GTCTATGGCA ACTGGAATGG CCCCCACCGC CTCTATCTGC AAATGAGCAC CCATGGGAAG   960
GTCCGCTTCC GGGACATCGC CTCACCCAAG TTCTCCATGC CCTCCCCTGT CCGCACGGTC   1020
ATCACCGCCG ACTTTGACAA TGACCAGGAG CTGGAGATCT TCTTCAACAA CATTGCCTAC   1080
CGCAGCTCCT CAGCCAACCG CCTCTTCCGC GTCATCCGTA GAGAGCACGG AGACCCCCTC   1140
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GTGACCGACT TCGACGGAGA CGGGATGCTG GACCTCATCT TGTCCCATGG AGAGTCCATG   1260
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CCCGTGGCAC ACTTTGGCCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA   1500
GATGGCAAGA TGGTGAGCCG GAACGTGGCC AGCGGGGAGA TGAACTCAGT GCTGGAGATC   1560
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AACAAGAAGT GCAGTCGGGG CTACGAGCCC AACGAGGATG GCACAGCCTG CGTGGGGACT   1800
CTCGGCCAGT CACCGGGCCC CCGCCCCACC ACCCCCACCG CTGCTGCTGC CACTGCCGCT   1860
GCTGCTGCCG CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT   1920
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CTGGGGTCGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA   1980
CCAGCGGATG GAGTCCAGCA GGGGAGTGGG AAAGTGGGCT TGTGCTGCTG CCTAGACAGT   2040
AGGGATGTAA AGGCCTGGGA GCTAGACCCT CCCCAAGCCC ATCCATGCAC ATTACTTAGC   2100
TAACAATTAG GGAGACTCGT AAGGCCAGGC CCTGTGCTGG GCACATAGCT GTGATCACAG   2160
CAGACAGGGT CGCTGCCCTG ATGGCGCTTA CATTCCAGTG GGTCTAATGA CCATATCTTA   2220
GGACACAGAT GTGCCCAGGG AGGTGGTGTC ACTGCACAGG AAGTATGAGG ACTTTAGTGT   2280
CCTGAGTTCA AATCCTGATT CAGGAACTCA CAAAGCTATG TGACCTTACA CCAGTCACTT   2340
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TTAGTGTGGA GATTAGATTA AATGTATGTA AGACACTTGG CACAAAACCT GGCACATAGT   2460
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Seq ID NO: 58 Protein Sequence
Protein Accession #: CAC08451.1

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EIYFLNTNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS   180
GRYSIYIANY AYGNVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI   240
LSSSASDIFC DNENGPNFLF HNRGDGTFVD AAASAGVDDP HQHGRGVALA DFNRDGKVDI   300
VYGNWNGPHR LYLQMSTHGK VRFRDIASPK FSMPSPVRTV ITADFDNDQE LEIFFNNIAY   360
RSSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRGTGGV VTDFDGDGML DLILSHGESM   420
AQPLSVFRGN QGFNNNWLRV VPRTRFGAFA RGAKVVLYTK KSGAHLRIID GGSGYLCEME   480
PVAHFGLGKD EASSVEVTWP DGKMVSRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECGQG   540
FSQQENGHCM DTNECIQFPF VCPRDKPVCV NTYGSYRCRT NKKCSRGYEP NEDGTACVGT   600
LGQSPGPRPT TPTAAAATAA AAAAAGAATA APVLVDGDLN LGSVVKESCE PSC
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Seq ID NO: 59 DNA sequence
Nucleic Acid Accession #: FGENESH
Coding sequence: 1..4794

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TCACCCTACT ACGCGCTGCG GGACCGGCAG GGGAACGCCA TCGGGGTCAC AGCCTGCGAC   240
ATCGACGGGG ACGGCCGGGA GGAGATCTAC TTCCTCAACA CCAATAATGC CTTCTCGGGC   300
CACAGCAGCT CAGCGCAGGT CCCTTCTGGG CTCCACAGAA ACAGGCCTGT GCTGAAGCCT   360
CCACCTACAA CCCCTGCAGG CCTCCTGGGT CTGCCTCCAC TCAGCGGAAG GGACTTTTCC   420
TCCTCCCTGG GTCAGGCTTC TCCGGACAGC AGGCAGGGAG AGAGGGTGCC GGTTCCCTGC   480
TGTCGGGGTG GACTGAGACC TACCCATGAA CCAGAACCAT TTCTTCTGAG ACCCAAATCA   540
GGGGTGGCCA CGTACACCGA CAAGTTGTTC AAGTTCCGCA ATAACCGGTG GGAAGACATC   600
CTGAGCGATG AGGTCAACGT GGCCCGTGGT GTGGCCAGCC TCTTTGCCGG ACGCTCTGTG   660
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GGTAATGTGG GCCCTGATGC CCTCATTGAA ATGGACCCTG AGGCCAGTGA CCTCTCCCGG   780
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TTCTCCCACA CTGCCTCTCC AAGCATTGGT GAGATATCTG GCAGAACCGA GGAGCGGGAA   900
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TCCAAAAGCC ATTTGGCTGA CAAGAACCTA TTTGGCCCAC CATGTTACTA TTCTGTCTGC   1140
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CTGAGAAGCT GGGAGGAAAG CAGGCAGAAG GGGCAGGCCA TGTCCAGATG TGCACTCAGG   1440
GAGCTGGGAG GTCCCTGGAG CCAAGCCACA CAGCACCTGC CTGCTAGAGA GCTGTATGAC   1500
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TTTAGGCTCA GGAAAGCACG GGAAGCAGAA TTCCCCCCAG GCTCCTCTGA GGAGCCTCTG   1920
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ATCCTCAGCA GCAGTGCCTC GGATATCTTC TGCGACAATG AGAATGGGCC TAACTTCCTT   2100
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GCCTTCATCG TTCACCTCAA ATATCACCTC TGCAGAGATT TTCCTCACTC CCTGTGCCAC   2220
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CCACATTGCC ATCATGGTTT GTCTATGAGC TTTACAAGGA CCGGGTCACG GTTCTATTCA   2340
TTCTTGACGC AAGGCTTGGC CTCCAGTGCC CACCGGAGGA CACTCAGCCT CCAGGGTTCT   2400
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ACTGCCTATT ACATTGTCCT GTGGTCTGCC ATCCCAGAGA GCCTGATGAC CCACAGCTAT   2520
TTGTCCTCTG AAAGAGTCAA CGTGGGTGTG GACGACCCCC ACCAGCATGG GCGAGGTGTC   2580
GCCCTGGCTG ACTTCAACCG TGATGGCAAA GTGGACATCG TCTATGGCAA CTGGAATGGC   2640
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CTCTTCCGAT GCTCCATCCT GGCTCGTGGC TCTTCATCCT TGACAGCTGG TGGGAGGAAC   2880
GGTCAGGGAG AAGGTTTAAG AATCAGAAGG GGAGGGTTCC CAGGGCCAGG GGGTCAGGCC   2940
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CGGGGTCCAA TCACTACCAG GAAAAGGGGC TACGGGGTCC AATCACTACC AGGAAAAGGG   3300
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GCTATGGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG CTCCAATCAC TACCAGGAAA   3840
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AACAACAACT GGCTGCGAGT GGTGCCACGC ACCCGGTTTG GGGCCTTTGC CAGGGGAGCT   4140
AAGGTCGTGC TCTACACCAA GAAGAGTGGG GCCCACCTGA GGATCATCGA CGGGGGCTCA   4200
GGCTACCTGT GTGAGATGGA GCCCGTGGCA CACTTTGGCC TGGGGAAGGA TGAAGCCAGC   4260
AGTGTGGAGG TGACGTGGCC AGATGGCAAG ATGGTGAGCC GGAACGTGGC CAGCGGGGAG   4320
ATGAACTCAG TGCTGGAGAT CCTCTACCCC CGGGATGAGG ACACACTTCA GGACCCAGCC   4380
CCACTGGAGT GTGGCCAAGG ATTCTCCCAG CAGGAAAATG GCCATTGCAT GGACACCAAT   4440
GAATGCATCC AGTTCCCATT CGTGTGCCCT CGAGACAAGC CCGTATGTGT CAACACCTAT   4500
GGAAGCTACA GGTGCCGGAC CAACAAGAAG TGCAGTCGGG GCTACGAGCC CAACGAGGAT   4560
GGCACAGCCT GCGTGGGTAC TGAGCTAGGC TCTAGGCATA CAATGACGTG GAAACCAAGG   4620
CCCAAAAAGG AGCTGCAACT TTCCCAAGGC ATCTGCACCC CCGTCTGGTC CTTTTTCCTG   4680
CCGGGTTGCC GGCTGCTCCT CAAAAGAGCT CAGCTCCAGG CTGCTCCCAG CACCCTTCTC   4740
CAGAAAGCTC CAGGTATTCC AGAAGCCCAA GTGTATGAAC AAGATCAGGA ATAA
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Seq ID NO: 60 Protein Sequence
Protein Accession #: FGENESH

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PPTTPAGLLG LPPLSGRDFS SSLGQASPDS RQGERVPVPC CRGGLRPTHE PEPFLLRPKS   180
GVATYTDKLF KFRNNRWEDI LSDEVNVARG VASLFAGRSV ACVDRKGSGR YSIYIANYAY   240
GNVGPDALIE MDPEASDLSR GILALRDVAA EAGVSKYTEG FSHTASPSIG EISGRTEERE   300
GGDPEEADEE HSGDGSTSQL CRLGWKDGQF KEEAAALVEE QREAGAAGVP RGRVRTALQT   360
SKSHLADKNL FGPPCYYSVC APSPAHPFPA RQAPQHYPVA PLVTQLMTHG RLAGKLARSV   420
PHPRAPGMDP KCKGRHAEPG LMAEALGAWP ALSTTVVPGG LRSWEESRQK GQAMSRCALR   480
ELGGPWSQAT QHLPARELYD LGEPPILQRT DGDPGRRRDS PKVTQECHLV ATMPALGGLE   540
GPGRVAKREI GRETGAVGRP LSHPLVPNFP SCLRPLEAGT VPGAALPGNP GNWVLDMAKA   600
LAWNQMEKEE GKIHGDHEPR FRLRKAREAE FPPGSSEEPL LQFPSGLRGS PVLQVGLGLA   660
SATHCGSMSF LGGRGVSVGP ILSSSASDIP CDNENGPNFL FHNRGDGTFV DAAASAERRL   720
AFIVHLKYHL CRDFPHSLCH LAETGPSSSC CPWHARLLQA PHCHHGLSMS FTRTGSRFYS   780
FLTQGLASSA HRRTLSLQGS QGAPPCLLAR APCVLGSLIP TAYYIVLWSA IPESLMTHSY   840
LSSERVNVGV DDPHQHGRGV ALADFNRDGK VDIVYGNWNG PHRLYLQMST HGKVRFRDIA   900
SPKFSMPSPV RTVITADFDN DQELEIFFNN IAYRSSSANR LFRCSILARG SSSLTAGGRN   960
GQGEGLRIRR GGFPGPGGQA KVNTGPLMKK QKGRKDEDWA RGCGNAGQSL AKEPASAIAG   1020
KGKGNVAQSV PRTQAPQDTK PHYHKKGLQG PITTRKRGYG VQSLPGKGAT GSNHYQEKGL   1080
RGPITTRKRG YGVQSLPGKG ATGSNHYQEK GLQGPITTRK RGYGLQSLPG KGATGSNHYH   1140
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NHYQEKGLQG PITTRKRGYR VQSLPQKGAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE   1260
AMGSNHYQEK GLRAPITTRK RGYGVQSLPQ KGATGSNVIR REHGDPLIEE LNPGDALEPE   1320
GRGTGGVVTD FDGDGMLDLI LSHGESMAQP LSVFRGNQGF NNNWLRVVPR TRFGAFARGA   1380
KVVLYTKKSG AHLRIIDGGS GYLCEMEPVA HFGLGKDEAS SVEVTWPDGK MVSRNVASGE   1440
MNSVLEILYP RDEDTLQDPA PLECGQGFSQ QENGHCMDTN ECIQFPFVCP RDKPVCVNTY   1500
GSYRCRTNKK CSRGYEPNED GTACVGTELG SRHTMTWKPR PKKELQLSQG ICTPVWSFFL   1560
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Seq ID NO: 61 DNA sequence
Nucleic Acid Accession #: NM_000584.1
Coding sequence: 75..374

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CACTGTGTGT AAACATGACT TCCAAGCTGG CCGTGGCTCT CTTGGCAGCC TTCCTGATTT   120
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GCATAAAGAC ATACTCCAAA CCTTTCCACC CCAAATTTAT CAAAGAACTG AGAGTGATTG   240
AGAGTGGACC ACACTGCGCC AACACAGAAA TTATTGTAAA GCTTTCTGAT GGAAGAGAGC   300
TCTGTCTGGA CCCCAAGGAA AACTGGGTGC AGAGGGTTGT GGAGAAGTTT TTGAAGAGGG   360
CTGAGAATTC ATAAAAAAAT TCATTCTCTG TGGTATCCAA GAATCAGTGA AGATGCCAGT   420
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CCAGATGCAA TACAAGATTC CTGGTTAAAT TTGAATTTCA GTAAACAATG AATAGTTTTT   540
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GAATGGGTTT GCTAGAATGT GATATTTGAA GCATCACATA AAAATGATGG GACAATAAAT   780
TTTGCCATAA AGTCAAATTT AGCTGGAAAT CCTGGATTTT TTTCTGTTAA ATCTGGCAAC   840
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GATATTAAAT GATGTTTTAT TAGATAAATT TCAATCAGGG TTTTTAGATT AAACAAAGAA  1200
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AGTACATTAT TGTTTATCTG AAAGTTTTAA TTGAACTAAC AATCCTAGTT TGATACTCCC  1320
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AACTATTAAA ACAGCCAAAA CTCCACAGTC AATATTAGTA ATTTCTTGCT GGTTGAAACT  1440
TGTTTATTAT GTACAAATAG ATTCTTATAA TATTATTTAA ATGACTGCAT TTTTAAATAC  1500
AAGGCTTTAT ATTTTTAACT TTAAGATGTT TTTATGTGCT CTCCAAATTT TTTTTACTGT  1560
TTCTGATTGT ATGGAAATAT AAAAGTAAAT ATGAAACATT TAAAATATAA TTTGTTGTCA  1620
AAGTAAAAAA AAAAAAAAA
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Seq ID NO: 62 Protein Sequence
Protein Accession #: NP_000575.1

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CANTEIIVKL SDGRELCLDP KENWVQRVVE KFLKRAENS
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Seq ID NO: 63 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 52-1146

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GTTGGTGGAG AGGCAGGTCC ATCTGTCACA CTACCCTGCC ACTACAGTGG AGCTGTCACA   180
TCCATGTGCT GGAATAGAGG CTCATGTTCT CTATTCACAT GCCAAAATGG CATTGTCTGG   240
ACCAATGGAA CCCACGTCAC CTATCGGAAG GACACACGCT ATAAGCTATT GGGGGACCTT   300
TCAAGAAGGG ATGTCTCTTT GACCATAGAA AATACAGCTG TGTCTGACAG TGGCGTATAT   360
TGTTGCCGTG TTGAGCACCG TGGGTGGTTC AATGACATGA AAATCACCGT ATCATTGGAG   420
ATTGTGCCAC CCAAGGTCAC GACTACTCCA ATTGTCACAA CTGTTCCAAC CGTCACGACT   480
GTTCGAACGA GCACCACTGT TCCAACGACA ACGACTGTTC CAATGACGAC TGTTCCAACG   540
ACAACTGTTC CAACAACAAT GAGCATTCCA ACGACAACGA CTGTTCTGAC GACAATGACT   600
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Seq ID NO: 64 Protein sequence:
Protein Accession #: NP_036338.1

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SLEIVPPKVT TTPIVTTVPT VTTVRTSTTV PTTTTVPTTT VPTTMSIPTT TTVPTTMTVS   180
TTTSVPTTTS IPTTTSVPVT TTVSTFVPPM PLPRQNHEPV ATSPSSPQPA ETHPTTLQGA   240
IRREPTSSPL YSYTTDGNDT VTESSDGLWN NNQTQLFLEH SLLTANTTKG IYAGVCISVL   300
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Seq ID NO: 65 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 2932-4764

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Seq ID NO: 66 Protein sequence:
Protein Accession #: EOS sequence

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GTTAAAACCT GTGAGAGGAT TGTACAGCTC TCTGAACCTC ACAGACCCAG GTCAAAAGGT  2340
TCTGAGAAAT ACTAGGTACA TTCATCCTCA CAGATTGCAA AGGTGCTTTG GGTGGGGGTT  2400
TAGTAATTTT CTGCTTAAAA AATGAGTATC TTGTAACCAT TACCTATATC TAAATATTCT  2460
TGAACAATTA GTAGATCCAG AAAGAAAAAA AAAATATGCT TCTCTGTGTG TGTACCTGTT  2520
```

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GTATGTCCTA ACTTATTAGA AAAATTTTAT ATCTTTTTAC ATGTGGGGGG CAGAAGGTAA   2580
AGCATGTTTG ACTTGTGAAA ATGGGATGTC AAACAGCCAT AAGTTCCCTG GTATTCACCT   2640
TCCTGTCCAT CTGTCCCCTC CATCGGTATA CCTTTATCCC TTTGAAAGGG TGCTTGTACA   2700
ATTTGATATA TTTTATTGAA GAGTTATCTC TTATTCTGAA TTAAATTAAG CATTTGTTTT   2760
ATTCTGAATT AAATTAAGCA TTTGTTTTAT TGCAGTAAAG TTTGTCCA
```

Seq ID NO: 68 Protein Sequence
Protein Accession #: NP_002440.1

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1          11         21         31         41         51
|          |          |          |          |          |
MASPSKGNDL FSPDEEGPAV VAGPGPGLGG AAGAAEERRV KVSSLPFSVE ALMSDKKPPK   60
ESPAVPPEGA SAGAHLRPLL LSGHRAREAH SPGPLVKPFE TASVKSGNSE DGAAWMQEPG   120
RYSPPPRHMS PTTCTLRKHK TNRKPRTPFT TSQLLALERK FRQKQYLSIA ERAEFSSSLN   180
LTETQVKIWF QNRSAKAKRL QEAELEKLKM AAKPMLPSSF SLPFPISSPL QAASIYAASY   240
PFHRPVLPIP PVGLYATPVG YGMYHLS
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Seq ID NO: 69 DNA sequence
Nucleic Acid Accession #: NM_005603.1
Coding sequence: 1..3756

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAGTACAG AAAGAGACTC AGAAACGACA TTTGACGAGG ATTCTCAGCC TAATGACGAA   60
GTGGTTCCCT ACAGTGATGA TGAAACAGAA GATGAACTTG ATGACCAGGG GTCTGCTGTT   120
GAACCAGAAC AAAACCGAGT CAACAGGGAA GCAGAGGAGA ACCGGGAGCC ATTCAGAAAA   180
GAATGTACAT GGCAAGTCAA AGCAAACGAT CGCAAGTACC ACGAACAACC TCACTTTATG   240
AACACAAAAT TCTTGTGTAT TAAGGAGAGT AAATATGCGA ATAATGCAAT TAAAACATAC   300
AAGTACAACG CATTTACCTT TATACCAATG AATCTGTTTG AGCAGTTTAA GAGAGCAGCC   360
AATTTATATT TCCTGGCTCT TCTTATCTTA CAGGCAGTTC CTCAAATCTC TACCCTGGCT   420
TGGTACACCA CACTAGTGCC CCTGCTTGTG GTGCTGGGCG TCACTGCAAT CAAAGACCTG   480
GTGGACGATG TGGCTCGCCA TAAAATGGAT AAGGAAATCA ACAATAGGAC GTGTGAAGTC   540
ATTAAGGATG GCAGGTTCAA AGTTGCTAAG TGGAAAGAAA TTCAAGTTGG AGACGTCATT   600
CGTCTGAAAA AAAATGATTT TGTTCCAGCT GACATTCTCC TGCTGTCTAG CTCTGAGCCT   660
AACAGCCTCT GCTATGTGGA AACAGCAGAA CTGGACGGAG AAACCAATTT AAAATTTAAG   720
ATGTCACTTG AAATCACAGA CCAGTACCTC CAAAGAGAAG ATACATTGGC TACATTTGAT   780
GGTTTTATTG AATGTGAAGA ACCCAATAAC CGACTAGATA AGTTTACAGG AACACTATTT   840
TGGAGAAACA CAAGTTTTCC TTTGGATGCT GATAAAATTT TGTTACGTGG CTGTGTAATT   900
AGGAACACCG ATTTCTGCCA CGGCTTAGTC ATTTTTGCAG GTGCTGACAC TAAAATAATG   960
AAGAATAGTG GGAAAACCAG ATTTAAAAGA ACTAAAATTG ATTACTTGAT GAACTACATG   1020
GTTTACACGA TCTTTGTTGT TCTTATTCTG CTTTCTGCTG GTCTTGCCAT CGGCCATGCT   1080
TATTGGGAAG CACAGGTGGG CAATTCCTCT TGGTACCTCT ATGATGGAGA AGACGATACA   1140
CCCTCCTACC GTGGATTCCT CATTTTCTGG GGCTATATCA TTGTTCTCAA CACCATGGTA   1200
CCCATCTCTC TCTATGTCAG CGTGGAAGTG ATTCGTCTTG GACAGAGTCA CTTCATCAAC   1260
TGGGACCTGC AAATGTACTA TGCTGAGAAG GACACACCCG CAAAAGCTAG AACCACCACA   1320
CTCAATGAAC AGCTCGGGCA GATCCATTAT ATCTTCTCTG ATAAGACGGG GACACTCACA   1380
CAAAATATCA TGACCTTTAA AAAGTGCTGT ATCAACGGGC AGATATATGG GGACCATCGG   1440
GATGCCTCTC AACACAACCA CAACAAAATA GAGCAAGTTG ATTTTAGCTG GAATACATAT   1500
GCTGATGGGA AGCTTGCATT TTATGACCAC TATCTTATTG AGCAAATCCA GTCAGGGAAA   1560
GAGCCAGAAG TACGACAGTT CTTCTTCTTG CTCGCAGTTT GCCACACAGT CATGGTGGAT   1620
AGGACTGATG GTCAGCTCAA CTACCAGGCA GCCTCTCCCG ATGAAGGTGC CCTGGTAAAC   1680
GCTGCCAGGA ACTTTGGCTT TGCCTTCCTC GCCAGGACCC AGAACACCAT CACCATCAGT   1740
GAACTGGGCA CTGAAAGGAC TTACAATGTT CTTGCCATTT TGGACTTCAA CAGTGACCGG   1800
AAGCGAATGT CTATCATTGT AAGAACCCCA GAAGGCAATA TCAAGCTTTA CTGTAAAGGT   1860
GCTGACACTG TTATTTATGA ACGGTTACAT CGAATGAATC CTACTAAGCA AGAAACACAG   1920
GATGCCCTGG ATATCTTTGC AAATGAAACT CTTAGAACCC TATGCCTTTG CTACAAGGAA   1980
ATTGAAGAAA AAGAATTTAC AGAATGGAAT AAAAAGTTTA TGGCTGCCAG TGTGGCCTCC   2040
ACCAACCGGG ACGAAGCTCT GGATAAAGTA TATGAGGAGA TTGAAAAAGA CTTAATTCTC   2100
CTGGGAGCTA CAGCTATTGA AGACAAGCTA CAGGATGGAG TTCCAGAAAC CATTTCAAAA   2160
CTTGCAAAAG CTGACATTAA GATCTGGGTG CTTACTGGAG ACAAAAAGGA AACTGCTGAA   2220
AATATAGGAT TTGCTTGTGA ACTTCTGACT GAAGACACCA CCATCTGCTA TGGGGAGGAT   2280
ATTAATTCTC TTCTTCATGC AAGGATGGAA AACCAGAGGA ATAGAGGTGG CGTCTACGCA   2340
AAGTTTGCAC CTCCTGTGCA GGAATCTTTT TTTCCACCCG GTGGAAACCG TGCCTTAATC   2400
ATCACTGGTT CTTGGTTGAA TGAAATTCTT CTCGAGAAAA AGACCAAGAG AAATAAGATT   2460
CTGAAGCTGA AGTTCCCAAG AACAGAAGAA GAAAGACGGA TGCGGACCCA AAGTAAAAGG   2520
AGGCTAGAAG CTAAGAAAGA GCAGCGGCAG AAAAACTTTG TGGACCTGGC CTGCGAGTGC   2580
AGCGCAGTCA TCTGCTGCCG CGTCACCCCC AAGCAGAAGG CCATGGTGGT GGACCTGGTG   2640
AAGAGGTACA AGAAAGCCAT CACGCTGGCC ATCGGAGATG GGGCCAATGA CGTGAACATG   2700
ATCAAAACTG CCCACATTGG CGTTGGAATA AGTGGACAAG AAGGAATGCA AGCTGTCATG   2760
TCGAGTGACT ATTCCTTTGC TCAGTTCCGA TATCTGCAGA GGCTACTGCT GGTGCATGGC   2820
CGATGGTCTT ACATAAGGAT GTGCAAGTTC CTACGATACT TCTTTTACAA AAACTTTGCC   2880
TTTACTTTGG TTCATTTCTG GTACTCCTTC TTCAATGGCT ACTCTGCGCA GACTGCATAC   2940
GAGGATTGGT TCATCACCCT CTACAACGTG CTGTACACCA GCCTGCCCGT GCTCCTCATG   3000
GGGCTGCTCG ACCAGGATGT GAGTGACAAA CTGAGCCTCC GATTCCCTGG GTTATACATA   3060
GTGGGACAAA GAGACTTACT ATTCAACTAT AAGAGATTCT TTGTAAGCTT GTTGCATGGG   3120
GTCCTAACAT CGATGATCCT CTTCTTCATA CCTCTTGGAG CTTATCTGCA AACCGTAGGG   3180
CAGGATGGAG AGGCACCTTC CGACTACCAG TCTTTTGCCG TCACCATTGC CTCTGCTCTT   3240
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GTAATAACAG TCAATTTCCA GATTGGCTTG GATACTTCTT ATTGGACTTT TGTGAATGCT   3300
TTTTCAATTT TTGGAAGCAT TGCACTTTAT TTTGGCATCA TGTTTGACTT TCATAGTGCT   3360
GGAATACATG TTCTCTTTCC ATCTGCATTT CAATTTACAG GCACAGCTTC AAACGCTCTG   3420
AGACAGCCAT ACATTTGGTT AACTATCATC CTGACTGTTG CTGTGTGCTT ACTACCCGTC   3480
GTTGCCATTC GATTCCTGTC AATGACCATC TGGCCATCAG AAAGTGATAA GATCCAGAAG   3540
CATCGCAAGC GGTTGAAGGC GGAGGAGCAG TGGCAGCGAC GGCAGCAGGT GTTCCGCCGG   3600
GGCGTGTCAA CGCGGCGCTC GGCCTACGCC TTCTCGCACC AGCGGGGCTA CGCGGACCTC   3660
ATCTCCTCCG GGCGCAGCAT CCGCAAGAAG CGCTCGCCGC TTGATGCCAT CGTGGCGGAT   3720
GGCACCGCGG AGTACAGGCG CACCGGGGAC AGCTGA
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Seq ID NO: 70 Protein Sequence
Protein Accession #: NP_005594.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSTERDSETT FDEDSQPNDE VVPYSDDETE DELDDQGSAV EPEQNRVNRE AEENREPFRK   60
ECTWQVKAND RKYHEQPHFM NTKFLCIKES KYANNAIKTY KYNAFTFIPM NLFEQFKRAA   120
NLYFLALLIL QAVPQISTLA WYTTLVPLLV VLGVTAIKDL VDDVARHKMD KEINNRTCEV   180
IKDGRFKVAK WKEIQVGDVI RLKKNDFVPA DILLLSSSEP NSLCYVETAE LDGETNLKFK   240
MSLEITDQYL QREDTLATFD GFIECEEPNN RLDKFTGTLF WRNTSFPLDA DKILLRGCVI   300
RNTDFCHGLV IFAGADTKIM KNSGKTRFKR TKIDYLMNYM VYTIFVVLIL LSAGLAIGHA   360
YWEAQVGNSS WYLYDGEDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN   420
WDLQMYYAEK DTPAKARTTT LNEQLGQIHY IFSDKTGTLT QNIMTFKKCC INGQIYGDHR   480
DASQHNHNKI EQVDFSWNTY ADGKLAFYDH YLIEQIQSGK EPEVRQFFFL LAVCHTVMVD   540
RTDGQLNYQA ASPDEGALVN AARNFGFAFL ARTQNTITIS ELGTERTYNV LAILDFNSDR   600
KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMNPTKQETQ DALDIFANET LRTLCLCYKE   660
IEEKEFTEWN KKFMAASVAS TNRDEALDKV YEEIEKDLIL LGATAIEDKL QDGVPETISK   720
LAKADIKIWV LTGDKKETAE NIGFACELLT EDTTICYGED INSLLHARME NQRNRGGVYA   780
KFAPPVQESF FPPGGNRALI ITGSWLNEIL LEKKTKRNKI LKLKFPRTEE ERRMRTQSKR   840
RLEAKKEQRQ KNFVDLACEC SAVICCRVTP KQKAMVVDLV KRYKKAITLA IGDGANDVNM   900
IKTAHIGVGI SGQEGMQAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKF LRYFFYKNFA   960
FTLVHFWYSF FNGYSAQTAY EDWFITLYNV LYTSLPVLLM GLLDQDVSDK LSLRFPGLYI   1020
VGQRDLLFNY KRFFVSLLHG VLTSMILFFI PLGAYLQTVG QDGEAPSDYQ SFAVTIASAL   1080
VITVNFQIGL DTSYWTFVNA FSIFGSIALY FGIMFDFHSA GIHVLFPSAF QFTGTASNAL   1140
RQPYIWLTII LTVAVCLLPV VAIRFLSMTI WPSESDKIQK HRKRLKAEEQ WQRRQQVFRR   1200
GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSPLDAIVAD GTAEYRRTGD S
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Seq ID NO: 71 DNA sequence
Nucleic Acid Accession #: NM_138784.1
Coding sequence: 334-816

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1          11         21         31         41         51
|          |          |          |          |          |
GGGGATACGG AAAACAGAAT AGAAGCACAG AACAAGGACT ATTGTATATA AGAGAAGCAG     60
GTGTTAATGT AAGTTGCTGT GGAATGACTG TTTTCAAGAA GAGAGAAGGA GCCAATATAT    120
CTACTTTCAT TAAGAAGCTG AAATTAAATT TGGATTTCCT TCTTTCCAAA GCTGAGACAC    180
GATGGCCAAA AAGCGATTGC TGTGATTGGA GCTGGAATTA GCGGACTGGG GGCCATCAAG    240
TGCTGCCTGG ATGAAGATCT GGAGCCCACC TGCTTTGAAA GAAATGATGA TATTGGACAT    300
CTCTGGAAAT TTCAAAAAAA TACTTCAGAG AAAATGCCTA GTATCTACAA ATCTGTGACC    360
ATCAATACTT CCAAGGAGAT GATGTGCTTC AGTGACTTCC CTGTCCCTGA TCATTTTCCC    420
AACTACATGC ACAACTCCAA ACTCATGGAC TACTTCGGGA TGTATGCCAC ACACTTTGGC    480
CTCCTGAATT ACATTCGTTT TAAGACTGAA GTGCAAAGTG TGAGGAAGCA CCCAGATTTT    540
TCTATCAATG GACAATGGGA TGTTGTTGTG GAGACTGAAG AGAAACAAGA GACTTTGGTC    600
TTTGATGGGG TCTTAGTTTG CAGTGGACAC CACACAGATC CCTACTTACC ACTTCAGTCC    660
TTCCCAGGCA TTGAGAAATT TGAAGGCTGT TATTTCCATA GTCGGGAATA CAAAAGTCCC    720
GAGGACTTTT CAGGGAAAAG AATCATAGTG ATCGGCATTG GAAATTCTGG AGTGGATATT    780
GCGGTGGAGC TCAGTCGTGT AGCAAAACAG ATTTGACCAG TAGGAACTGA GATTCAACGT    840
CCCCAAGACT GCAAAAGTAC CTACAATCAA ACAAATTAAT ATATTTCCTA ATTGGATCAG    900
CATGCAGACA AGTTTACAAA TATATTACAG AAAGATTTGA AGAGGGATTC TGGTTACGTT    960
CAGTTAAGCA GGACACTAAT CCTGAACAAT CTGATGTATT AAAGTTTCTA ATGTTTGTAT   1020
CTTTGGTTTG ATGCATACAA TAGAGTGGAA GTCTGTAGTA GTTAATATGA TGATAATTCG   1080
CTTCTAAATT TAAATCCTTA TTTATATATG AAGCATAGCT ATGTCAATGT CCAGGGAAGC   1140
ATTTTTAAAT AGTAAATCAG AAACATGTAA ACTAGTGAAT ACAATTTTCT ATTTTTCATT   1200
CAGAAATTTG TTGTCATAGA TGCAGCCTTT ATCTGGAAAT CAGTGGGCAG CTCTGGTCAA   1260
GCACAGCATG GCGACCACTG TGTAGTATTT TACCACCTAA TCCTTAGTAG CCAACACTGT   1320
TAAATCTGCA TAATGGGTAG CATATGAATA AAATAATATC TTGTAAAAAA AAAAAAAAAA   1380
AAAAAAAAAA AAAA
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Seq ID NO: 72 Protein sequence:
Protein Accession #: NP_620139.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPSIYKSVTI NTSKEMMCFS DFPVPDHFPN YMHNSKLMDY FGMYATHFGL LNYIRFKTEV     60
QSVRKHPDFS INGQWDVVVE TEEKQETLVF DGVLVCSGHH TDPYLPLQSF PGIEKFEGCY    120
FHSREYKSPE DFSGKRIIVI GIGNSGVDIA VELSRVAKQI
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Seq ID NO: 73 DNA sequence
Nucleic Acid Accession #: NM_003661.1
Coding sequence: 1..1152

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAGTGCAC TTTTCCTTGG TGTGGGAGTG AGGGCAGAGG AAGCTGGAGC GAGGGTGCAA    60
CAAAACGTTC CAAGTGGGAC AGATACTGGA GATCCTCAAA GTAAGCCCCT CGGTGACTGG    120
GCTGCTGGCA CCATGGACCC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTC    180
AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCCTGCTGA CTGATAATGA GGCCTGGAAC    240
GGATTCGTGG CTGCTGCTGA ACTGCCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG    300
GACAACCTTG CAAGACAAAT GATCATGAAA GACAAAAACT GGCACGATAA AGGCCAGCAG    360
TACAGAAACT GGTTTCTGAA AGAGTTTCCT CGGTTGAAAA GTGAGCTTGA GGATAACATA    420
AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAAGGCAC CACCATCGCC    480
AATGTGGTGT CTGGCTCTCT CAGCATTTCC TCTGGCATCC TGACCCTCGT CGGCATGGGT    540
CTGGCACCCT TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA    600
ATCACAGCCG CTTTGACCGG GATTACCAGC AGTACCATGG ACTACGGAAA GAAGTGGTGG    660
ACACAAGCCC AAGCCCACGA CCTGGTCATC AAAAGCCTTG ACAAATTGAA GGAGGTGAGG    720
GAGTTTTTGG GTGAGAACAT ATCCAACTTT CTTTCCTTAG CTGGCAATAC TTACCAACTC    780
ACACGAGGCA TTGGGAAGGA CATCCGTGCC ·CTCAGACGAG CCAGAGCCAA TCTTCAGTCA    840
GTACCGCATG CCTCAGCCTC ACGCCCCCGG GTCACTGAGC CAATCTCAGC TGAAAGCGGT    900
GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGGAAA TGAGCAGAGG AGTCAAGCTC    960
ACGGATGTGG CCCCTGTAAG CTTCTTTCTT GTGCTGGATG TAGTCTACCT CGTGTACGAA    1020
TCAAAGCACT TACATGAGGG GGCAAAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT    1080
CAGGAGCTGG AGGAGAAGCT AAACATTCTC AACAATAATT ATAAGATTCT GCAGGCGGAC    1140
CAAGAACTGT GA
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Seq ID NO: 74 Protein Sequence
Protein Accession #: NP_003652.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSALFLGVGV RAEEAGARVQ QNVPSGTDTG DPQSKPLGDW AAGTMDPESS IFIEDAIKYF    60
KEKVSTQNLL LLLTDNEAWN GFVAAAELPR NEADELRKAL DNLARQMIMK DKNWHDKGQQ    120
YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLSIS SGILTLVGMG    180
LAPFTEGGSL VLLEPGMELG ITAALTGITS STMDYGKKWW TQAQAHDLVI KSLDKLKEVR    240
EFLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPISAESG    300
EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVVYLVYE SKHLHEGAKS ETAEELKKVA    360
QELEEKLNIL NNNYKILQAD QEL
```

Seq ID NO: 75 DNA sequence
Nucleic Acid Accession #: NM_014452.1
Coding sequence: 1..1968

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGGGACCT CTCCGAGCAG CAGCACCGCC CTCGCCTCCT GCAGCCGCAT CGCCCGCCGA    60
GCCACAGCCA CGATGATCGC GGGCTCCCTT CTCCTGCTTG GATTCCTTAG CACCACCACA    120
GCTCAGCCAG AACAGAAGGC CTCGAATCTC ATTGGCACAT ACCGCCATGT TGACCGTGCC    180
ACCGGCCAGG TGCTAACCTG TGACAAGTGT CCAGCAGGAA CCTATGTCTC TGAGCATTGT    240
ACCAACACAA GCCTGCGCGT CTGCAGCAGT TGCCCTGTGG GGACCTTTAC CAGGCATGAG    300
AATGGCATAG AGAAATGCCA TGACTGTAGT CAGCCATGCC CATGGCCAAT GATTGAGAAA    360
TTACCTTGTG CTGCCTTGAC TGACCGAGAA TGCACTTGCC CACCTGGCAT GTTCCAGTCT    420
AACGCTACCT GTGCCCCCCA TACGGTGTGT CCTGTGGGTT GGGGTGTGCG GAAGAAAGGG    480
ACAGAGACTG AGGATGTGCG GTGTAAGCAG TGTGCTCGGG GTACCTTCTC AGATGTGCCT    540
TCTAGTGTGA TGAAATGCAA AGCATACACA GACTGTCTGA GTCAGAACCT GGTGGTGATC    600
AAGCCGGGGA CCAAGGAGAC AGACAACGTC TGTGGCACAC TCCCGTCCTT CTCCAGCTCC    660
ACCTCACCTT CCCCTGGCAC AGCCATCTTT CCACGCCCTG AGCACATGGA AACCCATGAA    720
GTCCCTTCCT CCACTTATGT TCCCAAAGGC ATGAACTCAA CAGAATCCAA CTCTTCTGCC    780
TCTGTTAGAC CAAAGGTACT GAGTAGCATC CAGGAAGGGA CAGTCCCTGA CAACACAAGC    840
TCAGCAAGGG GGAAGGAAGA CGTGAACAAG ACCCTCCCAA ACCTTCAGGT AGTCAACCAC    900
CAGCAAGGCC CCCACCACAG ACACATCCTG AAGCTGCTGC CGTCCATGGA GGCCACTGGG    960
GGCGAGAAGT CCAGCACGCC CATCAAGGGC CCCAAGAGGG GACATCCTAG ACAGAACCTA    1020
CACAAGCATT TTGACATCAA TGAGCATTTG CCCTGGATGA TTGTGCTTTT CCTGCTGCTG    1080
GTGCTTGTGG TGATTGTGGT GTGCAGTATC CGGAAAAGCT CGAGGACTCT GAAAAAGGGG    1140
CCCCGGCAGG ATCCCAGTGC CATTGTGGAA AAGGCAGGGC TGAAGAAATC CATGACTCCA    1200
ACCCAGAACC GGGAGAAATG GATCTACTAC TGCAATGGCC ATGGTATCGA TATCCTGAAG    1260
CTTGTAGCAG CCCAAGTGGG AAGCCAGTGG AAAGATATCT ATCAGTTTCT TTGCAATGCC    1320
AGTGAGAGGG AGGTTGCTGC TTTCTCCAAT GGGTACACAG CCGACCACGA GCGGGCCTAC    1380
GCAGCTCTGC AGCACTGGAC CATCCGGGGC CCCGAGGCCA GCCTCGCCCA GCTAATTAGC    1440
GCCCTGCGCC AGCACCGGAG AAACGATGTT GTGGAGAAGA TTCGTGGGCT GATGGAAGAC    1500
ACCACCCAGC TGGAAACTGA CAAACTAGCT CTCCCGATGA GCCCCAGCCC GCTTAGCCCG    1560
AGCCCCATCC CCAGCCCCAA CGCGAAACTT GAGAATTCCG CTCTCCTGAC GGTGGAGCCT    1620
TCCCCACAGG ACAAGAACAA GGGCTTCTTC GTGGATGAGT CGGAGCCCCT TCTCCGCTGT    1680
GACTCTACAT CCAGCGGCTC CTCCGCGCTG AGCAGGAACG GTTCCTTTAT TACCAAAGAA    1740
AAGAAGGACA CAGTGTTGCG GCAGGTACGC CTGGACCCCT GTGACTTGCA GCCTATCTTT    1800
GATGACATGC TCCACTTTCT AAATCCTGAG GAGCTGCGGG TGATTGAAGA GATTCCCCAG    1860
GCTGAGGACA AACTAGACCG GCTATTCGAA ATTATTGGAG TCAAGAGCCA GGAAGCCAGC    1920
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CAGACCCTCC TGGACTCTGT TTATAGCCAT CTTCCTGACC TGCTGTAG
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Seq ID NO: 76 Protein Sequence
Protein Accession #: NP_055267.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGTSPSSSTA LASCSRIARR ATATMIAGSL LLLGFLSTTT AQPEQKASNL IGTYRHVDRA   60
TGQVLTCDKC PAGTYVSEHC TNTSLRVCSS CPVGTFTRHE NGIEKCHDCS QPCPWPMIEK   120
LPCAALTDRE CTCPPGMFQS NATCAPHTVC PVGWGVRKKG TETEDVRCKQ CARGTFSDVP   180
SSVMKCKAYT DCLSQNLVVI KPGTKETDNV CGTLPSFSSS TSPSPGTAIF PRPEHMETHE   240
VPSSTYVPKG MNSTESNSSA SVRPKVLSSI QEGTVPDNTS SARGKEDVNK TLPNLQVVNH   300
QQGPHHRHIL KLLPSMEATG GEKSSTPIKG PKRGHPRQNL HKHFDINEHL PWMIVLFLLL   360
VLVVIVVCSI RKSSRTLKKG PRQDPSAIVE KAGLKKSMTP TQNREKWIYY CNGHGIDILK   420
LVAAQVGSQW KDIYQFLCNA SEREVAAFSN GYTADHERAY AALQHWTIRG PEASLAQLIS   480
ALRQHRRNDV VEKIRGLMED TTQLETDKLA LPMSPSPLSP SPIPSPNAKL ENSALLTVEP   540
SPQDKNKGFF VDESEPLLRC DSTSSGSSAL SRNGSFITKE KKDTVLRQVR LDPCDLQPIF   600
DDMLHPLNPE ELRVIEEIPQ AEDKLDRLFE IIGVKSQEAS QTLLDSVYSH LPDLL
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Seq ID NO: 77 DNA sequence
Nucleic Acid Accession #: NM_003105.3
Coding sequence: 123..6767

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1          11         21         31         41         51
|          |          |          |          |          |
GGCGCGGGCG GCCTGGAGCC CCGGGAGCGG CGCGCGCGGT CCCGGCCCAG CCGGCTCTCC   60
TGGCCTCGCG CTGCACATTC TCTCCTGGCG GCGGCGCCAC CTGCAGTAGC GTTCGCCCGA   120
ACATGGCGAC ACGGAGCAGC AGGAGGGAGT CGCGACTCCC GTTCCTATTC ACCCTGGTCG   180
CACTGCTGCC GCCCGGAGCT CTCTGCGAAG TCTGGACGCA GAGGCTGCAC GGCGGCAGCG   240
CGCCCTTGCC CCAGGACCGG GGCTTCCTCG TGGTGCAGGG CGACCCGCGC GAGCTGCGGC   300
TGTGGGCGCG CGGGGATGCC AGGGGGGCGA GCCGCGCGGA CGAGAAGCCG CTCCGGAGGA   360
AACGGAGCGC TGCCCTGCAG CCCGAGCCCA TCAAGGTGTA CGGACAGGTT AGTCTGAATG   420
ATTCCCACAA TCAGATGGTG GTGCACTGGG CTGGAGAGAA AAGCAACGTG ATCGTGGCCT   480
TGGCCCGAGA TAGCCTGGCA TTGGCGAGGC CCAAGAGCAG TGATGTGTAC GTGTCTTACG   540
ACTATGGAAA ATCATTCAAG AAAATTTCAG ACAAGTTAAA CTTTGGCTTG GGAAATAGGA   600
GTGAAGCTGT TATCGCCCAG TTCTACCACA GCCCTGCGGA CAACAAGCGG TACATCTTTG   660
CAGACGCTTA TGCCCAGTAC CTCTGGATCA CGTTTGACTT CTGCAACACT CTTCAAGGCT   720
TTTCCATCCC ATTTCGGGCA GCTGATCTCC TCCTACACAG TAAGGCCTCC AACCTTCTCT   780
TGGGCTTTGA CAGGTCCCAC CCCAACAAGC AGCTGTGGAA GTCAGATGAC TTTGGCCAGA   840
CCTGGATCAT GATTCAGGAA CATGTCAAGT CCTTTTCTTG GGGAATTGAT CCCTATGACA   900
AACCAAATAC CATCTACATT GAACGACACG AACCCTCTGG CTACTCCACT GTCTTCCGAA   960
GTACAGATTT CTTCCAGTCC CGGGAAAACC AGGAAGTGAT CCTTGAGGAA GTGAGAGATT   1020
TTCAGCTTCG GGACAAGTAC ATGTTTGCTA CAAAGGTGGT GCATCTCTTG GGCAGTGAAC   1080
AGCAGTCTTC TGTCCAGCTC TGGGTCTCCT TTGGCCGGAA GCCCATGAGA GCAGCCCAGT   1140
TTGTCACAAG ACATCCTATT AATGAATATT ACATCGCAGA TGCCTCCGAG GACCAGGTGT   1200
TTGTGTGTGT CAGCCACAGT AACAACCGCA CCAATTTATA CATCTCAGAG GCAGAGGGGC   1260
TGAAGTTCTC CCTGTCCTTG GAGAACGTGC TCTATTACAG CCCAGGAGGG GCCGGCAGTG   1320
ACACCTTGGT GAGGTATTTT GCAAATGAAC CATTTGCTGA CTTCCACCGA GTGGAAGGAT   1380
TGCAAGGAGT CTACATTGCT ACTCTGATTA ATGGTTCTAT GAATGAGGAG AACATGAGAT   1440
CGGTCATCAC CTTTGACAAA GGGGGAACCT GGGAGTTTCT TCAGGCTCCA GCCTTCACGG   1500
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Protein Accession #: NP_003096.1

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DAYAQYLWIT FDFCNTLQGF SIPFRAADLL LHSKASNLLL GFDRSHPNKQ LWKSDDFGQT   240
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VCVSHSNNRT NLYISEAEGL KFSLSLENVL YYSPGGAGSD TLVRYFANEP FADFHRVEGL   420
QGVYIATLIN GSMNEENMRS VITFDKGGTW EFLQAPAFTG YGEKINCELS QGCSLHLAQR   480
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Seq ID NO: 79 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 120-755

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Protein Accession #: NP_060606.1

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|          |          |          |          |          |
TTCTCCCGCA ACCTTCCCTT CGCTCCCTCC CGTCCCCCCC AGCTCCTAGC CTCCGACTCC   60
CTCCCCCCCT CACGCCCGCC CTCTCGCCTT CGCCGAACCA AAGTGGATTA ATTACACGCT  120
TTCTGTTTCT CTCCGTGCTG TTCTCTCCCG CTGTGCGCCT GCCCGCCTCT CGCTGTCCTC  180
TCTCCCCCTC GCCCTCTCTT CGGCCCCCCC CTTTCACGTT CACTCTGTCT CTCCCACTAT  240
CTCTGCCCCC CTCTATCCTT GATACAACAG CTGACCTCAT TTCCCGATAC CTTTTCCCCC  300
CCGAAAAGTA CAACATCTGG CCCGCCCCAG CCCGAAGACA GCCCGTCCTC CCTGGACAAT  360
CAGACGAATT CTCCCCCCCC CCCCAAAAAA AAAAGCCATC CCCCCGCTCT GCCCCGTCGC  420
ACATTCGGCC CCCGCGACTC GGCCAGAGCG GCGCTGGCAG AGGAGTGTCC GGCAGGAGGG  480
CCAACGCCCG CTGTTCGGTT TGCGACACGC AGCAGGGAGG TGGGCGGCAG CGTCGCCGGC  540
TTCCAGACAC CAATGGGAAT CCCAATGGGG AAGTCGATGC TGGTGCTTCT CACCTTCTTG  600
GCCTTCGCCT CGTGCTGCAT TGCTGCTTAC CGCCCCAGTG AGACCCTGTG CGGCGGGGAG  660
CTGGTGGACA CCCTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTCAG CAGGCCCGCA  720
AGCCGTGTGA GCCGTCGCAG CCGTGGCATC GTTGAGGAGT GCTGTTTCCG CAGCTGTGAC  780
CTGGCCCTCC TGGAGACGTA CTGTGCTACC CCCGCCAAGT CCGAGAGGGA CGTGTCGACC  840
CCTCCGACCG TGCTTCCGGA CAACTTCCCC AGATACCCCG TGGGCAAGTT CTTCCAATAT  900
GACACCTGGA AGCAGTCCAC CCAGCGCCTG CGCAGGGGCC TGCCTGCCCT CCTGCGTGCC  960
CGCCGGGGTC ACGTGCTCGC CAAGGAGCTC GAGGCGTTCA GGGAGGCCAA ACGTCACCGT 1020
CCCCTGATTG CTCTACCCAC CCAAGACCCC GCCCACGGGG GCGCCCCCCC AGAGATGGCC 1080
AGCAATCGGA AGTGAGCAAA ACTGCCGCAA GTCTGCAGCC CGGCGCCACC ATCCTGCAGC 1140
CTCCTCCTGA CCACGGACGT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCCACGT 1200
CCCCCTGGGG CTTCTCCTGA CCCAGTCCCC GTGCCCCGCC TCCCCGAAAC AGGCTACTCT 1260
CCTCGGCCCC CTCCATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAAACAT GTACAAAATC 1320
GATTGGCTTT AAACACCCTT CACATACCCT CCCCCC
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Seq ID NO: 84 Protein Sequence
Protein Accession #: NP_000603.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGIPMGKSML VLLTFLAFAS CCIAAYRPSE TLCGGELVDT LQFVCGDRGF YFSRPASRVS   60
RRSRGIVEEC CFRSCDLALL ETYCATPAKS ERDVSTPPTV LPDNFPRYPV GKFFQYDTWK  120
QSTQRLRRGL PALLRARRGH VLAKELEAFR EAKRHRPLIA LPTQDPAHGG APPEMASNRK  180
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Seq ID NO: 85 DNA sequence
Nucleic Acid Accession #: XM_092643.1
Coding sequence: 1-5352

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1          11         21         31         41         51
|          |          |          |          |          |
ATGACTGAAG CCATTACAGA AGCAGCAGTA GCCTCAAGTG AGGAGGTGTC AGAGGAAAGA   60
GACGACCTGG GGCCTCTTGA ATTACATGAC AGTGGTACCT TTCAACAAGT CGTGAACCTT  120
CTGGACATCA TTGACAGCGA GTCAGCAAAG ACGGACACAA CAGGGGCAGG CCTTGACATG  180
CGGAAGACCC TGGCCTCGGT GATAATCATG GAGAAGGCCA CCACTGAGCC TTCTGTAGTG  240
ATAAACACTC TCATCCGCTG CCTGCAGGTG CCAGAGATTT CCACCCAGCG CAAGGTCAAC  300
ATTTACAACA TCCTCCAGGA CATCATCCAG CAGGAGGGGG AGCTGGAGGA GCAGTGCGTG  360
CAGAGGCTGG TGGCCATTGC CTCCAAGGAG ATGAGGGAGA TCCCAGAGAT GGAGGGCTAT  420
ATGAAGGCAG AGGTGGCCAG CGACACACTG GTGGCTCTGT CCCGAAACCA CTTCAGCTTG  480
GTCATGTACG AGCTGCAGCA CCACCTCAAG CCCCTCAACC TCACTGATGA ATTTGTCATC  540
ATCACACTGG CCAAGCTGGC CAACGGCAAT GTGTTTGAGT TCATGCCATA CATGGGCATC  600
ACCCTGGCTA CCATATTCAC CATGCTGAGA CTTGCCAATG AAGCCAAGAT ACGCCAGGCG  660
ATCTGCAGTG CCATGGAGAC CTTCTGTGAG ACGGTGCAGT TTTATCTGAA GCACCTGGAG  720
GAGAGCGTGT ACCCCGTGAT GACTGAGGAG GAGTTTGCCC TGAAGGTGTT CCCCATGTAT  780
CGCTACTTCG TGACAGTGTG GCTGAGGCAC TACAACCCCG AGGTGAAGCT GGGGGTGATC  840
AAGTCCCTGA AGCCCATGCT CGGCCTCCTT CTGCCCAACG ATGACCTGCG GGAGCAGGTC  900
TACGACTACA TCCCCCTGCT GCTGGCGGAG TACCAGGGCA GTCTGGAGGT CTTGAGGCAG  960
ATCCTGGAAC TGTCAGTCAC CACCAACACC CCTGTCCCCC AAATGCAGCT ACACACCATT 1020
TTCACAGAAC TGCACGTCCA GGTGTGCAAC AAGGCCCCGG CCCAGCATCA GTACAGCAGC 1080
CAGAATCTGA TGGAGATGGT GCACTGCTTC GTAGCCCTTG CTCGCTCCTA CCCCAAGGAG 1140
CTGATGAAGT TCTTCTTCAG CCAGATGGAG ACAAACAAGG AGGCCGTCCG CGTGGGGACT 1200
CTGAATCTGA TTAGGGCTAT AGTGAGCGCA GATGAGCCCA GGATGAGTAT CAGGGCCATC 1260
TACCTGGCTA TCCGGGTAGT CAAGAACACC ATCTCTGATA CCCGGTCCAA GGTGAGGATG 1320
GCTATTCTCC ACATCATTGG GCAGTTGGCT CTCTGTGGCT ACCAGGAGAG AATCAAAGGC 1380
TGGGGCCTGA AGTACCTGTC TGTGCAGCTG ACCTTATCCA CCTACAAACT GACAAATCGC 1440
CGGGAGAAGT TTTATCAGAG GGACTTGGAG GAGAGGATGG TCCACAAAGT CACCATGGAC 1500
ACTGTGAAGA TCATTACCTC TTCTGTCAGT GGGATGACCA CCGAGTTTTG GGTGAGGCTG 1560
CTGTGCTACA TCATGGAGAC AGACTACGTG GAAGCTTTGA CTCCTATCTG TATCAGCCTC 1620
ACAAACCTGG CAGAACACCA GCTCCATGGC CAGGATGTGG ATGTCAGCGT GGCTGGCAAG 1680
AGCAGGCAAG TGGACCTGCC TGCACCTCAG AAGCTGCTGG CCCGTCTCCT GGTGCTGATG 1740
TCATCACCTT ACAAGGGGGA GGGTCGTGGG ATAGCCATGC TCAACCTCTT GAGGACCCTG 1800
AGCCAGAGCA TCGCACCCTC CATGGCCGAC ATGTGGGAGC TGGAGATTGC GCTACTGGTC 1860
CGGTACCTGG AAGAACATAC TGAGTTCACT TGGGATCAGA AAGCCTGGGA AGACAAGCTG 1920
ATTCAGTTTC TGCGAAACTC CCTCAAGAAG ACCCGGGGGT CTAGCTGGAG CCTGCGCTTG 1980
AGTAAAGAGC TGAACAACCA GATTGCGAGC TTTGACAGCC CCTCTCTGGA GAAGGGCTTT 2040
CTGTACCGGG CCTTGGGCTT CACCTTGGCC ACAGGCCTGG AGGCCAGCAA GGTGGAGGTC 2100
CTGCTGTTGG AGCTGCTGTA CAAGACGGAC TACAGCAATG ACTTTGACAG CGAGGGTGTG 2160
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ATTATGTGCT TTGGCCTGTG TGCCCGGGGC CAGGTAAAAA CGGTGCTGAA TGTGCTTCAT  2220
GACTTCGAGG AGAGGATCCA GGAGTCAGAG CAGTCCTGGC AGATCAGTGC TTGGCGGAAG  2280
GACCATCCCT GGAGGCGGGA GACAGTGAAA AGTGCCCTCA TGGTGATGTA TAGCTGCGTG  2340
GCCTCCTACT GCCACCCCCA GTTGCTCCTC AACCTCGTGG ACAGCCCCAT CACCGCTAAG  2400
ATCATTCACC ATTATGTCAG CAGCTGCCAG GACATCTGTC TCAAAATGGC CTTCATGAAG  2460
AGTGTTGTGC AGGTTACCAA GGCCATCAAC AACATCAAGG ACCTGGAGGA CTTTCACTTT  2520
GCCCAGAAGA CGACTCTTAC CAGCATTATA GTGGCGGTCA TCAAGGCAGA ACCGACTGAC  2580
AACCTGGTTT CTCCAGTGCG AGCCTTGGCG ATGGAGGCCC TCTCGCACCT GAGCAAGCTG  2640
AAGCCTTTCT ACTCCACAGA GGAAAACAGT GAGCTGATGG ATATCAGCAT ACATTCTGTA  2700
ATTTCTCTCC AACTCCCAGG AGAGGACAAT GAGTCCATTA AGACCCTGTA TGCAAATGCC  2760
CTGAGCTCCC TGGAGCAGCT GATGGAGAGC CTCCTGCAGA GGCAGCTGGA CCCCAAGGGG  2820
CTGCAGGAGA TGGTGCAGCT CCTGGAAAAG TGGATCTTGT CGGAGAAAGA ATGGGAGCGG  2880
GAAAAGGCCG TGAGCCTCCA TCTCTATCTC ATGTGGATTT ATGTCCACAG CACTGCTGTC  2940
TGTATCCACC TAAAGCTGGG GCAGTTTGGC ACAATGGTCG GACTCATTGC CCCGTGCACC  3000
TGTGATGCCC ATCAAAGAAC CCGCATGGCC TCAATGAATG TCCTGTCCAG CCTGCTAGAT  3060
CTTCACGCAA GCCAGACCTG CTCCTTGTGG GGCCCTTCCA AGCAGAAGGA GCTTGAGAAA  3120
TGTAAGGGGG ACCTCCAGAG CACAGATGTG GAGAAGATCT TCTGTGCATC CTCCAGAATC  3180
GCCAAGGTGG TCTGCATGGA GTTTAGCTGC GATGAGGTGG TCTCGCTCAT CCAGAAGCTC  3240
TGCGAGAACA CTGGGGCCAT GAACCTGCAG CATGACAAGG CCTCTGTCAC CTGGATAGCC  3300
TTCTTCCTCC AGATGCGGGC CAAGGAGCTG GAGGACAAGG TGGCCGAGAT CCTGAGTGCC  3360
ATCCTGGTGC ACCTGCCGGT GGTGGACCAC CCAGAGGTGC GGCGCCTTCT CATTGACGGC  3420
ATCCTGCTGC TGGCGCACCA CCACCAGGAG ACCATCCTCA CATCGCTCCT GAGGCAGCCA  3480
CTGCCCATGG AGAGCCACCT GGCAGAGGTG TGGCTGGCAG TGTCGGAGAA CGTGCCCTTC  3540
GCCCGGACCA TGCTCCACAG CCTGATGGGC CGGCTGCAGT CACGGCTCAG CCCCAGAATC  3600
AGTGCCACCT CCAAGGCTGA CATCTGGCGC CTGGCTGCGG TGGACCCCCT GATGACCCTG  3660
TGCACCATCC ACCTTCTCAT TCAGAAGCTG GATGAGAATG ACAAGCTCCC GGACTTCCTC  3720
CCTGACCTCA TCTACACCCT CCTGCTGCAG CTTGGAAGCA GCCACCGACC AGAGGCCGCC  3780
CCGCCGGTCT TGAAGATGTG GAAGCTGGTC CACACCACTC CTCTGCCGGA GGAGATGAAC  3840
CTGCAAAGGT GCTCTCGAGG GCGGGTCACT ATCAAGTCCA TGCAGCTCTT GTTCAAGAGA  3900
GTCAAGAGCC AGCACCTGGC ACATACCCTG GACGAGCAGG CAGTGTGGGA CCTCCTGCAG  3960
GACGGCGGGA CATTCCTGGA GGGTGTGAGC CTGCTGGCCA GGCTGTGCAT GCAGCACGTG  4020
GAGGGCCACA GGCAGAGGCT GGCCGAGCTG GTGCTCAGGG GCATGGACTC AGAAGTCCTG  4080
AGCTGCCGCA TCAGCAGCAC AGCGGTCTGC GTGGAAATGA GGCACCGGTT CATGAGCGGC  4140
CCAGTTCTGT ACCAGGAGAA GCTGCTGAAG CCGGCAGCTT TGCTGCTGGA GAAGGGTGCC  4200
GACCAGGAGG AAGACGAGGC CCTGCGGGTG CTGTCCCTGC GCGCCCTCGG CAACATGGCC  4260
CTGGGCGCCC CCAAGAAGGT GAAGCAGTAC CGGAAGGTCT TGCTGGAGAA GTGCCTGGGC  4320
CCCCTGAGGG AGCCCGTGAG CAACAGCGTG ACTGCCGAGG GCATGGAGGC CCTGACCAAG  4380
ATCCTGGCTG AGCTCCGGGA AGGGGATGTG GGGTCCTCTT TCGACGCCAT GTCTGAGCAG  4440
TGCAGGATCT TCTTCGACAA CGAGAGCGAG CTGCTGCGTC TGAAAGCCTT CATCCTCTTT  4500
GGAAAGCTGG CAAGGGTGGT CGGGATGTCC AAGAAGCATT TCTTCAAAGG GGAGGTGAAG  4560
AAGGCCTGGA TCCCCCTCAT GCTGCACTCC CAGGACCCCT GCTCCAATGC AGCCCAAGTA  4620
AGATACATCC TGGGCTTTGT GTCCCAGTCT GGGGCCCGCT GTTCCCCGAG GAAACAGGTC  4680
CTTGGGTCTG CTGGCTCGGC CTGTATGGCT ACCATGTTTC AGTGTGTGCA CTTCTGGGGC  4740
TGGAAGTCCC TGGAGCATCC CTCAGGGCCA AGTGATACCG CTACTGATGA CAAGATGACC  4800
GTTTTCCAGA CAACCATGTG CTCCATCCTG ACTCGGAAAA AGCCGGCTGT TCTCTACCGC  4860
TTCTTGCTAG AAACAATGGC CTATGTTAAA AATAACTTGT CAAGAATCAG AATCGCTGCT  4920
TGCAACTTGG CAGGAATTAT TATGAAGCAG ATGTCTACAC ATTATCTGAA AAAGCTGGAC  4980
TTCCCAGCAT TACGGAATTC CCTCCAGGAA CTACAGCTGG ACCCGGATCC CGGGCCCACT  5040
GGCCCAAAGG GTCGGAAACT AGCTTTGTGT CTTCACTCGG AGTTCATCCA CACGCATGCT  5100
GACAGCGTGC CTAAGGCCAG GCACTGTGCC AAGCGAGCAG GTAAACCAGG ACTTCCAAAC  5160
TGTTCCCAGT CCAACTGCCA AAGGAATTCA CCATCCGGGG TCCCATCAAC AGGAGAGAGC  5220
TGCTATGCTG TCCAAAATCC AACCCGTGCT AAAGCCTTCT CTGGAACAGT GGTCTTCAAA  5280
CTGTTTTGTG GAGCAAATGG TGACTTGATT TCCTGCCCAG TGATAAAGAG TATTGCTGCT  5340
AAACAAGCTT GA
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Seq ID NO: 86 Protein sequence:
Protein Accession #: XP_092643.1
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1          11         21         31         41         51
|          |          |          |          |          |
MTEAITEAAV ASSEEVSEER DDLGPLELHD SGTFQQVVNL LDIIDSESAK TDTTGAGLDM    60
RKTLASVIIM EKATTEPSVV INTLIRCLQV PEISTQRKVN IYNILQDIIQ QEGELEEQCV   120
QRLVAIASKE MREIPEMEGY MKAEVASDTL VALSRNHFSL VMYELQHHLK PLNLTDEFVI   180
ITLAKLANGN VFEFMPYMGI TLATIFTMLR LANEAKIRQA ICSAMETFCE TVQFYLKHLE   240
ESVYPVMTEE EFALKVFPMY RYFVTVWLRH YNPEVKLGVI KSLKPMLGLL LPNDDLREQV   300
YDYIPLLLAE YQGSLEVLRQ ILELSVTTNT PVPQMQLHTI FTELHVQVCN KAPAQHQYSS   360
QNLMEMVHCF VALARSYPKE LMKFFFSQME TNKEAVRVGT LNLIRAIVSA DEPRMSIRAI   420
YLAIRVVKNT ISDTRSKVRM AILHIIGQLA LCGYQERIKG WGLKYLSVQL TLSTYKLTNR   480
REKFYQRDLE ERMVHKVTMD TVKIITSSVS GMTTEFWVRL LCYIMETDYV EALTPICISL   540
TNLAEHQLHG QDVDVSVAGK SRQVDLPAPQ KLLARLLVLM SSPYKGEGRG IAMLNLLRTL   600
SQSIAPSMAD MWELEIALLV RYLEEHTEFT WDQKAWEDKL IQFLRNSLKK TRGSSWSLRL   660
SKELNNQIAS FDSPSLEKGF LYRALGFTLA TGLEASKVEV LLLELLYKTD YSNDFDSEGV   720
IMCFGLCARG QVKTVLNVLH DFEERIQESE QSWQISAWRK DHPWRRETVK SALMVMYSCV   780
ASYCHPQLLL NLVDSPITAK IIHHYVSSCQ DICLKMAFMK SVVQVTKAIN NIKDLEDFHF   840
AQKTTLTSII VAVIKAEPTD NLVSPVRALA MEALSHLSKL KPFYSTEENS ELMDISIHSV   900
ISLQLPGEDN ESIKTLYANA LSSLEQLMES LLQRQLDPKG LQEMVQLLEK WILSEKEWER   960
EKAVSLHLYL MWIYVHSTAV CIHLKLGQFG TMVGLIAPCT CDAHQRTRMA SMNVLSSLLD  1020
LHASQTCSLW GPSKQKELEK CKGDLQSTDV EKIFCASSRI AKVVCMEFSC DEVVSLIQKL  1080
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CENTGAMNLQ HDKASVTWIA FFLQMRAKEL EDKVAEILSA ILVHLPVVDH PEVRRLLIDG  1140
ILLLAHHHQE TILTSLLRQP LPMESHLAEV WLAVSENVPF ARTMLHSLMG RLQSRLSPRI  1200
SATSKADIWR LAAVDPLMTL CTIHLLIQKL DENDKLPDFL PDLIYTLLLQ LGSSHRPEAA  1260
PPVLKMWKLV HTTPLPEEMN LQRCSRGRVT IKSMQLLFKR VKSQHLAHTL DEQAVWDLLQ  1320
DGGTFLEGVS LLARLCMQHV EGHRQRLAEL VLRGMDSEVL SCRISSTAVC VEMRHRFMSG  1380
PVLYQEKLLK PAALLLEKGA DQEEDEALRV LSLRALGNMA LGAPKKVKQY RKVLLEKCLG  1440
PLREPVSNSV TAEGMEALTK ILAELREGDV GSSFDAMSEQ CRIFFDNESE LLRLKAFILF  1500
GKLARVVGMS KKHFFKGEVK KAWIPLMLHS QDPCSNAAQV RYILGFVSQS GARCSPRKQV  1560
LGSAGSACMA TMFQCVHFWG WKSLEHPSGP SDTATDDKMT VFQTTMCSIL TRKKPAVLYR  1620
FLLETMAYVK NNLSRIRIAA CNLAGIIMKQ MSTHYLKKLD FPALRNSLQE LQLDPDPGPT  1680
GPKGRKLALC LHSEFIHTHA DSVPKARHCA KRAGKPGLPN CSQSNCQRNS PSGVPSTGES  1740
CYAVQNPTRA KAFSGTVVFK LFCGANGDLI SCPVIKSIAA KQA
```

Seq ID NO: 87 DNA sequence
Nucleic Acid Accession #: CAT cluster

```
1          11         21         31         41         51
|          |          |          |          |          |
CACTTCTCCC TCTCCTTAGT TCTCCGGTAA CCAAACCTTC TCTCGTTATA TACCCAATGA   60
TAAAACCAAA GTAATGTTGT ACAGGTTAAA GATTCAAAAC AAACCATAGC AACTGAAACA   120
GGGTATCAGG ACGCAAATGC TTGGCTGGAA TGGATTAAAC ATTCTGTTGC AGGCTAAACA   180
AAAGCGCCTG TTACACTTGT GTGACAGGCA GGCCAGAGAC CCAAATTGTT CCCTTTCCAC   240
TTGGGTGGTC CTCTCACAGA CCGGGCATGA GCTGTGTGGT AGCTCTCTTC CAGAACCCCA   300
CAGCCTGGGG TGGTGAGTCA TGCAAGACTC TTTCACTGCT GTTCCCTGAG GTCAAGAGCC   360
CTGCAGGTCA GCCCTGAGGA CTATCCGGCC TCCAGCCCCT GATGTTAACT TCACCTCATG   420
CCTTTCACGG CAGGGGGAAA AGTTAGCATT CCTTGGAGAC TTAACAGGGT GCAGTGAAAC   480
CAGGCCTTTT GAAGAGCTTA CCAATCAGTC TGCCCTTGTT CATCCCCGAG CAGATGTGTG   540
GTGGTATTGC TGGGGACTAC TGCTGGGTAC TCTGCCAAGT AATTAGAGCA GCACTCATGC   600
TCTAGTCCAA CTGGCCATCC CTTTCACCCT AGCATTCTGT CAATATGATA AAAAAAAATG   660
TAAAGAAGTG CCTCACGTGG GTCCTTGACC CCCATGTTTA TATAAACACT ATTGGGTTCT   720
ATGAGGAGAA CCCGATGA
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Seq ID NO: 88 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..759

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCAGGAAG AAACAGGCTG GCAGCTTGGG GAAAGGATTC TTACATACCA CGGCGACCAG   60
GTAACTCTGT GCACAGACCC AGAAGAAAGT AGAAAAATAA GTTTTGGAGG AAACCTCATT   120
GTGAACACAC CTCACCAGGT CAGAACTATC CTAAGTCAGA AAGCAGAAAG GTGGCTTACT   180
GACTCCAGAA TCTTAAAGTA TGAGGCTATT CTCTTAGAAA AAGATGATTT AACATTAACC   240
ACTGATAATT CACTTAACCC AGCAGGTTTC CTAACAGGGG ATCTATATCA AAAGAGAGAG   300
CACACATGTT TAGTTTTAAT TAATTACCAT ACAAAGGTCC GACCAGACCT AGGAGAAACT   360
CCCTTCAGGA CGGGACAACA CTTTATAGAT GGTTCCTCCC AGGTGATAGA GGGAAAAAGA   420
TACAATGGGT ATTCAGTAAT TGATAGAGAA ACTCTTGTAG AAATAGAGTT AGGAAAATTG   480
CCTAATAATT GGTCTGCTCA AACATGTGAG CTGTTTGCAC TCAGCCAAGC CTTAAAGGAC   540
TTACAGAACC AGGAAGGAAC CATCTATACA GATTCTAAGT ACGCCTTTGG AGTGGCTCAT   600
ACATTTGGAA AAATTTGGAC TGAACGAGGT CTTATTAATA GCAAATGCCA AGACTTGGTC   660
CATAAGGAAT TAATCACCCA AGTATTAACT AACCTTCAGC TGCCAAAAGA AACAGCTATT   720
GACCATGTCC CCGGACACCA AAAAAGCCTT TCTTTTTAA
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Seq ID NO: 89 Protein Sequence
Protein Accession #: FGENESH predicted

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1          11         21         31         41         51
|          |          |          |          |          |
MQEETGWQLG ERILTYHGDQ VTLCTDPEES RKISFGGNLI VNTPHQVRTI LSQKAERWLT   60
DSRILKYEAI LLEKDDLTLT TDNSLNPAGF LTGDLYQKRE HTCLVLINYH TKVRPDLGET   120
PFRTGQHFID GSSQVIEGKR YNGYSVIDRE TLVEIELGKL PNNWSAQTCE LFALSQALKD   180
LQNQEGTIYT DSKYAFGVAH TFGKIWTERG LINSKCQDLV HKELITQVLT NLQLPKETAI   240
DHVPGHQKSL SF
```

Seq ID NO: 90 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence: 186..776

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1          11         21         31         41         51
|          |          |          |          |          |
AGAAACTCAG AGACCAAGTC CATTGAGAGA CTGAGGGGAA AGAGAGGAGA GAAAGAAAAA   60
GAGAGTGGGA ACAGTAAAGA GAAAGGAAGA CAACCTCCAG AGAAAGCCCC CGGAGACGTC   120
TCTCTGCAGA GAGGCGGCAG CACCCGGCTC ACCTGCGAAG CGCCTGGGAA GCGAGTGCCC   180
CTAACATGCG GCTGCCGCTG CTTGTGTCCG CGGGAGTCCT GCTGGTGGCT CTCCTGCCCT   240
GCCCGCCATG CAGGGCGCTC CTGAGCCGCG GGCCGGTCCC GGGAGCTCGG CAGGCGCCGC   300
AGCACCCTCA GCCCTTGGAT TTCTTCCAGC CGCCGCCGCA GTCCGAGCAG CCCCAGCAGC   360
CGCAGGCTCG GCCGGTCCTG CTCCGCATGG GAGAGGAGTA CTTCCTCCGC CTGGGGAACC   420
TCAACAAGAG CCCGGCCGCT CCCCTTTCGC CCGCCTCCTC GCTCCTCGCC GGAGGCAGCG   480
GCAGCCGCCC TTCGCCGGAA CAGGCGACCG CCAACTTTTT CCGCGTGTTG CTGCAGCAGC   540
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TGCTGCTGCC TCGGCGCTCG CTCGACAGCC CCGCGGCTCT CGCGGAGCGC GGCGCTAGGA   600
ATGCCCTCGG CGGCCACCAG GAGGCACCGG AGAGAGAAAG GCGGTCCGAG GAGCCTCCCA   660
TCTCCCTGGA TCTCACCTTC CACCTCCTCC GGGAAGTCTT GGAAATGGCC AGGGCCGAGC   720
AGTTAGCACA GCAAGCTCAC AGCAACAGGA AACTCATGGA GATTATTGGG AAATAAAACG   780
GTGCGTTTGG CCAAAAAGAA TCTGCATTTA GCACAAAAAA AATTTAAAAA AATACAGTAT   840
TCTGTACCAT AGCGCTGCTC TTATGCCATT TGTTTATTTT TATATAGCTT GAAACATAGA   900
GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAAGTGTA TTCACGTGCA   960
GCAGCAACAC AATGTTATTC GTTTTGTCTA CGTTTAGTTT CCGTTTCCAG GTGTTTATAG   1020
TGGTGTTTTA AAGAGAATGT AGACCTGTGA GAAAACGTTT TGTTTGAAAA AGCAGACAGA   1080
AGTCACTCAA TTGTTTTTGT TGTGGTCTGA GCCAAAGAGA ATGCCATTCT CTTGGGTGGG   1140
TAAGACTAAA TCTGTAAGCT CTTTGAAACA ACTTTCTCTT GTAAACGTTT CAGTAATAAA   1200
ACATCTTTCC AGTCCTTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT   1260
TAATAAAAGT TGCAAAGGT
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Seq ID NO: 91 Protein Sequence
Protein Accession #: NP_000747.1

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1          11         21         31         41         51
|          |          |          |          |          |
MRLPLLVSAG VLLVALLPCP PCRALLSRGP VPGARQAPQH PQPLDFFQPP PQSEQPQQPQ   60
ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SSLLAGGSGS RPSPEQATAN FFRVLLQQLL   120
LPRRSLDSPA ALAERGARNA LGGHQEAPER ERRSEEPPIS LDLTFHLLRE VLEMARAEQL   180
AQQAHSNRKL MEIIGK
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Seq ID NO: 92 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

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GCCCAGAAGG AGAACTCCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG   120
AGCACCCTGC CCCAGCGAGT CCTCCGGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCCTC   180
ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCCTGGCC AGAAGGTGAT GGAGAATAGC   240
AGTGGGACAC CCGACATCTT AACGCGGCAC TTCACAATTG ATGACTTTGA GATTGGGCGT   300
CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC   360
ATCGTGGCGC TCAAGGTCCT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG   420
CTGCGCAGAG AGATCGAAAT CCAGGCCCAC CTGCACCATC CCAACATCCT GCGTCTCTAC   480
AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG   540
CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CACGATCATG   600
GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA   660
AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTCGGCTGG   720
TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCCTGGA CTACCTGCCC   780
CCAGAGATGA TTGAGGGGCG CATGCACAAT GAGAAGGTGG ATCTGTGGTG CATTGGAGTG   840
CTTTGCTATG AGCTGCTGGT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACGAGACC   900
TATCGCCGCA TCGTCAAGGT GGACCTAAAG TTCCCCGCTT CTGTGCCCAC GGGAGCCCAG   960
GACCTCATCT CCAAACTGCT CAGGCATAAC CCCTCGGAAC GGCTGCCCCT GGCCCAGGTC   1020
TCAGCCCACC CTTGGGTCCG GGCCAACTCT CGGAGGGTGC TGCCTCCCTC TGCCCTTCAA   1080
TCTGTCGCCT GATGGTCCCT GTCATTCACT CGGGTGCGTG TGTTTGTATG TCTGTGTATG   1140
TATAGGGGAA AGAAGGGATC CCTAACTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT   1200
TTAATAAAGG CTGAAGCTTT TTGT
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Seq ID NO: 93 Protein Sequence
Protein Accession #: NP_004208

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1          11         21         31         41         51
|          |          |          |          |          |
MAQKENSYPW PYGRQTAPSG LSTLPQRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN   60
SSGTPDILTR HFTIDDFEIG RPLGKGKFGN VYLAREKKSH FIVALKVLFK SQIEKEGVEH   120
QLRREIEIQA HLHHPNILRL YNYFYDRRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI   180
MEELADALMY CHGKKVIHRD IKPENLLLGL KGELKIADFG WSVHAPSLRR KTMCGTLDYL   240
PPEMIEGRMH NEKVDLWCIG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA   300
QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPPSAL QSVA
```

Seq ID NO: 94 DNA sequence
Nucleic Acid Accession #: NM_007019.1
Coding sequence: 41..580

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGCG AGTTCCTGTC TCTCTGCCAA CGCCGCCCGG ATGGCTTCCC AAAACCGCGA   60
CCCAGCCGCC ACTAGCGTCG CCGCCGCCCG TAAAGGAGCT GAGCCGAGCG GGGGCGCCGC   120
CCGGGGTCCG GTGGGCAAAA GGCTACAGCA GGAGCTGATG ACCCTCATGA TGTCTGGCGA   180
TAAAGGGATT TCTGCCTTCC CTGAATCAGA CAACCTTTTC AAATGGGTAG GGACCATCCA   240
TGGAGCAGCT GGAACAGTAT ATGAAGACCT GAGGTATAAG CTCTCGCTAG AGTTCCCCAG   300
TGGCTACCCT TACAATGCGC CCACAGTGAA GTTCCTCACG CCCTGCTATC ACCCCAACGT   360
GGACACCCAG GGTAACATAT GCCTGGACAT CCTGAAGGAA AAGTGGTCTG CCCTGTATGA   420
TGTCAGGACC ATTCTGCTCT CCATCCAGAG CCTTCTAGGA GAACCCAACA TTGATAGTCC   480
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CTTGAACACA CATGCTGCCG AGCTCTGGAA AAACCCCACA GCTTTTAAGA AGTACCTGCA   540
AGAAACCTAC TCAAAGCAGG TCACCAGCCA GGAGCCCTGA CCCAGGCTGC CCAGCCTGTC   600
CTTGTGTCGT CTTTTTAATT TTTCCTTAGA TGGTCTGTCC TTTTTGTGAT TTCTGTATAG   660
GACTCTTTAT CTTGAGCTGT GGTATTTTTG TTTTGTTTTT GTCTTTTAAA TTAAGCCTCG   720
GTTGAGCCCT TGTATATTAA ATAAATGCAT TTTTGTCCTT TTTTAAAAAA AAAAAAAAAA   780
AAA
```

Seq ID NO: 95 Protein Sequence
Protein Accession #: NP_008950.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MASQNRDPAA TSVAAARKGA EPSGGAARGP VGKRLQQELM TLMMSGDKGI SAFPESDNLF   60
KWVGTIHGAA GTVYEDLRYK LSLEFPSGYP YNAPTVKFLT PCYHPNVDTQ GNICLDILKE   120
KWSALYDVRT ILLSIQSLLG EPNIDSPLNT HAAELWKNPT AFKKYLQETY SKQVTSQEP    179
```

Seq ID NO: 96 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

```
1          11         21         31         41         51
|          |          |          |          |          |
AGAACGGCTT CCGGCGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTCG   60
AAAACCACAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA   120
CCGAAGGTCC TGGAAGATAC TGCTCTTTGG TGTAATAAAC TTGATATGTA CTGGCTTCCT   180
GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACTT ACCTGACCAT   240
TTTTGATCTT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACAT TGAGGAAACC   300
TAGCCCTGTC TATTCATTTG GGTTTGAAAG ATTAGAAGTC CTGGCTGTAT TTGCCTCCAC   360
AGTCTTGGCA CAGTTGGGAG CTCTCTTTAT ATTAAAAGAA AGTGCAGAAC GCTTTTTGGA   420
ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA   480
CCTGTTCACG ATGCTTTCTA TTCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG   540
TACGAGCTGG CTTCAAGAGC ATGTTGCAGA TCTTAGTCGA AGCTTGTGTG GAATTATTCC   600
GGGACTTAGC AGTATCTTCC TTCCCCGAAT GAATCCATTT GTTTTGATTG ATCTTGCTGG   660
AGCATTTGCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCCGTAGA   720
CACTGCCTCT GCTATAGCTA TTGCCTTGAT GACATTTGGC ACTATGTATC CCATGAGTGT   780
GTACAGTGGG AAAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATTGGTC AGTTGGACAA   840
ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTTAGAA GTCCGAAATG AACATTTTTG   900
GACCCTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTCGAC GAGATGCCAA   960
TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTACTCTAAC   1020
TGTTCAAATT TTCAAGGATG ACTGGATTAG GCCTGCCTTA TTGTCTGGGC CTGTTGCAGC   1080
CAATGTCCTA AACTTTTCAG ATCATCACGT AATCCCAATG CCTCTTTTAA AGGGTACTGA   1140
TGATTTGAAC CCAGTTACAT CAACTCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC   1200
ATTTAACACT CCTGGGAAAA ATGTGAACCC AGTTATTCTT CTAAACACAC AAACAAGGCC   1260
TTATGGTTTT GGTCTCAATC ATGGACACAC ACCTTACAGC AGCATGCTTA ATCAAGGACT   1320
TGGAGTTCCA GGAATTGGAG CAACTCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG   1380
TAGATATGGA ACTAATAATA GAATTGGACA ACCAAGACCA TGATAGACTC TAACTTATTT   1440
TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAATCCAACT TTGCATTGAC   1500
TGTTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACATT TCATGAAACC   1560
TATGAAACTA TATTTTTGTA AAATGTATTT GTGACAGTGA AATCCTCGTA AATGTTAAAG   1620
GCTTTAAATA GGCTTCCTTT AGAAAATGTG TTTCTTTAAA TTTGGATTTT GGTATCTTTG   1680
GTTTTGTAGT TGACTGCAGT GTGATGTGAC CTTACCTTTA TAAGAGCCAC TTGATGGAGT   1740
AGATCTGTCA CATTACTAAG ATACGATATT TCTTTTTTTT TCCGAGACGG AGTCTTGCTC   1800
TGCCACTGTG CCCGGCCAAT ACATTATTAT TAACTTAAGG CTGTACTTTA TTAAGGCTTC   1860
CTTAGTTTTT GTTTTGTTTT GTTTTTTGAG ATGGAGTCTC ACTCTGTCGC CCAGGCTGGA   1920
ATGCAGTGGC ATGATCTCAG CTCACTGCAA CCTCTGCCTC CTGAGTTCAA ATGATTCTCC   1980
TGCCTCAGCC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCACGCCC AGCTAATTTT   2040
TGTATTTTTA GTAAAGACGG GGATTTCAC CATGTTGGCC AGGCTGGTCT TGAACTCCTG   2100
ACCTCATGAT CCACCCACCT TAGCCTCCCA AAGTGCTGGG ATTAGGTGTG AGCCACCGCA   2160
CCTGGCCGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATAA TACACATTTT   2220
GGGAAAGGGA AAAATGTCTG TTCAAAAAGT AAAGGTCTCT TTTATAGCTT TTCCAAACTT   2280
AATTGCTAAA TTTTTCTTTG AGGTTCTCCT GAATTATGTC TTACAAACTA AAAGCAAAAA   2340
TTTTTAGCAG AAATTTTGGA ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA   2400
GATTTTTGTT AAAGTTTCTC TCCTTTAAAA ATTTTAGTAC ATTTGTAAAT
```

Seq ID NO: 97 Protein Sequence
Protein Accession #: BAB70980.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGTIHLPRKP QRSFFGKLLR EFRLVAADRR SWKILLFGVI NLICTGFLLM WCSSTNSIAL   60
TAYTYLTIFD LFSLMTCLIS YWVTLRKPSP VYSFGFERLE VLAVFASTVL AQLGALFILK   120
ESAERFLEQP EIHTGRLLVG TFVALCFNLF TMLSIRNKPF AYVSEAASTS WLQEHVADLS   180
RSLCGIIPGL SSIFLPRMNP FVLIDLAGAF ALCITYMLIE INNYFAVDTA SAIAIALMTF   240
GTMYPMSVYS GKVLLQTTPP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GFGSLAGSVH   300
VRIRRDANEQ MVLAHVTNRL YTLVSTLTVQ IFKDDWIRPA LLSGPVAANV LNFSDHHVIP   360
MPLLKGTDDL NPVTSTPAKP SSPPPEFSFN TPGKNVNPVI LLNTQTRPYG FGLNHGHTPY   420
SSMLNQGLGV PGIGATQGLR TGFTNIPSRY GTNNRIGQPR P
```

Seq ID NO: 98 DNA sequence
Nucleic Acid Accession #: CAT cluster

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGACTTAA CCAATGCTTC ACAAATACCA AGAAAAAAAT ATTTCAATGT GATAAATATA   60
GGAAAGTTTT TCATAAATTT TCAAATTCAA ACTGACATAA GAGAAGACAT ACGGGAAAAA   120
AGACCTTTCA AATGTATAGA ATGTGGCAAA GCTTTTAACA AGTTTTCAAC CCTTACTACA   180
CATAAGAAAA TTCATACTAG AGAGAAACCC TACAAATGTG AAGAATGTGG CAAAGCCTTC   240
AACTGGTCCT CATACCTTAC TATACATAAG AGAATTCATA CTGGAGAGAA ACTCTACAAA   300
TGTGAAGAAT GTGGCAAAGC CTTCAACTGG TCCTCATACC TTACTGCATA TAAGATAACT   360
CATACTAGAG AGAAACCCTA CAAATGTGAA GAATGTGGCA AAGCCTTTAA GTACTCCTCG   420
AACCTCACTA CACATAAGAT AATTCATACT GGAGAGCATC TCTACAAGTG TGAAGAATGT   480
GGCAAAGCGT TTAACCATGC TGCATGCTTC TTTGTCATTT TGAAGATTTG A
```

Seq ID NO: 99 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..531

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGACTTAA CCAATGCTTC ACAAATACCA AGAAAAAAAT ATTTCAATGT GATAAATATA   60
GGAAAGTTTT TCATAAATTT TCAAATTCAA ACTGACATAA GAGAAGACAT ACGGGAAAAA   120
AGACCTTTCA AATGTATAGA ATGTGGCAAA GCTTTTAACA AGTTTTCAAC CCTTACTACA   180
CATAAGAAAA TTCATACTAG AGAGAAACCC TACAAATGTG AAGAATGTGG CAAAGCCTTC   240
AACTGGTCCT CATACCTTAC TATACATAAG AGAATTCATA CTGGAGAGAA ACTCTACAAA   300
TGTGAAGAAT GTGGCAAAGC CTTCAACTGG TCCTCATACC TTACTGCATA TAAGATAACT   360
CATACTAGAG AGAAACCCTA CAAATGTGAA GAATGTGGCA AAGCCTTTAA GTACTCCTCG   420
AACCTCACTA CACATAAGAT AATTCATACT GGAGAGCATC TCTACAAGTG TGAAGAATGT   480
GGCAAAGCGT TTAACCATGC TGCATGCTTC TTTGTCATTT TGAAGATTTG A
```

Seq ID NO: 100 Protein Sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
MDLTNASQIP RKKYFNVINI GKFFINFQIQ TDIREDIREK RPFKCIECGK AFNKFSTLTT   60
HKKIHTREKP YKCEECGKAF NWSSYLTIHK RIHTGEKLYK CEECGKAFNW SSYLTAYKIT   120
HTREKPYKCE ECGKAFKYSS NLTTHKIIHT GEHLYKCEEC GKAFNHAACF FVILKI
```

Seq ID NO: 101 DNA sequence
Nucleic Acid Accession #: NM_032589.1
Coding sequence: 147-422

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGT CTTGTTATGC AAATAGGCTT CCCACTTGGC AGGGGCCGTC TTGTCCACTC   60
GTTTCTGTAA ACATGGGTGG CAAAAAGAGA AGATGGAGCT GCCATTTAGA ACATGCCTAA   120
TCCCAGCTTC ATCTTGCTGA GCAAAAATGA AGGAGCCTGG ACCCAACTTT GTTACTGTGA   180
GAAAGGGTCT TCATTCATTC AAGATGGCAT TTGTTAAGCA CCTACTGCTG GAGTGCAGTG   240
GTTCAATCAC GGATCACTGC AGCCTCCACC TCCCAGTTCA AGAAATTCTC ATGTCTCAGC   300
CTCCTGAGCA GCTAGGATTA CAGACAAACC TTGGAAATCA AGAAAGTTCT GGAATGATGA   360
AGCTGTTCAT GCCAAGACCG AAAGTGCTGG CCCAGTATGA GTCCATTCAG TTCATGCCGT   420
GACAATTTTC TTGGAACTCC TTTTTATTGT TAGTTCTCAC TTGTTTCCAT ATTTAGTGAA   480
TGTACATTTA ATTGCAAAGC TGTCATTAAT AAAAATTCTT ATAGTACCTC ACTGCAC
```

Seq ID NO: 102 Protein sequence:
Protein Accession #: NP_115978.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MKEPGPNFVT VRKGLHSFKM AFVKHLLLEC SGSITDHCSL HLPVQEILMS QPPEQLGLQT   60
NLGNQESSGM MKLFMPRPKV LAQYESIQFM P
```

Seq ID NO: 103 DNA sequence
Nucleic Acid Accession #: NM_014501.1
Coding sequence: 60..737

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCGGACCGA AGAACGCAGG AAGGGGGCCG GGGGGACCCG CCCCCGGCCG GCCGCAGCCA   60
TGAACTCCAA CGTGGAGAAC CTACCCCCGC ACATCATCCG CCTGGTGTAC AAGGAGGTGA   120
CGACACTGAC CGCAGACCCA CCCGATGGCA TCAAGGTCTT TCCCAACGAG GAGGACCTCA   180
CCGACCTCCA GGTCACCATC GAGGGCCCTG AGGGGACCCC ATATGCTGGA GGTCTGTTCC   240
GCATGAAACT CCTGCTGGGG AAGGACTTCC CTGCCTCCCC ACCCAAGGGC TACTTCCTGA   300
CCAAGATCTT CCACCCGAAC GTGGGCGCCA ATGGCGAGAT CTGCGTCAAC GTGCTCAAGA   360
GGGACTGGAC GGCTGAGCTG GGCATCCGAC ACGTACTGCT GACCATCAAG TGCCTGCTGA   420
```

```
TCCACCCTAA CCCCGAGTCT GCACTCAACG AGGAGGCGGG CCGCCTGCTC TTGGAGAACT   480
ACGAGGAGTA TGCGGCTCGG GCCCGTCTGC TCACAGAGAT CCACGGGGGC GCCGGCGGGC   540
CCAGCGGCAG GGCCGAAGCC GGTCGGCCCC TGGCCAGTGG CACTGAAGCT TCCTCCACCG   600
ACCCTGGGGC CCCAGGGGGC CCGGGAGGGG CTGAGGGTCC CATGGCCAAG AAGCATGCTG   660
GCGAGCGCGA TAAGAAGCTG GCGGCCAAGA AAAAGACGGA CAAGAAGCGG GCGCTGCGGG   720
CGCTGCGGCG GCTGTAGTGG GCTCTCTTCC TCCTTCCACC GTGACCCCAA CCTCTCCTGT   780
CCCCTCCCTC CAACTCTGTC TCTAAGTTAT TTAAATTATG GCTGGGGTCG GGGAGGGTAC   840
AGGGGGCACT GGGACCTGGA TTTGTTTTTC TAAATAAAGT TGGAAAAGCA
```

Seq ID NO: 104 Protein Sequence
Protein Accession #: NP_055316.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MNSNVENLPP HIIRLVYKEV TTLTADPPDG IKVFPNEEDL TDLQVTIEGP EGTPYAGGLF   60
RMKLLLGKDF PASPPKGYFL TKIFHPNVGA NGEICVNVLK RDWTAELGIR HVLLTIKCLL   120
IHPNPESALN EEAGRLLLEN YEEYAARARL LTEIHGGAGG PSGRAEAGRA LASGTEASST   180
DPGAPGGPGG AEGPMAKKHA GERDKKLAAK KKTDKKRALR ALRRL
```

Seq ID NO: 105 DNA sequence
Nucleic Acid Accession #: NM_005101
Coding sequence: 76..573

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGCTGAGAG GCAGCGAACT CATCTTTGCC AGTACAGGAG CTTGTGCCGT GGCCCACAGC   60
CCACAGCCCA CAGCCATGGG CTGGGACCTG ACGGTGAAGA TGCTGGCGGG CAACGAATTC   120
CAGGTGTCCC TGAGCAGCTC CATGTCGGTG TCAGAGCTGA AGGCGCAGAT CACCCAGAAG   180
ATTGGCGTGC ACGCCTTCCA GCAGCGTCTG GCTGTCCACC CGAGCGGTGT GGCGCTGCAG   240
GACAGGGTCC CCCTTGCCAG CCAGGGCCTG GGCCCTGGCA GCACGGTCCT GCTGGTGGTG   300
GACAAATGCG ACGAACCTCT GAGCATCCTG GTGAGGAATA ACAAGGGCCG CAGCAGCACC   360
TACGAGGTCC GGCTGACGCA GACCGTGGCC CACCTGAAGC AGCAAGTGAG CGGGCTGGAG   420
GGTGTGCAGG ACGACCTGTT CTGGCTGACC TTCGAGGGGA AGCCCCTGGA GGACCAGCTC   480
CCGCTGGGGG AGTACGGCCT CAAGCCCCTG AGCACCGTGT TCATGAATCT GCGCCTGCGG   540
GGAGGCGGCA CAGAGCCTGG CGGGCGGAGC TAAGGGCCTC CACCAGCATC CGAGCAGGAT   600
CAAGGGCCGG AAATAAAGGC TGTTGTAAGA GAAT
```

Seq ID NO: 106 Protein Sequence
Protein Accession #: NP_005092

```
1          11         21         31         41         51
|          |          |          |          |          |
MGWDLTVKML AGNEFQVSLS SSMSVSELKA QITQKIGVHA FQQRLAVHPS GVALQDRVPL   60
ASQGLGPGST VLLVVDKCDE PLSILVRNNK GRSSTYEVRL TQTVAHLKQQ VSGLEGVQDD   120
LFWLTFEGKP LEDQLPLGEY GLKPLSTVFM NLRLRGGGTE PGGRS
```

Seq ID NO: 107 DNA sequence
Nucleic Acid Accession #: NM_006018
Coding sequence: 1..1161

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG   60
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT   120
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCTGGAAA   180
TCCAGCCGGA TTTTCCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG   240
CCGTTCGTGA TGGACTACTA TGTGCGGCGT TCAGACTGGA AGTTTGGGGA CATCCCTTGC   300
CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG   360
GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC   420
AATTGGACAG CAGCCATCAT CTCTTGCCTT CTGTGGGGCA TCACTGTTGG CCTAACAGTC   480
CACCTCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC   540
AGCATCTGCC ATACCTTCCG GTGGCACGAA GCTATGTTCC TCCTGGAGTT CCTCCTGCCC   600
CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG   660
GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT   720
GTCATCTGCT TCCTTCCCAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT   780
TCGGGCACGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC   840
AGCTTCACCT ACATGAACAG CATGCTGGAC CCCGTGGTGT ACTACTTCTC CAGCCCATCC   900
TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG   960
CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC   1020
GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCCTCTTA TCTGGGCCCA   1080
ACCTCAAATA ACCATTCCAA GAAGGGACAT TGTCACCAAG AACCAGCATC TCTGGAGAAA   1140
CAGTTGGGAT GTTGCATCGA G
```

Seq ID NO: 108 Protein Sequence
Protein Accession #: NP_006009.1

```
1          11         21         31         41         51
```

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|          |          |          |          |          |
MNRHHLQDHF LEIDKKNCCV FRDDFIAKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK   60
SSRIFLFNLA VADFLLIICL PFVMDYYVRR SDWKFGDIPC RLVLFMFAMN RQGSIIFLTV  120
VAVDRYFRVV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKKLLIQ NGPANVCISF  180
SICHTFRWHE AMFLLEFLLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVF  240
VICFLPSVVV RIRIFWLLHT SGTQNCEVYR SVDLAFFITL SFTYMNSMLD PVVYYFSSPS  300
FPNFFSTLIN RCLQRKMTGE PDNNRSTSVE LTGDPNKTRG APEALMANSG EPWSPSYLGP  360
TSNNHSKKGH CHQEPASLEK QLGCCIE
```

Seq ID NO: 109 DNA sequence
Nucleic Acid Accession #: NM_005030.2
Coding sequence: 63..1874

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGG AGCGGTGCGG AGGCTCTGCT CGGATCGAGG TCTGCAGCGC AGCTTCGGGA   60
GCATGAGTGC TGCAGTGACT GCAGGGAAGC TGGCACGGGC ACCGGCCGAC CCTGGGAAAG  120
CCGGGGTCCC CGGAGTTGCA GCTCCCGGAG CTCCGGCGGC GGCTCCACCG GCGAAAGAGA  180
TCCCGGAGGT CCTAGTGGAC CCACGCAGCC GGCGGCGCTA TGTGCGGGGC CGCTTTTTGG  240
GCAAGGGCGG CTTTGCCAAG TGCTTCGAGA TCTCGGACGC GGACACCAAG GAGGTGTTCG  300
CGGGCAAGAT TGTGCCTAAG TCTCTGCTGC TCAAGCCGCA CCAGAGGGAG AAGATGTCCA  360
TGGAAATATC CATTCACCGC AGCCTCGCCC ACCAGCACGT CGTAGGATTC CACGGCTTTT  420
TCGAGGACAA CGACTTCGTG TTCGTGGTGT TGGAGCTCTG CCGCCGGAGG TCTCTCCTGG  480
AGCTGCACAA GAGGAGGAAA GCCCTGACTG AGCCTGAGGC CCGATACTAC CTACGGCAAA  540
TTGTGCTTGG CTGCCAGTAC CTGCACCGAA ACCGAGTTAT TCATCGAGAC CTCAAGCTGG  600
GCAACCTTTT CCTGAATGAA GATCTGGAGG TGAAAATAGG GGATTTTGGA CTGGCAACCA  660
AAGTCGAATA TGACGGGGAG AGGAAGAAGA CCCTGTGTGG GACTCCTAAT TACATAGCTC  720
CCGAGGTGCT GAGCAAGAAA GGGCACAGTT TCGAGGTGGA TGTGTGGTCC ATTGGGTGTA  780
TCATGTATAC CTTGTTAGTG GGCAAACCAC CTTTTGAGAC TTCTTGCCTA AAAGAGACCT  840
ACCTCCGGAT CAAGAAGAAT GAATACAGTA TTCCCAAGCA CATCAACCCC GTGGCCGCCT  900
CCCTCATCCA GAAGATGCTT CAGACAGATC CCACTGCCCG CCCAACCATT AACGAGCTGC  960
TTAATGACGA GTTCTTTACT TCTGGCTATA TCCCTGCCCG TCTCCCCATC ACCTGCCTGA 1020
CCATTCCACC AAGGTTTTCG ATTGCTCCCA GCAGCCTGGA CCCCAGCAAC CGGAAGCCCC 1080
TCACAGTCCT CAATAAAGGC TTGGAGAACC CCCTGCCTGA GCGTCCCCGG GAAAAAGAAG 1140
AACCAGTGGT TCGAGAGACA GGTGAGGTGG TCGACTGCCA CCTCAGTGAC ATGCTGCAGC 1200
AGCTGCACAG TGTCAATGCC TCCAAGCCCT CGGAGCGTGG GCTGGTCAGG CAAGAGGAGG 1260
CTGAGGATCC TGCCTGCATC CCCATCTTCT GGGTCAGCAA GTGGGTGGAC TATTCGGACA 1320
AGTACGGCCT TGGGTATCAG CTCTGTGATA ACAGCGTGGG GGTGCTCTTC AATGACTCAA 1380
CACGCCTCAT CCTCTACAAT GATGGTGACA GCCTGCAGTA CATAGAGCGT GACGGCACTG 1440
AGTCCTACCT CACCGTGAGT TCCCATCCCA ACTCCTTGAT GAAGAAGATC ACCCTCCTTA 1500
AATATTTCCG CAATTACATG AGCGAGCACT TGCTGAAGGC AGGTGCCAAC ATCACGCCGC 1560
GCGAAGGTGA TGAGCTCGCC CGGCTGCCCT ACCTACGGAC CTGGTTCCGC ACCCGCAGCG 1620
CCATCATCCT GCACCTCAGC AACGGCAGCG TGCAGATCAA CTTCTTCCAG GATCACACCA 1680
AGCTCATCTT GTGCCCACTG ATGGCAGCCG TGACCTACAT CGACGAGAAG CGGGACTTCC 1740
GCACATACCG CCTGAGTCTC CTGGAGGAGT ACGGCTGCTG CAAGGAGCTG GCCAGCCGGC 1800
TCCGCTACGC CCGCACTATG GTGGACAAGC TGCTGAGCTC ACGCTCGGCC AGCAACCGTC 1860
TCAAGGCCTC CTAATAGCTG CCCTCCCCTC CGGACTGGTG CCCTCCTCAC TCCCACCTGC 1920
ATCTGGGGCC CATACTGGTT GGCTCCCGCG GTGCCATGTC TGCAGTGTGC CCCCCAGCCC 1980
CGGTGGCTGG GCAGAGCTGC ATCATCCTTG CAGGTGGGGG TTGCTGTGTA AGTTATTTTT 2040
GTACATGTTC GGGTGTGGGT TCTACAGCCT TGTCCCCCTC CCCCTCAACC CCACCATATG 2100
AATTGTACAG AATATTTCTA TTGAATTCGG AACTGTCCTT TCCTTGGCTT TATGCACATT 2160
AAACAGATGT GAATATTCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA
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Seq ID NO: 110 Protein Sequence
Protein Accession #: NP_005021.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MSAAVTAGKL ARAPADPGKA GVPGVAAPGA PAAAPPAKEI PEVLVDPRSR RRYVRGRFLG   60
KGGFAKCFEI SDADTKEVFA GKIVPKSLLL KPHQREKMSM EISIHRSLAH QHVVGFHGFF  120
EDNDFVFVVL ELCRRRSLLE LHKRRKALTE PEARYYLRQI VLGCQYLHRN RVIHRDLKLG  180
NLFLNEDLEV KIGDFGLATK VEYDGERKKT LCGTPNYIAP EVLSKKGHSF EVDVWSIGCI  240
MYTLLVGKPP FETSCLKETY LRIKKNEYSI PKHINPVAAS LIQKMLQTDP TARPTINELL  300
NDEFFTSGYI PARLPITCLT IPPRFSIAPS SLDPSNRKPL TVLNKGLENP LPERPREKEE  360
PVVRETGEVV DCHLSDMLQQ LHSVNASKPS ERGLVRQEEA EDPACIPIFW VSKWVDYSDK  420
YGLGYQLCDN SVGVLFNDST RLILYNDGDS LQYIERDGTE SYLTVSSHPN SLMKKITLLK  480
YFRNYMSEHL LKAGANITPR EGDELARLPY LRTWFRTRSA IILHLSNGSV QINFFQDHTK  540
LILCPLMAAV TYIDEKRDFR TYRLSLLEEY GCCKELASRL RYARTMVDKL LSSRSASNRL  600
KAS
```

Seq ID NO: 111 DNA sequence
Nucleic Acid Accession #: NM_005409.3
Coding sequence: 94..378

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1          11         21         31         41         51
|          |          |          |          |          |
TTCCTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG   60
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CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC   120
TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC   180
TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC   240
ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT   300
AAAGGACAAC GATGCCTAAA TCCCAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT   360
GAAAGAAAGA ATTTTTAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA   420
AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG   480
AGACTTTTCT ATGGTTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT   540
GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAATTCCA   600
CTGCCCAAAG GAGTCCAGCA ATTAAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT   660
GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTTGTATT ATACATTCAT   720
GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT   780
GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT   840
CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG   900
CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTTCAT GCAAATACAC ACTTCTTTCC   960
CCAAATATCA TGTAGCACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGGTTTGT   1020
TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA   1080
TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAATT AGCAGCACCG GTCTTAATTT   1140
GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC   1200
TGTACTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTTGAAA   1260
TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTTGAAAAA TAAGCAAATG TATACCTAGC   1320
AATCACTTTT ACTTTTTGTA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT   1380
TTGTTCATGC CTATATACTG TAAAATTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA   1440
GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTTCTTTT TTAAAAAAAA AAA
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Seq ID NO: 112 Protein Sequence
Protein Accession #: NP_005400.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSVKGMAIAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI   60
EVIITLKENK GQRCLNPKSK QARLIIKKVE RKNF
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Seq ID NO: 113 DNA sequence
Nucleic Acid Accession #: NM_001110.1
Coding sequence: 470..2716

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1          11         21         31         41         51
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GAATTCGAGG ATCCGGGTAC CATGGGCGGC GGCAGGCCTA GCAGCACGGG AACCGTCCCC   60
CGCGCGCATG CGCGCGCCCC TGAAGCGCCT GGGGGACGGG TATGGGCGGG AGGTAGGGGC   120
GCGGCTCCGC GTGCCAGTTG GGTGCCCGCG CGTCACGTGG TGAGGAAGGA GGCGGAGGTC   180
TGAGTTTCGA GGGAGGGGGG GAGAGAAGAG GGAACGAGCA AGGGAAGGAA AGCGGGGAAA   240
GGAGGAAGGA AACGAACGAG GGGGAGGGAG GTCCCTGTTT TGGAGGAGCT AGGAGCGTTG   300
CCGGCCCCTG AAGTGGAGCG AGAGGGAGGT GCTTCGCCGT TTCTCCTGCC AGGGGAGGTC   360
CCGGCTTCCC GTGGAGGCTC CGGACCAAGC CCCTTCAGCT TCTCCCTCCG GATCGATGTG   420
CTGCTGTTAA CCCGTGAGGA GGCGGCGGCG GCGGCAGCGG CAGCGGAAGA TGGTGTTGCT   480
GAGAGTGTTA ATTCTGCTCC TCTCCTGGGC GGCGGGGATG GGAGGTCAGT ATGGGAATCC   540
TTTAAATAAA TATATCAGAC ATTATGAAGG ATTATCTTAC AATGTGGATT CATTACACCA   600
AAAACACCAG CGTGCCAAAA GAGCAGTCTC ACATGAAGAC CAATTTTTAC GTCTAGATTT   660
CCATGCCCAT GGAAGACATT TCAACCTACG AATGAAGAGG GACACTTCCC TTTTCAGTGA   720
TGAATTTAAA GTAGAAACAT CAAATAAAGT ACTTGATTAT GATACCTCTC ATATTTACAC   780
TGGACATATT TATGGTGAAG AAGGAAGTTT TAGCCATGGG TCTGTTATTG ATGGAAGATT   840
TGAAGGATTC ATCCAGACTC GTGGTGGCAC ATTTTATGTT GAGCCAGCAG AGAGATATAT   900
TAAAGACCGA ACTCTGCCAT TTCACTCTGT CATTTATCAT GAAGATGATA TTAACTATCC   960
CCATAAATAC GGTCCTCAGG GGGGCTGTGC AGATCATTCA GTATTTGAAA GAATGAGGAA   1020
ATACCAGATG ACTGGTGTAG AGGAAGTAAC ACAGATACCT CAAGAAGAAC ATGCTGCTAA   1080
TGGTCCAGAA CTTCTGAGGA AAAAACGTAC AACTTCAGCT GAAAAAAATA CTTGTCAGCT   1140
TTATATTCAG ACTGATCATT TGTTCTTTAA ATATTACGGA ACACGAGAAG CTGTGATTGC   1200
CCAGATATCC AGTCATGTTA AAGCGATTGA TACAATTTAC CAGACCACAG ACTTCTCCGG   1260
AATCCGTAAC ATCAGTTTCA TGGTGAAACG CATAAGAATC AATACAACTG CTGATGAGAA   1320
GGACCCTACA AATCCTTTCC GTTTCCCAAA TATTGGTGTG GAGAAGTTTC TGGAATTGAA   1380
TTCTGAGCAG AATCATGATG ACTACTGTTT GGCCTATGTC TTCACAGACC GAGATTTTGA   1440
TGATGGCGTA CTTGGTCTGG CTTGGGTTGG AGCACCTTCA GGAAGCTCTG GAGGAATATG   1500
TGAAAAAAGT AAACTCTATT CAGATGGTAA GAAGAAGTCC TTAAACACTG GAATTATTAC   1560
TGTTCAGAAC TATGGGTCTC ATGTACCTCC CAAAGTCTCT CACATTACTT TTGCTCACGA   1620
AGTTGGACAT AACTTTGGAT CCCCACATGA TTCTGGAACA GAGTGCACAC CAGGAGAATC   1680
TAAGAATTTG GGTCAAAAAG AAAATGGCAA TTACATCATG TATGCAAGAG CAACATCTGG   1740
GGACAAACTT AACAACAATA AATTCTCACT CTGTAGTATT AGAAATATAA GCCAAGTTCT   1800
TGAGAAGAAG AGAAACAACT GTTTTGTTGA ATCTGGCCAA CCTATTTGTG GAAATGGAAT   1860
GGTAGAACAA GGTGAAGAAT GTGATTGTGG CTATAGTGAC CAGTGTAAAG ATGAATGCTG   1920
CTTCGATGCA AATCAACCAG AGGGAAGAAA ATGCAAACTG AAACCTGGGA AACAGTGCAG   1980
TCCAAGTCAA GGTCCTTGTT GTACAGCACA GTGTGCATTC AAGTCAAAGT CTGAGAAGTG   2040
TCGGGATGAT TCAGACTGTG CAAGGGAAGG AATATGTAAT GGCTTCACAG CTCTCTGCCC   2100
AGCATCTGAC CCTAAACCAA ACTTCACAGA CTGTAATAGG CATACACAAG TGTGCATTAA   2160
TGGGCAATGT GCAGGTTCTA TCTGTGAGAA ATATGGCTTA GAGGAGTGTA CGTGTGCCAG   2220
TTCTGATGGC AAAGATGATA AAGAATTATG CCATGTATGC TGTATGAAGA AAATGGACCC   2280
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ATCAACTTGT GCCAGTACAG GGTCTGTGCA GTGGAGTAGG CACTTCAGTG GTCGAACCAT   2340
CACCCTGCAA CCTGGATCCC CTTGCAACGA TTTTAGAGGT TACTGTGATG TTTTCATGCG   2400
GTGCAGATTA GTAGATGCTG ATGGTCCTCT AGCTAGGCTT AAAAAAGCAA TTTTTAGTCC   2460
AGAGCTCTAT GAAAACATTG CTGAATGGAT TGTGGCTCAT TGGTGGGCAG TATTACTTAT   2520
GGGAATTGCT CTGATCATGC TAATGGCTGG ATTTATTAAG ATATGCAGTG TTCATACTCC   2580
AAGTAGTAAT CCAAAGTTGC CTCCTCCTAA ACCACTTCCA GGCACTTTAA AGAGGAGGAG   2640
ACCTCCACAG CCCATTCAGC AACCCCAGCG TCAGCGGCCC CGAGAGAGTT ATCAAATGGG   2700
ACACATGAGA CGCTAACTGC AGCTTTTGCC TTGGTTCTTC CTAGTGCCTA CAATGGGAAA   2760
ACTTCACTCC AAAGAGAAAC CTATTAAGTC ATCATCTCCA AACTAAACCC TCACAAGTAA   2820
CAGTTGAAGA AAAAATGGCA AGAGATCATA TCCTCAGACC AGGTGGAATT ACTTAAATTT   2880
TAAAGCCTGA AAATTCCAAT TTGGGGGTGG GAGGTGGAAA AGGAACCCAA TTTTCTTATG   2940
AACAGATATT TTTAACTTAA TGGCACAAAG TCTTAGAATA TTATTATGTG CCCCGTGTTC   3000
CCTGTTCTTC GTTGCTGCAT TTTCTTCACT TGCAGGCAAA CTTGGCTCTC AATAAACTTT   3060
TACCACAAAT TGAAATAAAT ATATTTTTTT CAACTGCCAA TCAAGGCTAG GAGGCTCGAC   3120
CACCTCAACA TTGGAGACAT CACTTGCCAA TGTACATACC TTGTTATATG CAGACATGTA   3180
TTTCTTACGT ACACTGTACT TCTGTGTGCA ATTGTAAACA GAAATTGCAA TATGGATGTT   3240
TCTTTGTATT ATAAAATTTT TCCGCTCTTA ATTAAAAATT ACTGTTTAAT TGACATACTC   3300
AGGATAACAG AGAATGGTGG TATTCAGTGG TCCAGGATTC TGTAATGCTT TACACAGGCA   3360
GTTTTGAAAT GAAAATCAAT TTACCCCATG GTACCCGGAT CCTCGAATTC
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Seq ID NO: 114 Protein Sequence
Protein Accession #: NP_001101.1

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1          11         21         31         41         51
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MVLLRVLILL LSWAAGMGGQ YGNPLNKYIR HYEGLSYNVD SLHQKHQRAK RAVSHEDQFL   60
RLDFHAHGRH FNLRMKRDTS LFSDEFKVET SNKVLDYDTS HIYTGHIYGE EGSFSHGSVI   120
DGRFEGFIQT RGGTFYVEPA ERYIKDRTLP FHSVIYHEDD INYPHKYGPQ GGCADHSVFE   180
RMRKYQMTGV EEVTQIPQEE HAANGPELLR KKRTTSAEKN TCQLYIQTDH LFFKYYGTRE   240
AVIAQISSHV KAIDTIYQTT DFSGIRNISF MVKRIRINTT ADEKDPTNPF RFPNIGVEKF   300
LELNSEQNHD DYCLAYVFTD RDFDDGVLGL AWVGAPSGSS GGICEKSKLY SDGKKKSLNT   360
GIITVQNYGS HVPPKVSHIT FAHEVGHNFG SPHDSGTECT PGESKNLGQK ENGNYIMYAR   420
ATSGDKLNNN KFSLCSIRNI SQVLEKKRNN CFVESGQPIC GNGMVEQGEE CDCGYSDQCK   480
DECCFDANQP EGRKCKLKPG KQCSPSQGPC CTAQCAFKSK SEKCRDDSDC AREGICNGFT   540
ALCPASDPKP NFTDCNRHTQ VCINGQCAGS ICEKYGLEEC TCASSDGKDD KELCHVCCMK   600
KMDPSTCAST GSVQWSRHFS GRTITLQPGS PCNDFRGYCD VFMRCRLVDA DGPLARLKKA   660
IFSPELYENI AEWIVAHWWA VLLMGIALIM LMAGFIKICS VHTPSSNPKL PPPKPLPGTL   720
KRRRPPQPIQ QPQRQRPRES YQMGHMRR
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Seq ID NO: 115 DNA sequence
Nucleic Acid Accession #: NM_000577.2
Coding sequence: 41…520

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGG GAAGACCTCC TGTCCTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG   60
CCGACCCTCT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAACCA   120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAATGT   180
CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT   240
CCATGGAGGG AAGATGTGCC TGTCCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT   300
GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT   360
CATCCGCTCA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCCGCCTGCC CCGGTTGGTT   420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG   480
CGTCATGGTC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCCAG GCCTGCCTGT   540
TCCCATTCTT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCCCTGCCCC AGGGCTCCCG   600
GCTATGGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA   660
CCTGGTCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG   720
GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCCTGCA CAAAGCCCTT CCATGTCGCC   780
TCTGCATTCA GGATCAAACC CCGACCACCT GCCCAACCTG CTCTCCTCTT GCCACTGCCT   840
CTTCCTCCCT CATTCCACCT TCCCATGCCC TGGATCCATC AGGCCACTTG ATGACCCCCA   900
ACCAAGTGGC TCCCACACCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT   960
TTTAAGGGTT TGTGGAAAAT GAAAATTAGG ATTTCATGAT TTTTTTTTTT CAGTCCCCGT   1020
GAAGGAGAGC CCTTCATTTG GAGATTATGT TCTTTCGGGG AGAGGCTGAG GACTTAAAAT   1080
ATTCCTGCAT TTGTGAAATG ATGGTGAAAG TAAGTGGTAG CTTTTCCCTT CTTTTTCTTC   1140
TTTTTTTGTG ATGTCCCAAC TTGTAAAAAT TAAAAGTTAT GGTACTATGT TAGCCCCATA   1200
ATTTTTTTTT TCCTTTTAAA ACACTTCCAT AATCTGGACT CCTCTGTCCA GGCACTGCTG   1260
CCCAGCCTCC AAGCTCCATC TCCACTCCAG ATTTTTTACA GCTGCCTGCA GTACTTTACC   1320
TCCTATCAGA AGTTTCTCAG CTCCCAAGGC TCTGAGCAAA TGTGGCTCCT GGGGGTTCTT   1380
TCTTCCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCACTTGGAG   1440
ACTTGTATGA AAGATGGCTG TGCCTCTGCC TGTCTCCCCC ACCAGGCTGG GAGCTCTGCA   1500
GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG   1560
CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAAGT TCCCTACTTC   1620
CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAAAAT GCCTAAAAAA AAAAAAAAAA   1680
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA
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Seq ID NO: 116 Protein Sequence
Protein Accession #: NP_000568.1

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1          11         21         31         41         51
|          |          |          |          |          |
MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGPNVNLE EKIDVVPIEP    60
HALFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSENRK QDKRFAFIRS DSGPTTSFES    120
AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQEDE
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Seq ID NO: 117 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
GCACTTTAGC TCAGTGATGG ATTTTAAGAA CGATTACACC TGTCGCCTGT GGTCTGACTC    60
CAGGCACTCG CGTCAGGTAC TTCTGCTCCA GGATAGCTTT ATGAATTGCT CTGACAGCAT    120
CATCAATGGT TCCTTTCGTG CGCTTGGCTT TATTCATGAG GCTCAGGTCG GGGAAAGACT    180
GATGGTCCAC TGTGACAGCA AGACAGGTAA TGCAAATACG GATTTCATCT GGGTGGGTCC    240
AGATAACAGA CTGCTAGAGC CGGATAAAGA GATGGAAAAC TTTTACGTGT TTCACAATGG    300
AAGTCTGGTT ATAGAAAGCC CTCGTTTTGA GGATGCTGGA GTGTATTCTT GTATCGCAAT    360
GAATAAGCAA CGCCTGTTAA ATGAAACTGT GGACGTCACA ATAAATGTGA GCAATTTCAC    420
TGTAAGCAGA TCCCATGCTC ATGAGGCATT TAACACAGCT TTTACCACTC TTGCTGCTTG    480
CGTGGCCAGT ATCGTTTTGG TACTTTTGTA CCTCTATCTG ACTCCATGCC CCTGCAAGTG    540
TAAAACCAAG AGACAGAAAA ATATGCTACA CCAAAGCAAT GCCCATTCAT CGATTCTCAG    600
TCCTGGCCCC GCTAGTGATG CCTCCGCTGA TGAACGGAAG GCAGGTGCAG GTAAAAGAGT    660
GGTGTTTTTG GAACCCCTGA AGGATACTGC AGCAGGGCAG AACGGGAAAG TCAGGCTCTT    720
TCCCAGCGAG GCAGTGATAG CTGAGGGCAT CCTAAAGTCC ACGAGGGGGA AATCTGACTC    780
AGATTCAGTC AATTCAGTGT TTTCTGACAC ACCTTTTGTG GCGTCCACTT AA
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Seq ID NO: 118 DNA sequence
Nucleic Acid Accession #: AB032989.1
Coding sequence: 1..1316

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1          11         21         31         41         51
|          |          |          |          |          |
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TGCGGGCCGA GTGGACCCCC ACGCGCCTGA CCCAACTGCA CTCCCTGCTG CTGAGCCACA    120
ACCACCTGAA CTTCATCTCC TCTGAGGCCT TTTCCCCGGT ACCCAACCTG CGCTACCTGG    180
ACCTCTCCTC CAACCAGCTG CGTACACTGG ATGAGTTCCT GTTCAGTGAC CTGCAAGTAC    240
TGGAGGTGCT GCTGCTCTAC AATAACCACA TCATGGCGGT GGACCGGTGC GCCTTCGATG    300
ACATGGCCCA GCTGCAGAAA CTCTACTTGA GCCAGAACCA GATCTCTCGC TTCCCTCTGG    360
AACTGGTCAA GGAAGGAGCC AAGCTACCCA AACTAACGCT CCTGGATCTC TCTTCTAACA    420
AGCTGAAGAA CTTGCCATTG CCTGACCTGC AGAAGCTGCC GGCCTGGATC AAGAATGGGC    480
TGTACCTACA TAACAACCCC CTGAACTGCG ACTGTGAGCT CTACCAGCTG TTTTCACACT    540
GGCAGTATCG GCAGCTGAGC TCCGTGATGG ACTTTCAAGA GGATCTGTAC TGCATGAACT    600
CCAAGAAGCT GCACAATGTC TTCAACCTGA GTTTCCTCAA CTGTGGCGAG TACAAGGAGC    660
GTGCCTGGGA GGCCCACCTG GGTGACACCT TGATCATCAA GTGTGACACC AAGCAGCAAG    720
GGATGACCAA GGTGTGGGTG ACACCAAGTA ATGAACGGGT GCTAGATGAG GTGACCAATG    780
GCACAGTGAG TGTGTCTAAG GATGGCAGTC TTCTTTTCCA GCAGGTGCAG GTCGAGGACG    840
GTGGTGTGTA TACCTGCTAT GCCATGGGAG AGACTTTCAA TGAGACACTG TCTGTGGAAT    900
TGAAAGTGCA CAATTTCACC TTGCACGGAC ACCATGACAC CCTCAACACA GCCTATACCA    960
CCCTAGTGGG CTGTATCCTT AGTGTGGTCC TGGTCCTCAT ATACCTATAC CTCACCCCTT    1020
GCCGCTGCTG GTGCCGGGGT GTAGAGAAGC CTTCCAGCCA TCAAGGAGAC AGCCTCAGCT    1080
CTTCCATGCT TAGTACCACA CCCAACCATG ATCCTATGGC TGGTGGGGAC AAAGATGATG    1140
GTTTTGACCG GCGGGTGGCT TTCCTGGAAC CTGCTGGACC TGGGCAGGGT CAAAACGGCA    1200
AGCTCAAGCC AGGCAACACC CTGCCAGTGC CTGAGGCCAC AGGCAAGGGC CAACGGAGGA    1260
TGTCGGATCC AGAATCAGTC AGCTCGGTCT TCTCTGATAC GCCCATTGTG GTGTGAGCAG    1320
GATGGGTTGG TGGGGAGATT CTGCCCCAGG AGAGGTAATG CACCCCTGAA GGATATGAGG    1380
GGATGGAAGA GAGGGCTGGC TGCCCAAGGG AATGGATTCC TCCTGACCTC AAGGGAATTG    1440
GTCCCAGGTA CAACAGAGAG CAAGACCCCA AACAGGGCGT GGCTGCCACG ATTTTCAAAT    1500
GGGGGTATAT TAATCCTCAG GCAAATGCTA CACCCGTACC CAAAGCCCTG CCAATTCTCA    1560
GTGTGGTAGA GGAAGAGAAG CATGTCTGAG TTGGATGGGA ATGAGGAAGG AGTGAGGGGA    1620
AGAACAGATT CCCTAAACTT TCATGAGGTC ATCCCTAGCT CCTTAAGAGA AAAACATTTA    1680
GAAAAAAAAA TTTTTTCTAT CTCTGCCCAC CCACACCTGT GATGTTGTGT GTGTTGGGGG    1740
AGCTTCCACA GGAGCCACAC TGGGGAAAAG CTGTAGTATC TTCTTTGTTT AGCAAGTCAA    1800
ACTTCACAGC TGGGGAAGTT GAAAACCTTT GGAAAATGAG TCAGGAAAAG GCTGAGACCT    1860
CAATCGGTAA CAATTCCCCA AAGCTGTTGT AAGACTTTGC ATTAAAGCCT TTCTTTTTCC    1920
TGATGTGCCC TGGGTGGATG GATCTTTGCA GGAGCCTGGC CTGCTGCCTT TTAGTTACAA    1980
CAGCAATGTG GGATGTGGTA TCTGTGCCTT GTCCTGGGAC CAATGGCACA GAGGGTTATA    2040
GCATGAACTG AAGGGTCCAT GTCACAGCAT AGGTGCCAGC ACGAAACTTG TAGATGGGGG    2100
GTGAATTCCA GATAGGCTAA TTCCCTGGTT GGTGAAACCC TTGGTTAGTA TTTGATTCCC    2160
AGCATCTGTG TGTCAGGCCA GAGTGGGGGC TGCTGAAGGC AGAGCTTTTA TGGATGCCTG    2220
CCACAGACGT GGTACATGGG CCCACTTCAC GATAGAAGGA TGAAGGTAAA TCAGCCTCTA    2280
TTATGTAGCA TCCAGCTGGA CCTAGCTGAT TCTCAATGTA TGCCATCTCT TCATCCAGTC    2340
TCCTTATCAA GCTCAGGTGG GATTCTGAAT TTTCCCTAAT ATGCTGCTCT GTAAAGGGAG    2400
GAGTCCAAGA AAGCCTGGCC CCAGCTGGCT TAGAGTAGGC TTGGCGATAG TGAAAATCCA    2460
GTATATATCT CCTCTGTGTG GACAAGGTTG CCTTGCTCCT CTCAGAGATA CCACCTCTGC    2520
TGCAAAGTCA AAGCATGGGG TTTTGACATC AGAAGGGTTG GAATTGGGTG GTCTCTACCC    2580
CAGAATGGCA ATTTGGAGTG CAGCTTCAAG TTCTGCCCTC TCCACAGATT CCAGGCAATC    2640
CTGAAGCAGA GATAATCAGT AGTACTAAAC TTTCAGAAGG GGAGTTCTGC CACCCCATTC    2700
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CTCCATCGAG AGGTCTTTGC AGTTGTGGTT GTGAGGCCAG AGGAACTTAA GAAGAATGAG   2760
CTCAACATTC CATTCCATCC AAGGTTGCAG AATACTTTGA GTATGGAGAT GACCGATCCC   2820
TTTAACCTTT CCCTTTGACT ATACTGCATG CCCTGTGAGT GGCTGCTCTG AGCTTTGGCG   2880
GGGGATGAGC AGGGTGAAGG TGAAAATGTT CTCTGATGTT GGTTTTTCTT AGTGTCTCTT   2940
CTCTCCCACG TTTCTAGTCC ATTGGAAGTT CTCCAGATCC TCTAGATTTC TGACCTCTTT   3000
TTACATTCTA AGAGGTGTCA TTTACCTGTG GGTGAGGGGC TTGGAGGGCC TGACTATTAA   3060
GCTTCCTATT ATGATTGGGG AAGGGGACTC AACATCTTCC CCTTGTCTGG TCCTGGGAAC   3120
TCAAGACTGC TGTCCATCCT TTATTAGTAA CCTAGTTTTG TTGAGAGAGA GGTGCAGCAT   3180
TTCCCTCAAG TACCTGCATG CTCATAGGTA TGCATGCTTA TAGGTATGCA TGCACACCAG   3240
CACCTTGACT TCCACCAGGA CAGTGAATCT GTAGTCCCCA TTAATGATAC TCTCAGAATG   3300
GTCTCCACCA ATGTGCACAA CTTCATGCAC ACAATTGTAT TCCTCTTTAG GAGAGACAGT   3360
GACCATGCCA GGCTCTTCAA ATACACACTC CTGTATTTTC ATTTCTGAAC TCCCTGAAGC   3420
TTCACCCACA TCTCCATGGC ACTGAATCAC TTTTCTGCCC AGGCTGGAGT TAGAAGAACC   3480
ATGGGTTGAA GGCCTTGGGA GAAGAGGTGG TAAGGAGCTA CCTGGTTCTT TGGACTCCTC   3540
AGAAACCTCC CGTGAAGACT ATATATATGA GCAATATATG AGCAATTAAG ATAGAACTAG   3600
GTCATTGAAG GACTCAGAAG GAAACTGGCA AGGGGCTAAG TAGCTGTGAG CTGCTCTTCC   3660
TGTTAACTGT CCTCAGGAGA GAAAAGTTGT CTTGATTTAT TCCAGAGACT CCTGAGAATT   3720
TTGTTACTGG AGCTATAGGA ACTAGGACTC CCTCCTCAGA CTCATCAGGA AATCTGGGAA   3780
AATCTCATCT CCATGCTGCA GTCTCCCCGC TTGGCACCAT CTAGGGCTCT GAAGATCTTT   3840
AAAGTGAGCG TTAAATGAAG CAGGCCTTCT GGGGCATCGT GATGGAGCTC CTGAGGACTG   3900
GGAGGGCCGT TTTCTTCATA ATTCCTACCC AGTTTAGGGA ATGAGAAAAG GCCCTGTGGC   3960
TCTTAAGTCT CCTGACTATA TCCACTAGTT TGGCCTTGAG TTTGAGACAC CTGGTAGATG   4020
TACCTGGCTG CCCTACCAAG AGATTTGATT TGTTTCTTCC CGTGGTTTCA GGTGATAGAA   4080
CCCAAAGGTA GCTTTTTAAT TGGAGAATTG AATAATCAGC ATATGTAAGC GCACTAGAAC   4140
CCTGTGTTGA AAACTGCCAG GTGTGGGTAT AAGAAAAGGC CGAGAGATCA CCACCTCCTC   4200
TTACCCTACC CCACACCCAT AAACCAGACA TGTCTCCCAG GAAGCAGGTG TCCCTGGACA   4260
CAGAGGATGA CAGGGCTCTA CAATCTGTGT AATTATTATT ATTATTATTA TTTTGTATTT   4320
ATGGGGCCCA AGAAAGGGGC CAGGAGAGGG TACACCCCAG CTGGGGAGAG CAAAGCAGAT   4380
GGATCCAGTT TTCTGTGTGT TCTTACCTCT GTACTTCCTC GTAGCTCTGC TGACAAAGCA   4440
AGCAGGCCTC CCGTGTCCAA GACCCCATTC CTCCCACTTG TGTACACCTA GGCTGGCAAA   4500
TCTTGGAGCC TCTGGGCTCT GAAAACTAGA CAATGATCAT TAAACCTGGC TTGAGTCTCT   4560
GTTCTGGC
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Seq ID NO: 119 Protein Sequence
Protein Accession #: BAA86477.1

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1          11         21         31         41         51
|          |          |          |          |          |
HSLPSYTALL DLSHNNLSRL RAEWTPTRLT QLHSLLLSHN HLNFISSEAF SPVPNLRYLD   60
LSSNQLRTLD EFLFSDLQVL EVLLLYNNHI MAVDRCAFDD MAQLQKLYLS QNQISRFPLE   120
LVKEGAKLPK LTLLDLSSNK LKNLPLPDLQ KLPAWIKNGL YLHNNPLNCD CELYQLFSHW   180
QYRQLSSVMD FQEDLYCMNS KKLHNVFNLS FLNCGEYKER AWEAHLGDTL IIKCDTKQQG   240
MTKVWVTPSN ERVLDEVTNG TVSVSKDGSL LFQQVQVEDG GVYTCYAMGE TFNETLSVEL   300
KVHNFTLHGH HDTLNTAYTT LVGCILSVVL VLIYLYLTPC RCWCRGVEKP SSHQGDSLSS   360
SMLSTTPNHD PMAGGDKDDG FDRRVAFLEP AGPGQGQNGK LKPGNTLPVP EATGKGQRRM   420
SDPESVSSVF SDTPIVV
```

Seq ID NO: 120 DNA sequence
Nucleic Acid Accession #: NM_005071
Coding sequence: 9..1703

```
1          11         21         31         41         51
|          |          |          |          |          |
GATAGACCAT GAGCAGCCAT GGCAACAGCC TGTTCCTTCG GGAGAGCGGC CAGCGGCTGG   60
GCCGGGTGGG CTGGCTGCAG CGGCTGCAGG AAAGCCTGCA GCAGAGAGCA CTGCGCACGC   120
GCCTGCGCCT GCAGACCATG ACCCTCGAGC ACGTGCTGCG CTTCCTGCGC CGAAACGCCT   180
TCATTCTGCT GACGGTCAGC GCCGTGGTCA TTGGGGTCAG CCTGGCCTTT GCCCTGCGCC   240
CATATCAGCT CACCTACCGC CAGATCAAGT ACTTCTCTTT TCCTGGAGAG CTTCTGATGA   300
GGATGCTGCA GATGCTGGTG TTACCTCTCA TTGTCTCCAG CCTGGTCACA GGTATGGCAT   360
CCCTGGACAA CAAGGCCACG GGGCGGATGG GGATGCGGGC AGCTGTGTAC TACATGGTGA   420
CCACCATCAT CGCGGTCTTC ATCGGCATCC TCATGGTCAC CATCATCCAT CCCGGGAAGG   480
GCTCCAAGGA GGGGCTGCAC CGGGAGGGCC GGATCGAGAC CATCCCCACA GCTGATGCCT   540
TCATGGACCT GATCAGAAAT ATGTTTCCAC CAAACCTTGT GGAGGCCTGC TTCAAACAGT   600
TCAAGACGCA GTACAGCACG AGGGTGGTAA CCAGGACCAT GGTGAGGACA GAGAACGGGT   660
CTGAGCCGGG TGCCTCCATG CCTCCTCCAT TCTCAGTGGA GAACGGAACC AGCTTCCTGG   720
AAAATGTCAC TCGGGCCTTG GGTACCCTGC AGGAGATGCT GAGCTTTGAG GAGACTGTAC   780
CCGTGCCTGG CTCCGCCAAT GGCATCAACG CCCTGGGCCT CGTGGTCTTC TCTGTGGCCT   840
TTGGGCTGGT CATTGGTGGC ATGAAACACA AGGGCAGAGT CCTCAGGGAC TTCTTCGACA   900
GCCTCAATGA GGCTATTATG AGGCTGGTGG GCATCATTAT CTGGTATGCA CCTGTGGGCA   960
TCCTGTTCCT GATTGCTGGG AAGATTCTGG AGATGGAAGA CATGGCCGTC CTGGGGGGTC   1020
AGCTGGGCAT GTACACCCTG ACCGTCATCG TGGGCCTGTT CCTCCATGCC GGCATTGTCC   1080
TTCCCCTCAT CTACTTCCTC GTCACTCACC GGAACCCCTT CCCCTTCATT GGGGGCATGC   1140
TACAAGCCCT CATCACCGCT ATGGGCACGT CTTCCAGCTC GGCAACGCTG CCCATCACCT   1200
TCCGCTGCCT GGAGGAGGGC CTGGGTGTGG ACCGCCGCAT CACCAGGTTC GTCCTGCCCG   1260
TGGGCGCCAC GGTCAACATG GATGGCACTG CCCTCTACGA GGCCCTGGCT GCCATCTTCA   1320
TTGCTCAAGT TAACAACTAC GAGCTCAACC TGGGTCAGAT CACAACCATC AGCATCACGG   1380
CCACAGCAGC CAGTGTTGGG GCTGCTGGCA TCCCCCAGGC GGGTCTGGTC ACCATGGTCA   1440
TTGTGCTTAC GTCGGTCGGC TTGCCCACGG AAGACATCAC GCTCATCATC GCCGTGGACT   1500
```

```
GGTTCCTTGA CCGGCTTCGC ACAATGACCA ACGTACTGGG GGACTCAATT GGAGCGGCCG   1560
TCATCGAGCA CTTGTCTCAG CGGGAGCTGG AGCTTCAGGA AGCTGAGCTT ACCCTCCCCA   1620
GCCTGGGGAA ACCCTACAAG TCCCTCATGG CACAGGAGAA GGGGGCATCC CGGGGACGGG   1680
GAGGCAACGA GAGTGCTATG TGAGGGGCCT CCAGCTCTG
```

Seq ID NO: 121 Protein Sequence
Protein Accession #: NP_005062

```
1          11         21         31         41         51
|          |          |          |          |          |
MSSHGNSLFL RESGQRLGRV GWLQRLQESL QQRALRTRLR LQTMTLEHVL RFLRRNAFIL   60
LTVSAVVIGV SLAFALRPYQ LTYRQIKYFS FPGELLMRML QMLVLPLIVS SLVTGMASLD   120
NKATGRMGMR AAVYYMVTTI IAVFIGILMV TIIHPGKGSK EGLHREGRIE TIPTADAFMD   180
LIRNMFPPNL VEACFKQFKT QYSTRVVTRT MVRTENGSEP GASMPPPFSV ENGTSFLENV   240
TRALGTLQEM LSFEETVPVP GSANGINALG LVVFSVAFGL VIGGMKHKGR VLRDFFDSLN   300
EAIMRLVGII IWYAPVGILF LIAGKILEME DMAVLGGQLG MYTLTVIVGL FLHAGIVLPL   360
IYFLVTHRNP FPFIGGMLQA LITAMGTSSS SATLPITFRC LEEGLGVDRR ITRFVLPVGA   420
TVNMDGTALY EALAAIFIAQ VNNYELNLGQ ITTISITATA ASVGAAGIPQ AGLVTMVIVL   480
TSVGLPTEDI TLIIAVDWFL DRLRTMTNVL GDSIGAAVIE HLSQRELELQ EAELTLPSLG   540
KPYKSLMAQE KGASRGRGGN ESAM
```

Seq ID NO: 122 DNA sequence
Nucleic Acid Accession #: NM_031966.1
Coding sequence: 178..1479

```
1          11         21         31         41         51
|          |          |          |          |          |
ACGAACAGGC CAATAAGGAG GGAGCAGTGC GGGGTTTAAA TCTGAGGCTA GGCTGGCTCT   60
TCTCGGCGTG CTGCGGCGGA ACGGCTGTTG GTTTCTGCTG GTTGTAGGTC CTTGGCTGGT   120
CGGGCCTCCG GTGTTCTGCT TCTCCCCGCT GAGCTGCTGC CTGGTGAAGA GGAAGCCATG   180
GCGCTCCGAG TCACCAGGAA CTCGAAAATT AATGCTGAAA ATAAGGCGAA GATCAACATG   240
GCAGGCGCAA AGCGCGTTCC TACGGCCCCT GCTGCAACCT CCAAGCCCGG ACTGAGGCCA   300
AGAACAGCTC TTGGGGACAT TGGTAACAAA GTCAGTGAAC AACTGCAGGC CAAAATGCCT   360
ATGAAGAAGG AAGCAAAACC TTCAGCTACT GGAAAAGTCA TTGATAAAAA ACTACCAAAA   420
CCTCTTGAAA AGGTACCTAT GCTGGTGCCA GTGCCAGTGT CTGAGCCAGT GCCAGAGCCA   480
GAACCTGAGC CAGAACCTGA GCCTGTTAAA GAAGAAAAAC TTTCGCCTGA GCCTATTTTG   540
GTTGATACTG CCTCTCCAAG CCCAATGGAA ACATCTGGAT GTGCCCCTGC AGAAGAAGAC   600
CTGTGTCAGG CTTTCTCTGA TGTAATTCTT GCAGTAAATG ATGTGGATGC AGAAGATGGA   660
GCTGATCCAA ACCTTTGTAG TGAATATGTG AAAGATATTT ATGCTTATCT GAGACAACTT   720
GAGGAAGAGC AAGCAGTCAG ACCAAAATAC CTACTGGGTC GGGAAGTCAC TGGAAACATG   780
AGAGCCATCC TAATTGACTG GCTAGTACAG GTTCAAATGA AATTCAGGTT GTTGCAGGAG   840
ACCATGTACA TGACTGTCTC CATTATTGAT CGGTTCATGC AGAATAATTG TGTGCCCAAG   900
AAGATGCTGC AGCTGGTTGG TGTCACTGCC ATGTTTATTG CAAGCAAATA TGAAGAAATG   960
TACCCTCCAG AAATTGGTGA CTTTGCTTTT GTGACTGACA ACACTTATAC TAAGCACCAA   1020
ATCAGACAGA TGGAAATGAA GATTCTAAGA GCTTTAAACT TTGGTCTGGG TCGGCCTCTA   1080
CCTTTGCACT TCCTTCGGAG AGCATCTAAG ATTGGAGAGG TTGATGTCGA GCAACATACT   1140
TTGGCCAAAT ACCTGATGGA ACTAACTATG TTGGACTATG ACATGGTGCA CTTTCCTCCT   1200
TCTCAAATTG CAGCAGGAGC TTTTTGCTTA GCACTGAAAA TTCTGGATAA TGGTGAATGG   1260
ACACCAACTC TACAACATTA CCTGTCATAT ACTGAAGAAT CTCTTCTTCC AGTTATGCAG   1320
CACCTGGCTA AGAATGTAGT CATGGTAAAT CAAGGACTTA CAAAGCACAT GACTGTCAAG   1380
AACAAGTATG CCACATCGAA GCATGCTAAG ATCAGCACTC TACCACAGCT GAATTCTGCA   1440
CTAGTTCAAG ATTTAGCCAA GGCTGTGGCA AAGGTGTAAC TTGTAAACTT GAGTTGGAGT   1500
ACTATATTTA CAAATAAAAT TGGCACCATG TGCCATCTGT AAAAAAAAAA AAAAAAAAAA   1560
AAAAAAAAAA AAAAAAAA
```

Seq ID NO: 123 Protein Sequence
Protein Accession #: NP_114172.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MALRVTRNSK INAENKAKIN MAGAKRVPTA PAATSKPGLR PRTALGDIGN KVSEQLQAKM   60
PMKKEAKPSA TGKVIDKKLP KPLEKVPMLV PVPVSEPVPE PEPEPEPEPV KEEKLSPEPI   120
LVDTASPSPM ETSGCAPAEE DLCQAFSDVI LAVNDVDAED GADPNLCSEY VKDIYAYLRQ   180
LEEEQAVRPK YLLGREVTGN MRAILIDWLV QVQMKFRLLQ ETMYMTVSII DRFMQNNCVP   240
KKMLQLVGVT AMFIASKYEE MYPPEIGDFA FVTDNTYTKH QIRQMEMKIL RALNFGLGRP   300
LPLHFLRRAS KIGEVDVEQH TLAKYLMELT MLDYDMVHFP PSQIAAGAFC LALKILDNGE   360
WTPTLQHYLS YTEESLLPVM QHLAKNVVMV NQGLTKHMTV KNKYATSKHA KISTLPQLNS   420
ALVQDLAKAV AKV
```

Seq ID NO: 124 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 13-1424

```
1          11         21         31         41         51
|          |          |          |          |          |
TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT   60
CTTCCCCTGA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTTGG TGAAAGATAC   120
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```
TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACTTCCAG TGACAAAAAT GAAATATAGT   180
GGAAACTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC   240
GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCCGAT   300
GTCCATCATT TCAGGGAAAT GCCAGGGGGG CCCGTATGGA GGAAACATTA TATCACCTAC   360
AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGGAAA   420
GCTTTCCAAG TATGGAGTAA TGTTACCCCC TTGAAATTCA GCAAGATTAA CACAGGCATG   480
GCTGACATTT TGGTGGTTTT TGCCCGTGGA GCTCATGGAG ACTTCCATGC TTTTGATGGC   540
AAAGGTGGAA TCCTAGCCCA TGCTTTTGGA CCTGGATCTG GCATTGGAGG GGATGCACAT   600
TTCGATGAGG ACGAATTCTG GACTACACAT TCAGGAGGCA CAAACTTGTT CCTCACTGCT   660
GTTCACGAGA TTGGCCATTC CTTAGGTCTT GGCCATTCTA GTGATCCAAA GGCCGTAATG   720
TTCCCCACCT ACAAATATGT TGACATCAAC ACATTTCGCC TCTCTGCTGA TGACATACGT   780
GGCATTCAGT CCCTGTATGG AGACCCAAAA GAGAACCAAC GCTTGCCAAA TCCTGACAAT   840
TCAGAACCAG CTCTCTGTGA CCCCAATTTG AGTTTTGATG CTGTCACTAC CGTGGGAAAT   900
AAGATCTTTT TCTTCAAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAAGACC   960
AGTGTTAATT TAATTTCTTC CTTATGGCCA ACCTTGCCAT CTGGCATTGA AGCTGCTTAT  1020
GAAATTGAAG CCAGAAATCA AGTTTTTCTT TTTAAAGATG ACAAATACTG GTTAATTAGC  1080
AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTTGGTTT TCCTAACTTT  1140
GTGAAAAAAA TTGATGCAGC TGTTTTTAAC CCACGTTTTT ATAGGACCTA CTTCTTTGTA  1200
GATAACCAGT ATTGGAGGTA TGATGAAAGG AGACAGATGA TGGACCCTGG TTATCCCAAA  1260
CTGATTACCA AGAACTTCCA AGGAATCGGG CCTAAAATTG ATGCAGTCTT CTACTCTAAA  1320
AACAAATACT ACTATTTCTT CCAAGGATCT AACCAATTTG AATATGACTT CCTACTCCAA  1380
CGTATCACCA AAACACTGAA AAGCAATAGC TGGTTTGGTT GTTGAAAATG GTGTAATTAA  1440
TGGTTTTTGT TAGTTCACTT CAGCTTAATA AGTATTTATT GCATATTTGC TATGTCCTCA  1500
GTGTACCACT ACTTAGAGAT ATGTATCATA AAAATAAAAT CTGTAAACCA TAGGTAATGA  1560
TTATATAAAA TACATAATAT TTTTCAATTT TGAAAACTCT AATTGTCCAT TCTTGCTTGA  1620
CTCTACTATT AAGTTTGAAA ATAGTTACCT TCAAAGCAAG ATAATTCTAT TTGAAGCATG  1680
CTCTGTAAGT TGCTTCCTAA CATCCTTGGA CTGAGAAATT ATACTTACTT CTGGCATAAC  1740
TAAAATTAAG TATATATATT TTGGCTCAAA TAAAATTG
```

Seq ID NO: 125 Protein sequence:
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MKFLLILLLQ ATASGALPLN SSTSLEKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM    60
KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHHF REMPGGPVWR KHYITYRINN   120
YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHGD FHAFDGKGGI   180
LAHAFGPGSG IGGDAHFDED EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY   240
KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF   300
FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP   360
EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK   420
NFQGIGPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC
```

Seq ID NO: 126 DNA sequence
Nucleic Acid Accession #: NM_000077.2
Coding sequence: 272..742

```
1          11         21         31         41         51
|          |          |          |          |          |
CCCAACCTGG GGCGACTTCA GGTGTGCCAC ATTCGCTAAG TGCTCGGAGT TAATAGCACC    60
TCCTCCGAGC ACTCGCTCAC GGCGTCCCCT TGCCTGGAAA GATACCGCGG TCCCTCCAGA   120
GGATTTGAGG GACAGGGTCG GAGGGGGCTC TTCCGCCAGC ACCGGAGGAA GAAAGAGGAG   180
GGGCTGGCTG GTCACCAGAG GGTGGGGCGG ACCGCGTGCG CTCGGCGGCT GCGGAGAGGG   240
GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA   300
GCCTTCGGCT GACTGGCTGG CCACGGCCGC GGCCCGGGGT CGGGTAGAGG AGGTGCGGGC   360
GCTGCTGGAG GCGGGGGCGC TGCCCAACGC ACCGAATAGT TACGGTCGGA GGCCGATCCA   420
GGTCATGATG ATGGGCAGCG CCCGAGTGGC GGAGCTGCTG CTGCTCCACG GCGCGGAGCC   480
CAACTGCGCC GACCCCGCCA CTCTCACCCG ACCCGTGCAC GACGCTGCCC GGGAGGGCTT   540
CCTGGACACG CTGGTGGTGC TGCACCGGGC CGGGGCGCGG CTGGACGTGC GCGATGCCTG   600
GGGCCGTCTG CCCGTGGACC TGGCTGAGGA GCTGGGCCAT CGCGATGTCG CACGGTACCT   660
GCGCGCGGCT GCGGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG   720
TCCCTCAGAC ATCCCCGATT GAAAGAACCA GAGAGGCTCT GAGAAACCTC GGGAAACTTA   780
GATCATCAGT CACCGAAGGT CCTACAGGGC CACAACTGCC CCCGCCACAA CCCACCCCGC   840
TTTCGTAGTT TTCATTTAGA AAATAGAGCT TTTAAAAATG TCCTGCCTTT TAACGTAGAT   900
ATATGCCTTC CCCCACTACC GTAAATGTCC ATTTATATCA TTTTTTATAT ATTCTTATAA   960
AAATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTTCACTG TGTTGGAGTT TTCTGGAGTG  1020
AGCACTCACG CCCTAAGCGC ACATTCATGT GGGCATTTCT TGCGAGCCTC GCAGCCTCCG  1080
GAAGCTGTCG ACTTCATGAC AAGCATTTTG TGAACTAGGG AAGCTCAGGG GGGTTACTGG  1140
CTTCTCTTGA GTCACACTGC TAGCAAATGG CAGAACCAAA GCTCAAATAA AAATAAAATA  1200
ATTTTCATTC ATTCACTC
```

Seq ID NO: 127 Protein Sequence
Protein Accession #: NP_000068.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEPAAGSSME PSADWLATAA ARGRVEEVRA LLEAGALPNA PNSYGRRPIQ VMMMGSARVA    60
ELLLLHGAEP NCADPATLTR PVHDAAREGF LDTLVVLHRA GARLDVRDAW GRLPVDLAEE   120
```

```
LGHRDVARYL RAAAGGTRGS NHARIDAAEG PSDIPD
```

Seq ID NO: 128 DNA sequence
Nucleic Acid Accession #: NM_058196.1
Coding sequence: 104..421

```
1          11         21         31         41         51
|          |          |          |          |          |
TGTGTGGGGG TCTGCTTGGC GGTGAGGGGG CTCTACACAA GCTTCCTTTC CGTCATGCCG    60
GCCCCCACCC TGGCTCTGAC CATTCTGTTC TCTCTGGCAG GTCATGATGA TGGGCAGCGC    120
CCGAGTGGCG GAGCTGCTGC TGCTCCACGG CGCGGAGCCC AACTGCGCCG ACCCCGCCAC    180
TCTCACCCGA CCCGTGCACG ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT    240
GCACCGGGCC GGGGCGCGGC TGGACGTGCG CGATGCCTGG GGCCGTCTGC CCGTGGACCT    300
GGCTGAGGAG CTGGGCCATC GCGATGTCGC ACGGTACCTG CGCGCGGCTG CGGGGGGCAC    360
CAGAGGCAGT AACCATGCCC GCATAGATGC CGCGGAAGGT CCCTCAGACA TCCCCGATTG    420
AAAGAACCAG AGAGGCTCTG AGAAACCTCG GGAAACTTAG ATCATCAGTC ACCGAAGGTC    480
CTACAGGGCC ACAACTGCCC CCGCCACAAC CCACCCCGCT TTCGTAGTTT TCATTTAGAA    540
AATAGAGCTT TTAAAAATGT CCTGCCTTTT AACGTAGATA TAAGCCTTCC CCCACTACCG    600
TAAATGTCCA TTTATATCAT TTTTTATATA TTCTTATAAA AATGTAAAAA AGAAAAACAC    660
CGCTTCTGCC TTTTCACTGT GTTGGAGTTT TCTGGAGTGA GCACTCACGC CCTAAGCGCA    720
CATTCATGTG GGCATTTCTT GCGAGCCTCG CAGCCTCCGG AAGCTGTCGA CTTCATGACA    780
AGCATTTTGT GAACTAGGGA AGCTCAGGGG GGTTACTGGC TTCTCTTGAG TCACACTGCT    840
AGCAAATGGC AGAACCAAAG CTCAAATAAA AATAAAATAA TTTTCATTCA TTCACTC
```

Seq ID NO: 129 Protein Sequence
Protein Accession #: NP_478103.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MMMGSARVAE LLLLHGAEPN CADPATLTRP VHDAAREGFL DTLVVLHRAG ARLDVRDAWG    60
RLPVDLAEEL GHRDVARYLR AAAGGTRGSN HARIDAAEGP SDIPD
```

Seq ID NO: 130 DNA sequence
Nucleic Acid Accession #: NM_058197.1
Coding sequence: 272..646

```
1          11         21         31         41         51
|          |          |          |          |          |
CCCAACCTGG GGCGACTTCA GGTGTGCCAC ATTCGCTAAG TGCTCGGAGT TAATAGCACC    60
TCCTCCGAGC ACTCGCTCAC GGCGTCCCCT TGCCTGGAAA GATACCGCGG TCCCTCCAGA    120
GGATTTGAGG GACAGGGTCG GAGGGGGCTC TTCCGCCAGC ACCGGAGGAA GAAAGAGGAG    180
GGGCTGGCTG GTCACCAGAG GGTGGGGCGG ACCGCGTGCG CTCGGCGGCT GCGGAGAGGG    240
GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA    300
GCCGGCGGCG GGGAGCAGCA TGGAGCCTTC GGCTGACTGG CTGGCCACGG CCGCGGCCCG    360
GGGTCGGGTA GAGGAGGTGC GGGCGCTGCT GGAGGCGGGG GCGCTGCCCA ACGCACCGAA    420
TAGTTACGGT CGGAGGCCGA TCCAGGTGGG TAGAAGGTCT GCAGCGGGAG CAGGGGATGG    480
CGGGCGACTC TGGAGGACGA AGTTTGCAGG GGAATTGGAA TCAGGTAGCG CTTCGATTCT    540
CCGGAAAAAG GGGAGGCTTC CTGGGGAGTT TTCAGAAGGG GTTTGTAATC ACAGACCTCC    600
TCCTGGCGAC GCCCTGGGGG CTTGGGAAAC CAAGGAAGAG GAATGAGGAG CCACGCGCGT    660
ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTTGTAT TAGATGGAAG    720
TCATGATGAT GGGCAGCGCC CGAGTGGCGG AGCTGCTGCT GCTCCACGGC GCGGAGCCCA    780
ACTGCGCCGA CCCCGCCACT CTCACCCGAC CCGTGCACGA CGCTGCCCGG GAGGGCTTCC    840
TGGACACGCT GGTGGTGCTG CACCGGGCCG GGGCGCGGCT GGACGTGCGC GATGCCTGGG    900
GCCGTCTGCC CGTGGACCTG GCTGAGGAGC TGGGCCATCG CGATGTCGCA CGGTACCTGC    960
GCGCGGCTGC GGGGGGCACC AGAGGCAGTA ACCATGCCCG CATAGATGCC GCGGAAGGTC    1020
CCTCAGACAT CCCCGATTGA AAGAACCAGA GAGGCTCTGA GAAACCTCGG GAACTTAGAT    1080
CATCAGTCAC CGAAGGTCCT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCCGCTTT    1140
CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAATGTCC TGCCTTTTAA CGTAGATATA    1200
TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA    1260
TGTAAAAAAG AAAAACACCG CTTCTGCCTT TTCACTGTGT TGGAGTTTTC TGGAGTGAGC    1320
ACTCACGCCC TAAGCGCACA TTCATGTGGG CATTTCTTGC GAGCCTCGCA GCCTCCGGAA    1380
GCTGTCGACT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTACTGGCTT    1440
CTCTTGAGTC ACACTGCTAG CAAATGGCAG AACCAAAGCT CAAATAAAAA TAAAATAATT    1500
TTCATTCATT CACTC
```

Seq ID NO: 131 Protein Sequence
Protein Accession #: NP_478104.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEPAAGSSME PAAGSSMEPS ADWLATAAAR GRVEEVRALL EAGALPNAPN SYGRRPIQVG    60
RRSAAGAGDG GRLWRTKFAG ELESGSASIL RKKGRLPGEF SEGVCNHRPP PGDALGAWET    120
KEEE
```

Seq ID NO: 132 DNA sequence
Nucleic Acid Accession #: NM_058195.1
Coding sequence: 163..684

```
1          11         21         31         41         51
|          |          |          |          |          |
CCTCCCTACG GGCGCCTCCG GCAGCCCTTC CCGCGTGCGC AGGGCTCAGA GCCGTTCCGA   60
GATCTTGGAG GTCCGGGTGG GAGTGGGGGT GGGGTGGGGG TGGGGGTGAA GGTGGGGGGC   120
GGGCGCGCTC AGGGAAGGCG GGTGCGCGCC TGCGGGGCGG AGATGGGCAG GGGGCGGTGC   180
GTGGGTCCCA GTCTGCAGTT AAGGGGGCAG GAGTGGCGCT GCTCACCTCT GGTGCCAAAG   240
GGCGGCGCAG CGGCTGCCGA GCTCGGCCCT GGAGGCGGCG AGAACATGGT GCGCAGGTTC   300
TTGGTGACCC TCCGGATTCG GCGCGCGTGC GGCCCGCCGC GAGTGAGGGT TTTCGTGGTT   360
CACATCCCGC GGCTCACGGG GGAGTGGGCA GCGCCAGGGG CGCCCGCCGC TGTGGCCCTC   420
GTGCTGATGC TACTGAGGAG CCAGCGTCTA GGGCAGCAGC CGCTTCCTAG AAGACCAGGT   480
CATGATGATG GGCAGCGCCC GAGTGGCGGA GCTGCTGCTG CTCCACGGCG CGGAGCCCAA   540
CTGCGCCGAC CCCGCCACTC TCACCCGACC CGTGCACGAC GCTGCCCGGG AGGGCTTCCT   600
GGACACGCTG GTGGTGCTGC ACCGGGCCGG GGCGCGGCTG GACGTGCGCG ATGCCTGGGG   660
CCGTCTGCCC GTGGACCTGG CTGAGGAGCT GGGCCATCGC GATGTCGCAC GGTACCTGCG   720
CGCGGCTGCG GGGGGCACCA GAGGCAGTAA CCATGCCCGC ATAGATGCCG CGGAAGGTCC   780
CTCAGACATC CCCGATTGAA AGAACCAGAG AGGCTCTGAG AAACCTCGGG AAACTTAGAT   840
CATCAGTCAC CGAAGGTCCT ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCCGCTTT   900
CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAATGTCC TGCCTTTTAA CGTAGATATA   960
TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA   1020
TGTAAAAAAG AAAAACACCG CTTCTGCCTT TTCACTGTGT TGGAGTTTTC TGGAGTGAGC   1080
ACTCACGCCC TAAGCGCACA TTCATGTGGG CATTTCTTGC GAGCCTCGCA GCCTCCGGAA   1140
GCTGTCGACT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTACTGGCTT   1200
CTCTTGAGTC ACACTGCTAG CAAATGGCAG AACCAAAGCT CAAATAAAAA TAAAATAATT   1260
TTCATTCATT CACTC
```

Seq ID NO: 133 Protein Sequence
Protein Accession #: NP_478102.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGRGRCVGPS LQLRGQEWRC SPLVPKGGAA AAELGPGGGE NMVRRFLVTL RIRRACGPPR   60
VRVFVVHIPR LTGEWAAPGA PAAVALVLML LRSQRLGQQP LPRRPGHDDG QRPSGGAAAA   120
PRRGAQLRRP RHSHPTRARR CPGGLPGHAG GAAPGRGAAG RARCLGPSAR GPG
```

Seq ID NO: 134 DNA sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 1..1077

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGGGTTCA ACTTGACGCT TGCAAAATTA CCAAATAACG AGCTGCACGG CCAAGAGAGT   60
CACAATTCAG GCAACAGGAG CGACGGGCCA GGAAAGAACA CCACCCTTCA CAATGAATTT   120
GACACAATTG TCTTGCCGGT GCTTTATCTC ATTATATTTG TGGCAAGCAT CTTGCTGAAT   180
GGTTTAGCAG TGTGGATCTT CTTCCACATT AGGAATAAAA CCAGCTTCAT ATTCTATCTC   240
AAAAACATAG TGGTTGCAGA CCTCATAATG ACGCTGACAT TTCCATTTCG AATAGTCCAT   300
GATGCAGGAT TTGGACCTTG GTACTTCAAG TTTATTCTCT GCAGATACAC TTCAGTTTTG   360
TTTTATGCAA ACATGTATAC TTCCATCGTG TTCCTTGGGC TGATAAGCAT TGATCGCTAT   420
CTGAAGGTGG TCAAGCCATT TGGGGACTCT CGGATGTACA GCATAACCTT CACGAAGGTT   480
TTATCTGTTT GTGTTTGGGT GATCATGGCT GTTTTGTCTT TGCCAAACAT CATCCTAACA   540
AATGGTCAGC CAACAGAGGA CAATATCCAT GACTGCTCAA AACTTAAAAG TCCTTTGGGG   600
GTCAAATGGC ATACGGCAGT CACCTATGTG AACAGCTGCT TGTTTGTGGC CGTGCTGGTG   660
ATTCTGATCG GATGTTACAT AGCCATATCC AGGTACATCC ACAAATCCAG CAGGCAATTC   720
ATAAGTCAGT CAAGCCGAAA GCGAAAACAT AACCAGAGCA TCAGGGTTGT TGTGGCTGTG   780
TTTTTTACCT GCTTTCTACC ATATCACTTG TGCAGAATTC CTTTTACTTT TAGTCACTTA   840
GACAGGCTTT TAGATGAATC TGCACAAAAA ATCCTATATT ACTGCAAAGA AATTACACTT   900
TTCTTGTCTG CGTGTAATGT TTGCCTGGAT CCAATAATTT ACTTTTTCAT GTGTAGGTCA   960
TTTTCAAGAA GGCTGTTCAA AAAATCAAAT ATCAGAACCA GGAGTGAAAG CATCAGATCA   1020
CTGCAAAGTG TGAGAAGATC GGAAGTTCGC ATATATTATG ATTACACTGA TGTGTAA
```

Seq ID NO: 135 Protein Sequence
Protein Accession #: NP_076404

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1          11         21         31         41         51
|          |          |          |          |          |
MGFNLTLAKL PNNELHGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN   60
GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFPFRIVH DAGFGPWYFK FILCRYTSVL   120
FYANMYTSIV FLGLISIDRY LKVVKPFGDS RMYSITFTKV LSVCVWVIMA VLSLPNIILT   180
NGQPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF   240
ISQSSRKRKH NQSIRVVVAV FFTCFLPYHL CRIPFTFSHL DRLLDESAQK ILYYCKEITL   300
FLSACNVCLD PIIYFFMCRS FSRRLFKKSN IRTRSESIRS LQSVRRSEVR IYYDYTDV
```

Seq ID NO: 136 DNA sequence
Nucleic Acid Accession #: NM_005329.1
Coding sequence: 1..1662

```
1          11         21         31         41         51
|          |          |          |          |          |
```

```
ATGCCGGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA   60
GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTCATCCA CACGGAAAAG   120
CACTACCTGT CCTTCGGCCT GTACGGCGCC ATCCTGGGCC TGCACCTGCT CATTCAGAGC   180
CTTTTTGCCT TCCTGGAGCA CCGGCGCATG CGACGTGCCG GCCAGGCCCT GAAGCTGCCC   240
TCCCCGCGGC GGGGCTCGGT GGCACTGTGC ATTGCCGCGT ACCAGGAGGA CCCTGACTAC   300
TTGCGCAAGT GCCTGCGCTC GGCCCAGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG   360
GTGGTGGATG GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG   420
GGCGGCACCG AGCAGGCCGG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG   480
GGTGAGACGG AGGCCAGCCT GCAGGAGGGC ATGGACCGTG TGCGGGATGT GGTGCGGGCC   540
AGCACCTTCT CGTGCATCAT GCAGAAGTGG GGAGGCAAGC GCGAGGTCAT GTACACGGCC   600
TTCAAGGCCC TCGGCGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG   660
GATCCAGCCT GCACCATCGA GATGCTTCGA GTCCTGGAGG AGGATCCCCA AGTAGGGGGA   720
GTCGGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCCTT CCTGAGCAGC   780
GTGCGGTACT GGATGGCCTT CAACGTGGAG CGGGCCTGCC AGTCCTACTT TGGCTGTGTG   840
CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCCTGGAG   900
GACTGGTACC ATCAGAAGTT CCTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC   960
ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC   1020
ACAGAGACCC CCACTAAGTA CCTCCGGTGG CTCAACCAGC AAACCCGCTG GAGCAAGTCT   1080
TACTTCCGGG AGTGGCTCTA CAACTCTCTG TGGTTCCATA AGCACCACCT CTGGATGACC   1140
TACGAGTCAG TGGTCACGGG TTTCTTCCCC TTCTTCCTCA TTGCCACGGT TATACAGCTT   1200
TTCTACCGGG GCCGCATCTG GAACATTCTC CTCTTCCTGC TGACGGTGCA GCTGGTGGGC   1260
ATTATCAAGG CCACCTACGC CTGCTTCCTT CGGGGCAATG CAGAGATGAT CTTCATGTCC   1320
CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCCGGCCA AGATCTTTGC CATTGCTACC   1380
ATCAACAAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTCATTGGC   1440
CTCATTCCTG TGTCCATCTG GGTGGCAGTT CTCCTGGGAG GGCTGGCCTA CACAGCTTAT   1500
TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCCTTG TCTCTGGGGC TATACTGTAT   1560
GGCTGCTACT GGGTGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCG GCGATGTGGG   1620
AAGAAGCCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA
```

Seq ID NO: 137 Protein Sequence
Protein Accession #: NP_005320.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPVQLTTALR VVGTSLFALA VLGGILAAYV TGYQFIHTEK HYLSFGLYGA ILGLHLLIQS   60
LFAFLEHRRM RRAGQALKLP SPRRGSVALC IAAYQEDPDY LRKCLRSAQR ISFPDLKVVM   120
VVDGNRQEDA YMLDIFHEVL GGTEQAGFFV WRSNFHEAGE GETEASLQEG MDRVRDVVRA   180
STFSCIMQKW GGKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG   240
VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQQFLE   300
DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRW LNQQTRWSKS   360
YFREWLYNSL WFHKHHLWMT YESVVTGFFP FFLIATVIQL FYRGRIWNIL LFLLTVQLVG   420
IIKATYACFL RGNAEMIFMS LYSLLYMSSL LPAKIFAIAT INKSGWGTSG RKTIVVNFIG   480
LIPVSIWVAV LLGGLAYTAY CQDLFSETEL AFLVSGAILY GCYWVALLML YLAIIARRCG   540
KKPEQYSLAF AEV
```

Seq ID NO: 138 DNA Sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89..631

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT   60
CTGAGAGCCG GGCAGAGGCT CCGGAGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC   120
GACGGGCGAT GCTGATGGCC CAGGAGGCCC TGGCATTCCT GATGGCCCAG GGGGCAATGC   180
TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCCCGGGGCG CAGGGGCAGC   240
AAGGGCCTCG GGGCCGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTTCAGG   300
GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCCGCCTGC TTGAGTTCTA   360
CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA   420
GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCACTG TGTCCGGCAA   480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC   540
CTGTCTCCAG CAGCTTTCCC TGTTGATGTG GATCACGCAG TGCTTTCTGC CCGTGTTTTT   600
GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCCAGCCT GGCGCCCCTT CCTAGGTCAT   660
GCCTCCTCCC CTAGGGAATG GTCCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT   720
GTTTGTCGCT GGAGGAGGAC GGCTTACATG TTTGTTTCTG TAGAAAATAA AACTGAGCTA   780
```

Seq ID NO: 139 Protein Sequence
Protein Accession #: NP_001318.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQAEGRGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA   60
PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAELARRSLA QDAPPLPVPG   120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQQLSLLM WITQCFLPVF LAQPPSGQRR   180
```

Seq ID NO: 140 DNA Sequence
Nucleic Acid Accession #: Eos sequence

Coding sequence: 53..459

```
1          11         21         31         41         51
|          |          |          |          |          |
CCTCGTGGGC CCTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGGAGC CATGCAGGCC   60
GAAGGCCAGG GCACAGGGGG TTCGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT   120
CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA   180
GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCCGCGGGGT   240
CCGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGCCG   300
GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC   360
ATCAGCTCCT GTCTCCAGCA GCTTTCCCTG TTGATGTGGA TCACGCAGTG CTTTCTGCCC   420
GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCTTCC   480
TAGGTCATGC CTCCTCCCCT AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTGTGGGG   540
GCCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTTCTGTA GAAAATAAAG   600
CTGAGCTA
```

Seq ID NO: 141 Protein Sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA   60
PRGPHGGAAS AQDGRCPCGA RRPDSRLLQF RLTAADHRQL QLSISSCLQQ LSLLMWITQC   120
FLPVFLAQAP SGQRR
```

Seq ID NO: 142 DNA Sequence
Nucleic Acid Accession #: NM_130467.2
Coding sequence: 246..638

```
1          11         21         31         41         51
|          |          |          |          |          |
AGGCAGAGCT CTGCAAGGAG AGGTTGTGTC TTCGTTCTTT CCGCCATCTT CGTTCTTTCC   60
AACATCTTCG TTCTTTCTCA CTGACCGAGA CTCAGCCGGT AGGTCTGCAG AGTGGTCTTC   120
CTGGTAATTT AGTTGTGAGT GAATGTGTGG AGGAGCCAGC GGGCTTAGGA CAGGTCCTGT   180
GGCACAGTCC GTGGCTTTGA GGGAAAAGGG CCTCGCGGTG GTCCTCCGCC TTCCCCCAGG   240
TCGTGATGCA GGCGCCATGG GCCGGTAATC GTGGCTGGGC TGGAACGAGG GAGGAAGTGA   300
GAGATATGAG TGAGCATGTA ACAAGATCCC AATCCTCAGA AAGAGGAAAT GACCAAGAGT   360
CTTCCCAGCC AGTTGGACCT GTGATTGTCC AGCAGCCCAC TGAGGAAAAA CGTCAAGAAG   420
AGGAACCACC AACTGATAAT CAGGGTATTG CACCTAGTGG GGAGATCAAA AATGAAGGAG   480
CACCTGCTGT TCAAGGGACT GATGTGGAAG CTTTTCAACA GGAACTGGCT CTGCTTAAGA   540
TAGAGGATGC ACCTGGAGAT GGTCCTGATG TCAGGGAGGG GACTCTGCCC ACTTTTGATC   600
CCACTAAAGT GCTGGAAGCA GGTGAAGGGC AACTATAGGT TTAAACCAAG ACAAATGAAG   660
ACTGAAACCA AGAATATTGT TCTTATGCTG GAAATTTGAC TGCTAACATT CTCTTAATAA   720
AGTTTTACAG TTTTC
```

Seq ID NO: 143 Protein Sequence
Protein Accession #: NP_569734

```
1          11         21         31         41         51
|          |          |          |          |          |
MSEHVTRSQS SERGNDQESS QPVGPVIVQQ PTEEKRQEEE PPTDNQGIAP SGEIKNEGAP   60
AVQGTDVEAF QQELALLKIE DAPGDGPDVR EGTLPTFDPT KVLEAGEGQL
```

Seq ID NO: 144 DNA Sequence
Nucleic Acid Accession #: NM_001476.1
Coding sequence: 82..435

```
1          11         21         31         41         51
|          |          |          |          |          |
GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCCTGCCGT CCGGACTCTT TTTCCTCTAC   60
TGAGATTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACCTATTA TTGGCCTAGA   120
CCAAGGCGCT ATGTACAGCC TCCTGAAGTG ATTGGGCCTA TGCGGCCCGA GCAGTTCAGT   180
GATGAAGTGG AACCAGCAAC ACCTGAAGAA GGGGAACCAG CAACTCAACG TCAGGATCCT   240
GCAGCTGCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA   300
GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCCTGAT   360
GGGCAGGAGG TGGACCCGCC AAATCCAGAG GAGGTGAAAA CGCCTGAAGA AGGTGAAAAG   420
CAATCACAGT GTTAAAAGAA GACACGTTGA AATGATGCAG GCTGCTCCTA TGTTGGAAAT   480
TTGTTCATTA AAATTCTCCC AATAAAGCTT TACAGCCTTC TGCAAAA
```

Seq ID NO: 145 Protein Sequence
Protein Accession #: NP_001467.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSWRGRSTYY WPRPRRYVQP PEVIGPMRPE QFSDEVEPAT PEEGEPATQR QDPAAAQEGE   60
DEGASAGQGP KPEADSQEQG HPQTGCECED GPDGQEVDPP NPEEVKTPEE GEKQSQC
```

Seq ID NO: 146 DNA Sequence
Nucleic Acid Accession #: NM_005562
Coding sequence: 90..3671

```
1          11         21         31         41         51
|          |          |          |          |          |
ACAGCGGAGC GCAGAGTGAG AACCACCAAC CGAGGCGCCG GGCAGCGACC CCTGCAGCGG   60
AGACAGAGAC TGAGCGGCCC GGCACCGCCA TGCCTGCGCT CTGGCTGGGC TGCTGCCTCT   120
GCTTCTCGCT CCTCCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA   180
ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAAACT GGTAATGGAT   240
TCCGCTGCCT CAACTGCAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAATG   300
GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAAGGTT   360
CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAGGT GTGACAGGAG   420
CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCAAG   480
ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG   540
ACGCGGGCCG CTGTGTCTGC AAGCCAGCTG TTACTGGAGA ACGCTGTGAT AGGTGTCGAT   600
CAGGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGCTATG   660
GGCATTCAGC CAGCTGCCGC AGCTCTGCAG AATACAGTGT CCATAAGATC ACCTCTACCT   720
TTCATCAAGA TGTTGATGGC TGGAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC   780
AATGGTCACA GCGCCATCAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT   840
TTGTGGCTCC TGCCAAATTT CTTGGGAATC AACAGGTGAG CTATGGGCAA AGCCTGTCCT   900
TTGACTACCG TGTGGACAGA GGAGGCAGAC ACCCATCTGC CCATGATGTG ATTCTGGAAG   960
GTGCTGGTCT ACGGATCACA GCTCCCTTGA TGCCACTTGG CAAGACACTG CCTTGTGGGC   1020
TCACCAAGAC TTACACATTC AGGTTAAATG AGCATCCAAG CAATAATTGG AGCCCCCAGC   1080
TGAGTTACTT TGAGTATCGA AGGTTACTGC GGAATCTCAC AGCCCTCCGC ATCCGAGCTA   1140
CATATGGAGA ATACAGTACT GGGTACATTG ACAATGTGAC CCTGATTTCA GCCCGCCCTG   1200
TCTCTGGAGC CCCAGCACCC TGGGTTGAAC AGTGTATATG TCCTGTTGGG TACAAGGGGC   1260
AATTCTGCCA GGATTGTGCT TCTGGCTACA AGAGAGATTC AGCGAGACTG GGGCCTTTTG   1320
GCACCTGTAT TCCTTGTAAC TGTCAAGGGG GAGGGGCCTG TGATCCAGAC ACAGGAGATT   1380
GTTATTCAGG GGATGAGAAT CCTGACATTG AGTGTGCTGA CTGCCCAATT GGTTTCTACA   1440
ACGATCCGCA CGACCCCCGC AGCTGCAAGC CATGTCCCTG TCATAACGGG TTCAGCTGCT   1500
CAGTGATGCC GGAGACGGAG GAGGTGGTGT GCAATAACTG CCCTCCCGGG GTCACCGGTG   1560
CCCGCTGTGA GCTCTGTGCT GATGGCTACT TTGGGGACCC CTTTGGTGAA CATGGCCCAG   1620
TGAGGCCTTG TCAGCCCTGT CAATGCAACA ACAATGTGGA CCCCAGTGCC TCTGGGAATT   1680
GTGACCGGCT GACAGGCAGG TGTTTGAAGT GTATCCACAA CACAGCCGGC ATCTACTGCG   1740
ACCAGTGCAA AGCAGGCTAC TTCGGGGACC CATTGGCTCC CAACCCAGCA GACAAGTGTC   1800
GAGCTTGCAA CTGTAACCCC ATGGGCTCAG AGCCTGTAGG ATGTCGAAGT GATGGCACCT   1860
GTGTTTGCAA GCCAGGATTT GGTGGCCCCA ACTGTGAGCA TGGAGCATTC AGCTGTCCAG   1920
CTTGCTATAA TCAAGTGAAG ATTCAGATGG ATCAGTTTAT GCAGCAGCTT CAGAGAATGG   1980
AGGCCCTGAT TTCAAAGGCT CAGGGTGGTG ATGGAGTAGT ACCTGATACA GAGCTGGAAG   2040
GCAGGATGCA GCAGGCTGAG CAGGCCCTTC AGGACATTCT GAGAGATGCC CAGATTTCAG   2100
AAGGTGCTAG CAGATCCCTT GGTCTCCAGT TGGCCAAGGT GAGGAGCCAA GAGAACAGCT   2160
ACCAGAGCCG CCTGGATGAC CTCAAGATGA CTGTGGAAAG AGTTCGGGCT CTGGGAAGTC   2220
AGTACCAGAA CCGAGTTCGG GATACTCACA GGCTCATCAC TCAGATGCAG CTGAGCCTGG   2280
CAGAAAGTGA AGCTTCCTTG GGAAACACTA ACATTCCTGC CTCAGACCAC TACGTGGGGC   2340
CAAATGGCTT TAAAAGTCTG GCTCAGGAGG CCACAAGATT AGCAGAAAGC CACGTTGAGT   2400
CAGCCAGTAA CATGGAGCAA CTGACAAGGG AAACTGAGGA CTATTCCAAA CAAGCCCTCT   2460
CACTGGTGCG CAAGGCCCTG CATGAAGGAG TCGGAAGCGG AAGCGGTAGC CCGGACGGTG   2520
CTGTGGTGCA AGGGCTTGTG GAAAAATTGG AGAAAACCAA GTCCCTGGCC CAGCAGTTGA   2580
CAAGGGAGGC CACTCAAGCG GAAATTGAAG CAGATAGGTC TTATCAGCAC AGTCTCCGCC   2640
TCCTGGATTC AGTGTCTCGG CTTCAGGGAG TCAGTGATCA GTCCTTTCAG GTGGAAGAAG   2700
CAAAGAGGAT CAAACAAAAA GCGGATTCAC TCTCAACGCT GGTAACCAGG CATATGGATG   2760
AGTTCAAGCG TACACAAAAG AATCTGGGAA ACTGGAAAGA AGAAGCACAG CAGCTCTTAC   2820
AGAATGGAAA AAGTGGGAGA GAGAAATCAG ATCAGCTGCT TTCCCGTGCC AATCTTGCTA   2880
AAAGCAGAGC ACAAGAAGCA CTGAGTATGG GCAATGCCAC TTTTTATGAA GTTGAGAGCA   2940
TCCTTAAAAA CCTCAGAGAG TTTGACCTGC AGGTGGACAA CAGAAAAGCA GAAGCTGAAG   3000
AAGCCATGAA GAGACTCTCC TACATCAGCC AGAAGGTTTC AGATGCCAGT GACAAGACCC   3060
AGCAAGCAGA AAGAGCCCTG GGGAGCGCTG CTGCTGATGC ACAGAGGGCA AAGAATGGGG   3120
CCGGGGAGGC CCTGGAAATC TCCAGTGAGA TTGAACAGGA GATTGGGAGT CTGAACTTGG   3180
AAGCCAATGT GACAGCAGAT GGAGCCTTGG CCATGGAAAA GGGACTGGCC TCTCTGAAGA   3240
GTGAGATGAG GGAAGTGGAA GGAGAGCTGG AAAGGAAGGA GCTGGAGTTT GACACGAATA   3300
TGGATGCAGT ACAGATGGTG ATTACAGAAG CCCAGAAGGT TGATACCAGA GCCAAGAACG   3360
CTGGGGTTAC AATCCAAGAC ACACTCAACA CATTAGACGG CCTCCTGCAT CTGATGGACC   3420
AGCCTCTCAG TGTAGATGAA GAGGGGCTGG TCTTACTGGA GCAGAAGCTT TCCCGAGCCA   3480
AGACCCAGAT CAACAGCCAA CTGCGGCCCA TGATGTCAGA GCTGGAAGAG AGGGCACGTC   3540
AGCAGAGGGG CCACCTCCAT TTGCTGGAGA CAAGCATAGA TGGGATTCTG GCTGATGTGA   3600
AGAACTTGGA GAACATTAGG GACAACCTGC CCCCAGGCTG CTACAATACC CAGGCTCTTG   3660
AGCAACAGTG AAGCTGCCAT AAATATTTCT CAACTGAGGT TCTTGGGATA CAGATCTCAG   3720
GGCTCGGGAG CCATGTCATG TGAGTGGGTG GGATGGGGAC ATTTGAACAT GTTTAATGGG   3780
TATGCTCAGG TCAACTGACC TGACCCCATT CCTGATCCCA TGGCCAGGTG GTTGTCTTAT   3840
TGCACCATAC TCCTTGCTTC CTGATGCTGG GCAATGAGGC AGATAGCACT GGGTGTGAGA   3900
ATGATCAAGG ATCTGGACCC CAAAGAATAG ACTGGATGGA AAGACAAACT GCACAGGCAG   3960
ATGTTTGCCT CATAATAGTC GTAAGTGGAG TCCTGGAATT TGGACAAGTG CTGTTGGGAT   4020
ATAGTCAACT TATTCTTTGA GTAATGTGAC TAAAGGAAAA AACTTTGACT TTGCCCAGGC   4080
ATGAAATTCT TCCTAATGTC AGAACAGAGT GCAACCCAGT CACACTGTGG CCAGTAAAAT   4140
ACTATTGCCT CATATTGTCC TCTGCAAGCT TCTTGCTGAT CAGAGTTCCT CCTACTTACA   4200
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ACCCAGGGTG TGAACATGTT CTCCATTTTC AAGCTGGAAG AAGTGAGCAG TGTTGGAGTG   4260
AGGACCTGTA AGGCAGGCCC ATTCAGAGCT ATGGTGCTTG CTGGTGCCTG CCACCTTCAA   4320
GTTCTGGACC TGGGCATGAC ATCCTTTCTT TTAATGATGC CATGGCAACT TAGAGATTGC   4380
ATTTTTATTA AAGCATTTCC TACCAGCAAA GCAAATGTTG GGAAAGTATT TACTTTTTCG   4440
GTTTCAAAGT GATAGAAAAG TGTGGCTTGG GCATTGAAAG AGGTAAAATT CTCTAGATTT   4500
ATTAGTCCTA ATTCAATCCT ACTTTTCGAA CACCAAAAAT GATGCGCATC AATGTATTTT   4560
ATCTTATTTT CTCAATCTCC TCTCTCTTTC CTCCACCCAT AATAAGAGAA TGTTCCTACT   4620
CACACTTCAG CTGGGTCACA TCCATCCCTC CATTCATCCT TCCATCCATC TTTCCATCCA   4680
TTACCTCCAT CCATCCTTCC AACATATATT TATTGAGTAC CTACTGTGTG CCAGGGGCTG   4740
GTGGGACAGT GGTGACATAG TCTCTGCCCT CATAGAGTTG ATTGTCTAGT GAGGAAGACA   4800
AGCATTTTTA AAAAATAAAT TTAAACTTAC AAACTTTGTT TGTCACAAGT GGTGTTTATT   4860
GCAATAACCG CTTGGTTTGC AACCTCTTTG CTCAACAGAA CATATGTTGC AAGACCCTCC   4920
CATGGGGGCA CTTGAGTTTT GGCAAGGCTG ACAGAGCTCT GGGTTGTGCA CATTTCTTTG   4980
CATTCCAGCT GTCACTCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA   5040
TAACACCAGT GGGAATTGCT GGAGGAACCA GAGGCACTTC CACCTTGGCT GGGAAGACTA   5100
TGGTGCTGCC TTGCTTCTGT ATTTCCTTGG ATTTTCCTGA AAGTGTTTTT AAATAAAGAA   5160
CAATTGTTAG ATGCC
```

Seq ID NO: 147 Protein Sequence
Protein Accession #: NP_005553

```
1          11         21         31         41         51
|          |          |          |          |          |
MPALWLGCCL CFSLLLPAAR ATSRREVCDC NGKSRQCIFD RELHRQTGNG FRCLNCNDNT   60
DGIHCEKCKN GFYRHRERDR CLPCNCNSKG SLSARCDNSG RCSCKPGVTG ARCDRCLPGF   120
HMLTDAGCTQ DQRLLDSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGGN   180
PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDVDGWKA VQRNGSPAKL QWSQRHQDVF   240
SSAQRLDPVY FVAPAKFLGN QQVSYGQSLS FDYRVDRGGR HPSAHDVILE GAGLRITAPL   300
MPLGKTLPCG LTKTYTFRLN EHPSNNWSPQ LSYFEYRRLL RNLTALRIRA TYGEYSTGYI   360
DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTCIPCNCQG   420
GGACDPDTGD CYSGDENPDI ECADCPIGFY NDPHDPRSCK PCPCHNGFSC SVMPETEEVV   480
CNNCPPGVTG ARCELCADGY FGDPFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK   540
CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCNPMGS EPVGCRSDGT CVCKPGFGGP   600
NCEHGAFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEQAL   660
QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLDDLKM TVERVRALGS QYQNRVRDTH   720
RLITQMQLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR   780
ETEDYSKQAL SLVRKALHEG VGSGSGSPDG AVVQGLVEKL EKTKSLAQQL TREATQAEIE   840
ADRSYQHSLR LLDSVSRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG   900
NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQEALSM GNATFYEVES ILKNLREFDL   960
QVDNRKAEAE EAMKRLSYIS QKVSDASDKT QQAERALGSA AADAQRAKNG AGEALEISSE   1020
IEQEIGSLNL EANVTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE   1080
AQKVDTRAKN AGVTIQDTLN TLDGLLHLMD QPLSVDEEGL VLLEQKLSRA KTQINSQLRP   1140
MMSELEERAR QQRGHLHLLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ
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Seq ID NO: 148 DNA Sequence
Nucleic Acid Accession #: NM_021048.2
Coding sequence: 327..1436

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGG AGAAGCGAGG TTCTCGTTCT GAGGGACAGG CTTGAGATCG GCTGAAGAGA   60
GCGGGCCCAG GCTCTGTGAG GAGGCAAGGG AGGTGAGAAC CTTGCTCTCA GAGGGTGACT   120
CAAGTCAACA CAGGGAACCC CTCTTTTCTA CAGACACAGT GGGTCGCAGG ATCTGACAAG   180
AGTCCAGGTT CTCAGGGGAC AGGGAGAGCA AGAGGTCAAG AGCTGTGGGA CACCACAGAG   240
CAGCACTGAA GGAGAAGACC TGCCTGTGGG TCCCCATCGC CCAAGTCCTG CCCACACTCC   300
CACCTGCTAC CCTGATCAGA GTCATCATGC CTCGAGCTCC AAAGCGTCAG CGCTGCATGC   360
CTGAAGAAGA TCTTCAATCC CAAAGTGAGA CACAGGGCCT CGAGGGTGCA CAGGCTCCCC   420
TGGCTGTGGA GGAGGATGCT TCATCATCCA CTTCCACCAG CTCCTCTTTT CCATCCTCTT   480
TTCCCTCCTC CTCCTCTTCC TCCTCCTCCT CCTGCTATCC TCTAATACCA AGCACCCCAG   540
AGGAGGTTTC TGCTGATGAT GAGACACCAA ATCCTCCCCA GAGTGCTCAG ATAGCCTGCT   600
CCTCCCCCTC GGTCGTTGCT TCCCTTCCAT TAGATCAATC TGATGAGGGC TCCAGCAGCC   660
AAAAGGAGGA GAGTCCAAGC ACCCTACAGG TCCTGCCAGA CAGTGAGTCT TTACCCAGAA   720
GTGAGATAGA TGAAAAGGTG ACTGATTTGG TGCAGTTTCT GCTCTTCAAG TATCAAATGA   780
AGGAGCCGAT CACAAAGGCA GAAATACTGG AGAGTGTCAT AAAAAATTAT GAAGACCACT   840
TCCCTTTGTT GTTTAGTGAA GCCTCCGAGT GCATGCTGCT GGTCTTTGGC ATTGATGTAA   900
AGGAAGTGGA TCCCACTGGC CACTCCTTTG TCCTTGTCAC CTCCCTGGGC CTCACCTATG   960
ATGGGATGCT GAGTGATGTC CAGAGCATGC CCAAGACTGG CATTCTCATA CTTATCCTAA   1020
GCATAATCTT CATAGAGGGC TACTGCACCC CTGAGGAGGT CATCTGGGAA GCACTGAATA   1080
TGATGGGGCT GTATGATGGG ATGGAGCACC TCATTTATGG GGAGCCCAGG AAGCTGCTCA   1140
CCCAAGATTG GGTGCAGGAA AACTACCTGG AGTACCGGCA GGTGCCTGGC AGTGATCCTG   1200
CACGGTATGA GTTTCTGTGG GGTCCAAGGG CTCATGCTGA AATTAGGAAG ATGAGTCTCC   1260
TGAAATTTTT GGCCAAGGTA AATGGGAGTG ATCCAAGATC CTTCCCACTG TGGTATGAGG   1320
AGGCTTTGAA AGATGAGGAA GAGAGAGCCC AGGACAGAAT TGCCACCACA GATGATACTA   1380
CTGCCATGGC CAGTGCAAGT TCTAGCGCTA CAGGTAGCTT CTCCTACCCT GAATAAAGTA   1440
AGACAGATTC TTCACTGTGT TTTAAAAGGC AAGTCAAATA CCACATGATT TTACTCATAT   1500
GTGGAATCTA AAAAAAAAAA AAAAAAAA
```

Seq ID NO: 149 Protein Sequence
Protein Accession #: NP_066386.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPRAPKRQRC MPEEDLQSQS ETQGLEGAQA PLAVEEDASS STSTSSSFPS SFPSSSSSSS   60
SSCYPLIPST PEEVSADDET PNPPQSAQIA CSSPSVVASL PLDQSDEGSS SQKEESPSTL   120
QVLPDSESLP RSEIDEKVTD LVQFLLFKYQ MKEPITKAEI LESVIKNYED HFPLLFSEAS   180
ECMLLVFGID VKEVDPTGHS FVLVTSLGLT YDGMLSDVQS MPKTGILILI LSIIFIEGYC   240
TPEEVIWEAL NMMGLYDGME HLIYGEPRKL LTQDWVQENY LEYRQVPGSD PARYEFLWGP   300
RAHAEIRKMS LLKFLAKVNG SDPRSFPLWY EEALKDEEER AQDRIATTDD TTAMASASSS   360
ATGSFSYPE
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Seq ID NO: 150 DNA Sequence
Nucleic Acid Accession #: NM_003695
Coding sequence: 12..398

```
1          11         21         31         41         51
|          |          |          |          |          |
CGACATCAGA GATGAGGACA GCATTGCTGC TCCTTGCAGC CCTGGCTGTG GCTACAGGGC   60
CAGCCCTTAC CCTGCGCTGC CACGTGTGCA CCAGCTCCAG CAACTGCAAG CATTCTGTGG   120
TCTGCCCGGC CAGCTCTCGC TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA   180
ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCCTG CAAGGCCAGG   240
TCAGCAGCGG CACCAGCTCC ACCCAGTGCT GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC   300
ACAACGCTGC ACCCACCCGC ACCGCCCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC   360
TGAGCCTCCT GGCCGTCATC TTAGCCCCCA GCCTGTGACC TTCCCCCCAG GGAAGGCCCC   420
TCATGCCTTT CCTTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCCAG CCGGCAACGG   480
GGGTGCCAGG AGCCCCAGGC TGAGGGCTTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG   540
CATGGAATGC TGATGACTTG GAGCAGGCCC CACAGACCCC ACAGAGGATG AAGCCACCCC   600
ACAGAGGATG CAGCCCCCAG CTGCATGGAA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG   660
GATTTCACAC TCCTTCTGTT TTGTTGCCGT TTATTTTGTA CTCAAATCTC TACATGGAGA   720
TAAATGATTT AAACC
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Seq ID NO: 151 Protein Sequence
Protein Accession #: NP_003686

```
1          11         21         31         41         51
|          |          |          |          |          |
MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCPA SSRFCKTTNT VEPLRGNLVK   60
KDCAESCTPS YTLQGQVSSG TSSTQCCQED LCNEKLHNAA PTRTALAHSA LSLGLALSLL   120
AVILAPSL
```

Seq ID NO: 152 DNA Sequence
Nucleic Acid Accession #: NM_006398.1
Coding sequence: 19..516

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCCCCTTGT CTGCAGAGAT GGCTCCCAAT GCTTCCTGCC TCTGTGTGCA TGTCCGTTCC   60
GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAATCAAA   120
GAACATGTCC GGTCTAAGAC CAAGGTTCCT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC   180
AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC   240
CACCTTACCC TGAAAGTGGT GAAGCCCAGT GATGAGGAGC TGCCCTTGTT TCTTGTGGAG   300
TCAGGTGATG AGGCAAAGAG GCACCTCCTC CAGGTGCGAA GGTCCAGCTC AGTGGCACAA   360
GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC   420
AATGGAAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC   480
TTACTCTTCC TGGCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGGATG GGGTGTTGGC   540
AGGGGTCAAA AAGCTTATTT CTTTTAATCT CTTACTCAAC GAACACATCT TCTGATGATT   600
TCCCAAAATT AATGAGAATG AGATGAGTAG AGTAAGATTT GGGTGGGATG GGTAGGATGA   660
AGTATATTGC CCAACTCTAT GTTTCTTTGA TTCTAACACA ATTAATTAAG TGACATGATT   720
TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTTAA GGCAAAATAG AGCATTC
```

Seq ID NO: 153 Protein Sequence
Protein Accession #: NP_006389.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAPNASCLCV HVRSEEWDLM TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR   60
RSLSSYGIDK EKTIHLTLKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE   120
TKTGIIPETQ IVTCNGKRLE DGKMMADYGI RKGNLLFLAS YCIGG
```

Seq ID NO: 154 DNA Sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74..2788

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1          11         21         31         41         51
|          |          |          |          |          |
GTGGGTCACG TGAACCACTT TTCGCGCGAA ACCTGGTTGT TGCTGTAGTG GCGGAGAGGA   60
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TCGTGGTACT GCTATGGCGG AATCATCGGA ATCCTTCACC ATGGCATCCA GCCCGGCCCA   120
GCGTCGGCGA GGCAATGATC CTCTCACCTC CAGCCCTGGC CGAAGCTCCC GGCGTACTGA   180
TGCCCTCACC TCCAGCCCTG GCCGTGACCT TCCACCATTT GAGGATGAGT CCGAGGGGCT   240
CCTAGGCACA GAGGGGCCCC TGGAGGAAGA AGAGGATGGA GAGGAGCTCA TTGGAGATGG   300
CATGGAAAGG GACTACCGCG CCATCCCAGA GCTGGACGCC TATGAGGCCG AGGGACTGGC   360
TCTGGATGAT GAGGACGTAG AGGAGCTGAC GGCCAGTCAG AGGGAGGCAG CAGAGCGGGC   420
CATGCGGCAG CGTGACCGGG AGGCTGGCCG GGGCCTGGGC CGCATGCGCC GTGGGCTCCT   480
GTATGACAGC GATGAGGAGG ACGAGGAGCG CCCTGCCCGC AAGCGCCGCC AGGTGGAGCG   540
GGCCACGGAG GACGGCGAGG AGGACGAGGA GATGATCGAG AGCATCGAGA ACCTGGAGGA   600
TCTCAAAGGC CACTCTGTGC GCGAGTGGGT GAGCATGGCG GGCCCCCGGC TGGAGATCCA   660
CCACCGCTTC AAGAACTTCC TGCGCACTCA CGTCGACAGC CACGGCCACA ACGTCTTCAA   720
GGAGCGCATC AGCGACATGT GCAAAGAGAA CCGTGAGAGC CTGGTGGTGA ACTATGAGGA   780
CTTGGCAGCC AGGGAGCACG TGCTGGCCTA CTTCCTGCCT GAGGCACCGG CGGAGCTGCT   840
GCAGATCTTT GATGAGGCTG CCCTGGAGGT GGTACTGGCC ATGTACCCCA AGTACGACCG   900
CATCACCAAC CACATCCATG TCCGCATCTC CCACCTGCCT CTGGTGGAGG AGCTGCGCTC   960
GCTGAGGCAG CTGCATCTGA ACCAGCTGAT CCGCACCAGT GGGGTGGTGA CCAGCTGCAC   1020
TGGCGTCCTG CCCCAGCTCA GCATGGTCAA GTACAACTGC AACAAGTGCA ATTTCGTCCT   1080
GGGTCCTTTC TGCCAGTCCC AGAACCAGGA GGTGAAACCA GGCTCCTGTC CTGAGTGCCA   1140
GTCGGCCGGC CCCTTTGAGG TCAACATGGA GGAGACCATC TATCAGAACT ACCAGCGTAT   1200
CCGAATCCAG GAGAGTCCAG GCAAAGTGGC GGCTGGCCGG CTGCCCCGCT CCAAGGACGC   1260
CATTCTCCTC GCAGATCTGG TGGACAGCTG CAAGCCAGGA GACGAGATAG AGCTGACTGG   1320
CATCTATCAC AACAACTATG ATGGCTCCCT CAACACTGCC AATGGCTTCC CTGTCTTTGC   1380
CACTGTCATC CTAGCCAACC ACGTGGCCAA GAAGGACAAC AAGGTTGCTG TAGGGGAACT   1440
GACCGATGAA GATGTGAAGA TGATCACTAG CCTCTCCAAG GATCAGCAGA TCGGAGAGAA   1500
GATCTTTGCC AGCATTGCTC CTTCCATCTA TGGTCATGAA GACATCAAGA GAGGCCTGGC   1560
TCTGGCCCTG TTCGGAGGGG AGCCCAAAAA CCCAGGTGGC AAGCACAAGG TACGTGGTGA   1620
TATCAACGTG CTCTTGTGCG GAGACCCTGG CACAGCGAAG TCGCAGTTTC TCAAGTATAT   1680
TGAGAAAGTG TCCAGCCGAG CCATCTTCAC CACTGGCCAG GGGGCGTCGG CTGTGGGCCT   1740
CACGGCGTAT GTCCAGCGGC ACCCTGTCAG CAGGGAGTGG ACCTTGGAGG CTGGGGCCCT   1800
GGTTCTGGCT GACCGAGGAG TGTGTCTCAT TGATGAATTT GACAAGATGA ATGACCAGGA   1860
CAGAACCAGC ATCCATGAGG CCATGGAGCA ACAGAGCATC TCCATCTCGA AGGCTGGCAT   1920
CGTCACCTCC CTGCAGGCTC GCTGCACGGT CATTGCTGCC GCCAACCCCA TAGGAGGGCG   1980
CTACGACCCC TCGCTGACTT TCTCTGAGAA CGTGGACCTC ACAGAGCCCA TCATCTCACG   2040
CTTTGACATC CTGTGTGTGG TGAGGGACAC CGTGGACCCA GTCCAGGACG AGATGCTGGC   2100
CCGCTTCGTG GTGGGCAGCC ACGTCAGACA CCACCCCAGC AACAAGGAGG AGGAGGGGCT   2160
GGCCAATGGC AGCGCTGCTG AGCCCGCCAT GCCCAACACG TATGGCGTGG AGCCCCTGCC   2220
CCAGGAGGTC CTGAAGAAGT ACATCATCTA CGCCAAGGAG AGGGTCCACC CGAAGCTCAA   2280
CCAGATGGAC CAGGACAAGG TGGCCAAGAT GTACAGTGAC CTGAGGAAAG AATCTATGGC   2340
GACAGGCAGC ATCCCCATTA CGGTGCGGCA CATCGAGTCC ATGATCCGCA TGGCGGAGGC   2400
CCACGCGCGC ATCCATCTGC GGGACTATGT GATCGAAGAC GACGTCAACA TGGCCATCCG   2460
CGTGATGCTG GAGAGCTTCA TAGACACACA GAAGTTCAGC GTCATGCGCA GCATGCGCAA   2520
GACTTTTGCC CGCTACCTTT CATTCCGGCG TGACAACAAT GAGCTGTTGC TCTTCATACT   2580
GAAGCAGTTA GTGGCAGAGC AGGTGACATA TCAGCGCAAC CGCTTTGGGG CCCAGCAGGA   2640
CACTATTGAG GTCCCTGAGA AGGACTTGGT GGATAAGGCT CGTCAGATCA ACATCCACAA   2700
CCTCTCTGCA TTTTATGACA GTGAGCTCTT CAGGATGAAC AAGTTCAGCC ACGACCTGAA   2760
AAGGAAAATG ATCCTGCAGC AGTTCTGAGG CCCTATGCCA TCCATAAGGA TTCCTTGGGA   2820
TTCTGGTTTG GGGTGGTCAG TGCCCTCTGT GCTTTATGGA CACAAAACCA GAGCACTTGA   2880
TGAACTCGGG GTACTAGGGT CAGGGCTTAT AGCAGGATGT CTGGCTGCAC CTGGCATGAC   2940
TGTTTGTTTC TCCAAGCCTG CTTTGTGCTT CTCACCTTTG GGTGGGATGC CTTGCCAGTG   3000
TGTCTTACTT GGTTGCTGAA CATCTTGCCA CCTCCGAGTG CTTTGTCTCC ACTCAGTACC   3060
TTGGATCAGA GCTGCTGAGT TCAGGATGCC TGCGTGTGGT TTAGGTGTTA GCCTTCTTAC   3120
ATGGATGTCA GGAGAGCTGC TGCCCTCTTG GCGTGAGTTG CGTATTCAGG CTGCTTTTGC   3180
TGCCTTTGGC CAGAGAGCTG GTTGAAGATG TTTGTAATCG TTTTCAGTCT CCTGCAGGTT   3240
TCTGTGCCCC TGTGGTGGAA GAGGGCACGA CAGTGCCAGC GCAGCGTTCT GGGCTCCTCA   3300
GTCGCAGGGG TGGGATGTGA GTCATGCGGA TTATCCACTC GCCACAGTTA TCAGCTGCCA   3360
TTGCTCCCTG TCTGTTTCCC CACTCTCTTA TTTGTGCATT CGGTTTGGTT TCTGTAGTTT   3420
TAATTTTTAA TAAAGTTGAA TAAAATATAA AAAAAAAAAA AAAAAA
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Seq ID NO: 155 Protein Sequence
Protein Accession #: AAH17490.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAESSESFTM ASSPAQRRRG NDPLTSSPGR SSRRTDALTS SPGRDLPPFE DESEGLLGTE   60
GPLEEEEDGE ELIGDGMERD YRAIPELDAY EAEGLALDDE DVEELTASQR EAAERAMRQR   120
DREAGRGLGR MRRGLLYDSD EEDEERPARK RRQVERATED GEEDEEMIES IENLEDLKGH   180
SVREWVSMAG PRLEIHHRFK NFLRTHVDSH GHNVFKERIS DMCKENRESL VVNYEDLAAR   240
EHVLAYFLPE APAELLQIFD EAALEVVLAM YPKYDRITNH IHVRISHLPL VEELRSLRQL   300
HLNQLIRTSG VVTSCTGVLP QLSMVKYNCN KCNFVLGPFC QSQNQEVKPG SCPECQSAGP   360
FEVNMEETIY QNYQRIRIQE SPGKVAAGRL PRSKDAILLA DLVDSCKPGD EIELTGIYHN   420
NYDGSLNTAN GFPVFATVIL ANHVAKKDNK VAVGELTDED VKMITSLSKD QQIGEKIFAS   480
IAPSIYGHED IKRGLALALF GGEPKNPGGK HKVRGDINVL LCGDPGTAKS QFLKYIEKVS   540
SRAIFTTGQG ASAVGLTAYV QRHPVSREWT LEAGALVLAD RGVCLIDEFD KMNDQDRTSI   600
HEAMEQQSIS ISKAGIVTSL QARCTVIAAA NPIGGRYDPS LTFSENVDLT EPIISRFDIL   660
CVVRDTVDPV QDEMLARFVV GSHVRHHPSN KEEEGLANGS AAEPAMPNTY GVEPLPQEVL   720
KKYIIYAKER VHPKLNQMDQ DKVAKMYSDL RKESMATGSI PITVRHIESM IRMAEAHARI   780
HLRDYVIEDD VNMAIRVMLE SFIDTQKFSV MRSMRKTFAR YLSFRRDNNE LLLFILKQLV   840
AEQVTYQRNR FGAQQDTIEV PEKDLVDKAR QINIHNLSAF YDSELFRMNK FSHDLKRKMI   900
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LQQF

Seq ID NO: 156 DNA Sequence
Nucleic Acid Accession #: NM_002497.1
Coding sequence: 135..1472

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGTA GGGGTGGCGG GTCAGTGCTG CTCGGGGGCT TCTCCATCCA GGTCCCTGGA   60
GTTCCTGGTC CCTGGAGCTC CGCACTTGGC GCGCAACCTG CGTGAGGCAG CGCGACTCTG   120
GCGACTGGCC GGCCATGCCT TCCCGGGCTG AGGACTATGA AGTGTTGTAC ACCATTGGCA   180
CAGGCTCCTA CGGCCGCTGC CAGAAGATCC GGAGGAAGAG TGATGGCAAG ATATTAGTTT   240
GGAAAGAACT TGACTATGGC TCCATGACAG AAGCTGAGAA ACAGATGCTT GTTTCTGAAG   300
TGAATTTGCT TCGTGAACTG AAACATCCAA ACATCGTTCG TTACTATGAT CGGATTATTG   360
ACCGGACCAA TACAACACTG TACATTGTAA TGGAATATTG TGAAGGAGGG GATCTGGCTA   420
GTGTAATTAC AAAGGGAACC AAGGAAAGGC AATACTTAGA TGAAGAGTTT GTTCTTCGAG   480
TGATGACTCA GTTGACTCTG GCCCTGAAGG AATGCCACAG ACGAAGTGAT GGTGGTCATA   540
CCGTATTGCA TCGGGATCTT AAACCAGCCA ATGTTTTCCT GGATGGCAAG CAAAACGTCA   600
AGCTTGGAGA CTTTGGGCTA GCTAGAATAT TAAACCATGA CACGAGTTTT GCAAAAACAT   660
TTGTTGGCAC ACCTTATTAC ATGTCTCCTG AACAAATGAA TCGCATGTCC TACAATGAGA   720
AATCAGATAT CTGGTCATTG GGCTGCTTGC TGTATGAGTT ATGTGCATTA ATGCCTCCAT   780
TTACAGCTTT TAGCCAGAAA GAACTCGCTG GGAAAATCAG AGAAGGCAAA TTCAGGCGAA   840
TTCCATACCG TTACTCTGAT GAATTGAATG AAATTATTAC GAGGATGTTA AACTTAAAGG   900
ATTACCATCG ACCTTCTGTT GAAGAAATTC TTGAGAACCC TTTAATAGCA GATTTGGTTG   960
CAGACGAGCA AAGAAGAAAT CTTGAGAGAA GAGGGCGACA ATTAGGAGAG CCAGAAAAAT   1020
CGCAGGATTC CAGCCCTGTA TTGAGTGAGC TGAAACTGAA GGAAATTCAG TTACAGGAGC   1080
GAGAGCGAGC TCTCAAAGCA AGAGAAGAAA GATTGGAGCA GAAAGAACAG GAGCTTTGTG   1140
TTCGTGAGAG ACTAGCAGAG GACAAACTGG CTAGAGCAGA AAATCTGTTG AAGAACTACA   1200
GCTTGCTAAA GGAACGGAAG TTCCTGTCTC TGGCAAGTAA TCCAGAACTT CTTAATCTTC   1260
CATCCTCAGT AATTAAGAAG AAAGTTCATT TCAGTGGGGA AAGTAAAGAG AACATCATGA   1320
GGAGTGAGAA TTCTGAGAGT CAGCTCACAT CTAAGTCCAA GTGCAAGGAC CTGAAGAAAA   1380
GGCTTCACGC TGCCCAGCTG CGGGCTCAAG CCCTGTCAGA TATTGAGAAA AATTACCAAC   1440
TGAAAAGCAG ACAGATCCTG GGCATGCGCT AGCCAGGTAG AGAGACACAG AGCTGTGTAC   1500
AGGATGTAAT ATTACCAACC TTTAAAGACT GATATTCAAA TGCTGTAGTG TTGAATACTT   1560
GGCCCCATGA GCCATGCCTT TCTGTATAGT ACACATGATA TTTCGGAATT GGTTTTACTG   1620
TTCTTCAGCA ACTATTGTAC AAAATGTTCA CATTTAATTT TTCTTTCTTC TTTTAAGAAC   1680
ATATTATAAA AAGAATACTT TCTTGGTTGG GCTTTTAATC CTGTGTGTGA TTACTAGTAG   1740
GAACATGAGA TGTGACATTC TAAATCTTGG GAGAAAAAAT AATATTAGGA AAAAAATATT   1800
TATGCAGGAA GAGTAGCACT CACTGAATAG TTTTAAATGA CTGAGTGGTA TGCTTACAAT   1860
TGTCATGTCT AGATTTAAAT TTTAAGTCTG AGATTTTAAA TGTTTTTGAG CTTAGAAAAC   1920
CCAGTTAGAT GCAATTTGGT CATTAATACC ATGACATCTT GCTTATAAAT ATTCCATTGC   1980
TCTGTAGTTC AAATCTGTTA GCTTTGTGAA AATTCATCAC TGTGATGTTT GTATTCTTTT   2040
TTTTTTTCTG TTTAACAGAA TATGAGCTGT CTGTCATTTA CCTACTTCTT TCCCACTAAA   2100
TAAAAGAATT CTTCAGTTA
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Seq ID NO: 157 Protein Sequence
Protein Accession #: NP_002488.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPSRAEDYEV LYTIGTGSYG RCQKIRRKSD GKILVWKELD YGSMTEAEKQ MLVSEVNLLR   60
ELKHPNIVRY YDRIIDRTNT TLYIVMEYCE GGDLASVITK GTKERQYLDE EFVLRVMTQL   120
TLALKECHRR SDGGHTVLHR DLKPANVFLD GKQNVKLGDF GLARILNHDT SFAKTFVGTP   180
YYMSPEQMNR MSYNEKSDIW SLGCLLYELC ALMPPFTAFS QKELAGKIRE GKFRRIPYRY   240
SDELNEIITR MLNLKDYHRP SVEEILENPL IADLVADEQR RNLERRGRQL GEPEKSQDSS   300
PVLSELKLKE IQLQERERAL KAREERLEQK EQELCVRERL AEDKLARAEN LLKNYSLLKE   360
RKPLSLASNP ELLNLPSSVI KKKVHFSGES KENIMRSENS ESQLTSKSKC KDLKKRLHAA   420
QLRAQALSDI EKNYQLKSRQ ILGMR
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Seq ID NO: 158 DNA Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
TGAGTTTGCC CCCTTACCCC CATCCCAGTG AATATTTGCA ATTCCTAAAG ACGTGTTTTG   60
ATTGTCACAC CTGGGTGGGG AACATGCTAC TGGCATCTAA TGCATAGAGG GCAGTAATGC   120
TGCTAAACAT CTTTCAACGC ACAGGACAGA GCCCCACAAA AGAGAATTAT CTAGCCCCAA   180
ATGTCCATAA CACTGCTGTT GAGAAAACCT ACCGCAGGAT CTTACTGGGC TTCATAGGTA   240
AGCTTGCCTT TGTTCTGGCT TCTGTAGATA TATAAAATAA AGACACTGCC CAGTCCCTCC   300
CTCAACGTCC CGAGCCAGGG CTCAAGGCAA TTCCAATAAC AGTAGAATGA ACACTAAATA   360
TTGATTTCAA AATCTCAGCA ACTAGAAGAA TGACCAACCA TCCTGGTTGG CCTGGGACTG   420
TCCTAGTTTT AGCATTGAAA GTTTCAGGTT CCAGGAAAGC CCTCAGGCCT GGGCTGCTGG   480
TCACCCTAGC AGCTGAGGGA CTCTTCAATA CAGAATTAGT CTTTGTGCAC TGGAGATGAA   540
TATACTTTAA TTTGTAACAT GTGAAAACAT CTATAAACAT CTACTGAAGC CTGTTCTGTC   600
TGCACCGACA TTTTCATTGA GTACGGATTC TTCCTACCAG ATACAGCTGC TCTACAACTT   660
TCGAGGGCTG GTATAAAACT AGCTTTTACC TATTTTTAAA AATTACATGA ATAGTAAAAA   720
CTTGGATTAA CCCAGTATTC GGGTATTTTC AATTTCCTTG GGAGCTTAGA GGACGGACAA   780
ATAAAAAGAT TATTTCAACA TCAAATATAY GCTATTGTTT ACATATGAAG ATAACCACAT   840
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ATATGTATAA ATTCACCGTT ACTTTTTAGC AATACTATAA AATCCAACAG AAAAAAATAG   900
CATTTACTAT
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Seq ID NO: 159 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 264..782

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1          11         21         31         41         51
|          |          |          |          |          |
CCCTGCTCCA GTCACACCCG GAAGCTGACT GGTCCACGCA CAGCTGAAGC ATGAGGAAAC   60
TCATCGCGGG ACTAATTTTC CTTAAAATTT AGACTTGCAC AGTAAGGACT TCAACTGACC   120
TTCCTCAGAC TGAGAACTGT TTCCAGTATA TACATCAAGT CACTGAGATC TCCAGCACCC   180
TGCCGGTGGC ACTACTGAGA GACGAGGTGC CAGGGTGGTT CCTGAAAGTG CCTGAGCCCC   240
AACTTATCAG CAAGGAGCTC ATCATGCTGA CAGAAGTCAT GGAGGTCTGG CATGGCTTAG   300
TGATCGCGGT GGTGTCCCTC TTCCTGCAGG CCTGCTTCCT CACCGCCATC AACTACCTGC   360
TCAGCAGGCA CATGGCCCAC AAGAGTGAAC AGATACTGAA AGCGGCCAGT CTCCAGGTTC   420
CCAGGCCCAG CCCTGGCCAC CATCATCCAC CTGCTGTCAA AGAGATGAAG GAGACTCAGA   480
CAGAGAGAGA CATCCCAATG TCTGATTCCC TTTACAGGCA TGACAGCGAC ACACCCTCAG   540
ATAGCTTGGA TAGCTCCTGC AGTTCGCCTC CTGCCTGCCA GGCCACAGAG GATGTGGATT   600
ACACACAAGT CGTCTTTTCT GACCCTGGAG AACTAAAAAA TGACTCCCCG CTGGACTATG   660
AGAACATAAA GGAAATCACA GATTATGTCA ATGTCAATCC AGAAAGACAC AAGCCCAGTT   720
TCTGGTATTT TGTCAACCCT GCTCTGTCTG AGCCAGCGGA ATATGATCAA GTGGCCATGT   780
GAATTCCAAA TATTTTTAAT GGGGTCCAGT TCTCTATGGA TTCTTACATT TAATTTGTAG   840
GGAAATGCCA TTTTTCCCCC TTAAACAAGG CATGGGGCTC ACAAGTCTAT GGAGACAGGC   900
CAAAAAGAAT GTGGAGAAGA AAACTGATAA ATACACAGAG GTCCTCAAGA CCCATGGACT   960
CCTGGTCTGT ACCCAAAAAA GCTGTTCGTT CCTCAAAAAC AAAAACAAGG CTTGGCTGGG   1020
AAAACAGGCC AATGCCCCGG CAAGAAAGGT TGAGATCAGA TGTTAGGAAG AACTTTCAGG   1080
TAAAGTATGA GAACTATGGA GTCCATCAGC AGAGATAGTA GTGAAGTCTC TCCCCAGGGA   1140
AAATTTTAAA AAGGTTGAAT CAGCTGTTGT AGAGTTCTAT TTGGCAATCT CATGGTTAAA   1200
TGACTTCCCT TTGAGCTCTT TAATTATTGG CAATAAACAA CTTCTTTAAA AGTTTTAAAT   1260
AAAATAGCAA CCACCACCA
```

Seq ID NO: 160 Protein Sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MLTEVMEVWH GLVIAVVSLF LQACFLTAIN YLLSRHMAHK SEQILKAASL QVPRPSPGHH   60
HPPAVKEMKE TQTERDIPMS DSLYRHDSDT PSDSLDSSCS SPPACQATED VDYTQVVFSD   120
PGELKNDSPL DYENIKEITD YVNVNPERHK PSFWYFVNPA LSEPAEYDQV AM
```

Seq ID NO: 161 DNA Sequence
Nucleic Acid Accession #: NM_012152
Coding sequence: 43..1104

```
1          11         21         31         41         51
|          |          |          |          |          |
CTTCTTTAAA TTTCTTTCTA GGATGTTCAC TTCTTCTCCA CAATGAATGA GTGTCACTAT   60
GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTCGA TGACTGGACA   120
GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT   180
TCTAATTCTC TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC   240
TACCTGTTGG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTGCCTA TGTATTCCTG   300
ATGTTTAACA CAGGCCCAGT TTCAAAAACT TTGACTGTCA ACCGCTGGTT TCTCCGTCAG   360
GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG   420
AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA   480
CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTTATGG GGGCGGTCCC CACACTGGGC   540
TGGAATTGCC TCTGCAACAT CTCTGCCTGC TCTTCCCTGG CCCCCATTTA CAGCAGGAGT   600
TACCTTGTTT TCTGGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGTAC   660
CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG   720
TCCATCAGCC GCCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG   780
GCGTTTGTGG TATGCTGGAC CCCGGGCCTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC   840
AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC   900
GTCGTGAACC CCATCATCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG   960
ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA   1020
GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA   1080
GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCCACCCA GGTGATGACT   1140
GTCTTAGG
```

Seq ID NO: 162 Protein Sequence
Protein Accession #: NP_036284

```
1          11         21         31         41         51
|          |          |          |          |          |
MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFF CLFIFFSNSL VIAAVIKNRK   60
FHFPFYYLLA NLAAADFFAG IAYVFLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL   120
LVIAVERHMS IMRMRVHSNL TKKRVTLLIL LVWAIAIFMG AVPTLGWNCL CNISACSSLA   180
PIYSRSYLVF WTVSNLMAFL IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT   240
```

```
VMTVLGAFVV CWTPGLVVLL LDGLNCRQCG VQHVKRWFLL LALLNSVVNP IIYSYKDEDM   300
YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS
```

Seq ID NO: 163 DNA Sequence
Nucleic Acid Accession #: NM_020242
Coding sequence: 72..4240

```
1          11         21         31         41         51
|          |          |          |          |          |
CAGTCGCGCG CGGTGCAGTC GGGAGGTGGA GGCACCGGCT GCATTGTTTT CGGGATCGAG   60
GGGTGAGGGC GCTATGGCAC CCGGCTGCAA AACTGAGTTA CGCAGCGTGA CAAATGGTCA   120
GTCTAACCAA CCAAGTAATG AAGGTGATGC CATCAAAGTT TTTGTGCGAA TTCGTCCTCC   180
TGCAGAAAGA TCTGGGTCAG CTGATGGAGA GCAGAACTTA TGCTTATCTG TGCTGTCCTC   240
CACGAGTCTC CGGCTGCACT CCAACCCTGA GCCCAAGACC TTCACGTTTG ATCATGTTGC   300
AGATGTGGAT ACCACTCAGG AATCTGTATT TGCAACTGTG GCTAAAAGCA TTGTGGAGTC   360
TTGCATGAGC GGTTATAATG GTACCATCTT TGCATATGGA CAGACTGGCT CAGGGAAGAC   420
ATTTACTATG ATGGGACCAT CTGAATCTGA TAATTTTTCT CATAACCTGA GAGGAGTAAT   480
CCCACGAAGT TTTGAATATT TGTTTTCCTT AATTGATCGT GAAAAAGAAA AGGCTGGAGC   540
TGGAAAGAGT TTCCTTTGTA AGTGTTCCTT TATTGAAATC TACAACGAGC AGATATATGA   600
TCTACTGGAC TCTGCATCGG CTGGACTGTA CTTAAGGGAG CATATCAAGA AGGGAGTCTT   660
TGTTGTTGGT GCGGTGGAGC AGGTGGTAAC CTCAGCTGCT GAAGCCTATC AGGTGCTGTC   720
TGGAGGATGG AGGAATAGAC GTGTGGCATC AACATCAATG AACAGAGAAT CGTCTAGGTC   780
TCATGCCGTC TTTACAATTA CAATAGAGTC AATGGAGAAA AGTAATGAGA TTGTGAATAT   840
ACGGACCTCC CTACTCAACC TGGTGGATTT AGCAGGATCT GAAAGGCAAA AAGATACCCA   900
TGCAGAAGGG ATGAGATTGA AGGAAGCAGG TAACATAAAT CGATCATTGA GCTGCCTGGG   960
CCAAGTGATT ACAGCACTTG TCGACGTGGG TAATGGAAAA CAGAGACATG TTTGCTACAG   1020
AGACTCCAAA CTTACCTTCT TACTACGGGA TTCCCTTGGA GGTAATGCCA AAACAGCCAT   1080
AATTGCAAAT GTTCATCCTG GATCCAGGTG TTTTGGGGAA ACCCTATCAA CACTTAACTT   1140
TGCTCAAAGA GCCAAGCTGA TTAAAAACAA GGCAGTAGTA AATGAAGACA CCCAAGGAAA   1200
TGTGAGCCAG CTCCAAGCTG AAGTGAAGAG GCTCAAAGAA CAACTGGCGG AGCTTGCTTC   1260
AGGACAGACA CCACCAGAAA GCTTCCTGAC CAGAGACAAA AAGAAGACTA ACTATATGGA   1320
GTATTTCCAG GAAGCAATGT TATTCTTTAA GAAATCTGAA CAGGAAAAGA AGTCTCTGAT   1380
AGAAAAAGTT ACCCAATTAG AAGACCTCAC CCTCAAAAAG GAAAAATTTA TTCAATCTAA   1440
TAAAATGATT GTGAAATTCC GAGAGGATCA AATAATACGC TTGGAAAAGC TCCACAAGGA   1500
ATCCCGGGGA GGTTTTCTGC CTGAGGAGCA GGATCGTTTG CTCTCAGAAT TAAGGAATGA   1560
GATTCAAACT CTGCGAGAAC AAATAGAGCA CCACCCCAGA GTTGCAAAGT ATGCTATGGA   1620
AAATCATTCC CTCAGGGAGG AGAATAGAAG ACTGAGATTA TTAGAGCCTG TGAAAAGAGC   1680
TCAAGAAATG GATGCCCAGA CCATTGCAAA ACTAGAAAAA GCTTTCTCTG AAATAAGTGG   1740
CATGGAGAAA AGTGACAAAA ATCAGCAAGG ATTTTCACCT AAAGCTCAGA AAGAGCCATG   1800
TTTGTTTGCA AACACTGAGA AGTTAAAAGC ACAACTCCTG CAAATTCAGA CAGAGCTGAA   1860
TAATTCAAAG CAAGAATATG AAGAATTCAA AGAACTTACT AGGAAAAGGC AGCTAGAATT   1920
GGAATCAGAG CTTCAGTCTT TGCAAAAAGC GAACCTTAAT CTTGAAAACC TTTTGGAAGC   1980
AACAAAAGCC TGCAAGCGGC AAGAAGTTTC TCAGCTGAAT AAAATTCATG CTGAAACACT   2040
TAAGATTATA ACTACACCAA CCAAGGCCTA CCAACTTCAT TCCCGACCAG TACCAAAATT   2100
AAGCCCTGAA ATGGGAAGCT TTGGCTCTCT ATACACTCAG AATTCTAGCA TATTAGATAA   2160
TGATATATTA AATGAGCCAG TTCCTCCTGA GATGAATGAA CAAGCTTTTG AGGCCATTTC   2220
TGAAGAGCTT AGAACAGTGC AGGAACAAAT GAGTGCTCTT CAAGCCAAAC TGGATGAAGA   2280
AGAGCATAAA AACCTAAAGC TTCAGCAGCA TGTTGACAAA CTGGAACATC ATTCTACCCA   2340
AATGCAGGAG CTTTTCTCAT CAGAAAGAAT TGATTGGACC AAACAGCAGG AAGAGCTTCT   2400
CTCACAGTTG AATGTCCTTG AAAAGCAGCT TCAAGAGACT CAAACTAAAA ATGACTTTTT   2460
GAAAAGTGAG GTACATGACC TGCGAGTAGT CCTTCATTCT GCTGACAAGG AGCTTTCTTC   2520
AGTGAAATTG GAATATAGTT CATTCAAAAC GAATCAGGAG AAAGAATTCA ACAAACTTTC   2580
TGAAAGACAC ATGCATGTAC AGCTTCAATT AGATAATCTC AGGTTAGAAA ACGAAAAGCT   2640
GCTTGAGAGC AAAGCCTGCC TACAGGATTC CTATGACAAC TTACAAGAAA TAATGAAATT   2700
TGAGATTGAC CAACTTTCAA GAAACCTCCA AAACTTCAAA AAAGAAAATG AAACTCTGAA   2760
ATCTGATCTG AATAATTTGA TGGAGCTTCT TGAGGCAGAA AAAGAACGCA ATAACAAATT   2820
ATCATTACAG TTTGAAGAAG ATAAAGAAAA CAGTTCTAAA GAAATCTTAA AAGTTCTTGA   2880
GGCTGTACGT CAGGAGAAAC AGAAAGAGAC GGCCAAGTGT GAGCAGCAGA TGGCAAAAGT   2940
ACAGAAACTA GAAGAGAGCT TGCTTGCTAC TGAAAAAGTG ATCAGTTCCC TGGAAAAGTC   3000
TAGAGATTCT GATAAGAAAG TTGTAGCTGA CCTCATGAAC CAGATCCAGG AGCTAAGAAC   3060
ATCGGTCTGT GAGAAAACAG AAACTATAGA CACCCTGAAA CAAGAACTGA AGGACATAAA   3120
TTGCAAATAC AACTCTGCTT TGGTTGACAG AGAAGAGAGC AGAGTGTTGA TCAAGAAGCA   3180
GGAAGTGGAT ATTCTGGATC TGAAAGAAAC CCTTAGGCTG AGAATACTTT CTGAGGACAT   3240
AGAGAGGGAT ATGCTCTGTG AGGACCTGGC TCATGCCACT GAGCAGCTGA ACATGCTCAC   3300
AGAGGCCTCA AAAAAACACT CGGGGCTGCT GCAGTCTGCC CAGGAAGAAC TGACCAAGAA   3360
GGAAGCCCTG ATTCAGGAAC TTCAGCACAA GCTAAACCAA AAGAAAGAGG AAGTAGAACA   3420
GAAGAAGAAT GAATATAACT TCAAAATGAG GCAACTAGAA CATGTGATGG ATTCTGCTGC   3480
TGAGGATCCC CAGAGTCCTA AGACACCACC TCACTTTCAA ACACATTTGG CAAAACTCCT   3540
GGAAACACAA GAACAAGAGA TAGAAGATGG AAGAGCCTCT AAGACTTCTT TGGAACACCT   3600
TGTAACAAAG CTAAATGAAG ACAGAGAAGT CAAAAATGCT GAAATCCTCA GAATGAAGGA   3660
GCAGTTGCGT GAAATGGAAA ACCTACGCCT GGAAAGTCAG CAGTTAATAG AGAAAAACTG   3720
GCTCCTGCAA GGTCAGCTGG ATGATATTAA AAGACAAAAG GAAAACAGTG ATCAGAATCA   3780
TCCAGATAAT CAACAGCTGA AGAATGAACA AGAAGAAAGT ATCAAAGAAA GACTTGCAAA   3840
AAGTAAAATA GTTGAAGAAA TGCTGAAAAT GAAAGCAGAC CTAGAAGAAG TCCAAAGTGC   3900
CCTTTACAAC AAAGAGATGG AATGCCTTAG AATGACTGAT GAAGTCGAAC GAACCCAAAC   3960
TTTGGAGTCT AAAGCATTCC AGGAAAAAGA ACAACTGAGA TCAAAGCTGG AAGAAATGTA   4020
TGAAGAAAGA GAGAGAACAT CCCAGGAGAT GGAAATGTTA AGGAAGCAGG TGGAGTGTCT   4080
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TGCTGAGGAA AATGGAAAGT TGGTAGGTCA CCAAAATTTG CATCAGAAGA TTCAGTACGT   4140
AGTGCGACTA AAGAAGGAAA ATGTCAGGCT TGCTGAGGAG ACAGAAAAGT TGCGTGCCGA   4200
AAATGTATTT TTAAAAGAAA AGAAAAGAAG TGAATCTTGA GGATTCCGGT CAGCTACCTA   4260
GGCATCACCT TGTTTGAAGA TGTTTCTTCT CTTTTACAAG TAAGACCTAC TCCTGGCCAC   4320
TTAGGAGAGC TGAATTTATG GACCTTAATT ATTAAATGTT TATAAGGTGG TGGTAACCAC   4380
CTCAAGTTTC TGATGAACAT TCTGCATCCA TATACACCCT GTGACAGTCA GCAGTCTGCT   4440
ATTAAGTGGC CTACTTCAAG GCTTTGAATC AACTTAAGGG AAAACCTTTT GTCTTTGTAA   4500
AAATAAAAGC CTGTAGCTAA GGTTTACAGT GGACATTAGC CAGATCATTT TCTTCTTAGA   4560
TTATGCCATA ATCTCCTTTG ATTCTTATGG AAGTTCTAAC AATATATGGT GGTTCCAACA   4620
CCTGCAGTGA GTTTAATGAC TGACTTAGTA GCAGGTACAA GAAGCAAACT TGTTAATATA   4680
GATTATTTTT GTATTCTTAC TTTAGGTATT TTACTTGAGC ATTTTCCATG ACTGTAAATA   4740
AAGCCATTTT TTAAGATAAA AAAAAAAAAA AAAAA
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Seq ID NO: 164 Protein Sequence
Protein Accession #: NP_064627

```
1          11         21         31         41         51
|          |          |          |          |          |
MAPGCKTELR SVTNGQSNQP SNEGDAIKVF VRIRPPAERS GSADGEQNLC LSVLSSTSLR   60
LHSNPEPKTF TFDHVADVDT TQESVFATVA KSIVESCMSG YNGTIFAYGQ TGSGKTFTMM   120
GPSESDNFSH NLRGVIPRSF EYLFSLIDRE KEKAGAGKSF LCKCSFIEIY NEQIYDLLDS   180
ASAGLYLREH IKKGVFVVGA VEQVVTSAAE AYQVLSGGWR NRRVASTSMN RESSRSHAVF   240
TITIESMEKS NEIVNIRTSL LNLVDLAGSE RQKDTHAEGM RLKEAGNINR SLSCLGQVIT   300
ALVDVGNGKQ RHVCYRDSKL TFLLRDSLGG NAKTAIIANV HPGSRCFGET LSTLNFAQRA   360
KLIKNKAVVN EDTQGNVSQL QAEVKRLKEQ LAELASGQTP PESFLTRDKK KTNYMEYFQE   420
AMLFFKKSEQ EKKSLIEKVT QLEDLTLKKE KFIQSNKMIV KFREDQIIRL EKLHKESRGG   480
FLPEEQDRLL SELRNEIQTL REQIEHHPRV AKYAMENHSL REENRRLRLL EPVKRAQEMD   540
AQTIAKLEKA FSEISGMEKS DKNQQGFSPK AQKEPCLFAN TEKLKAQLLQ IQTELNNSKQ   600
EYEEFKELTR KRQLELESEL QSLQKANLNL ENLLEATKAC KRQEVSQLNK IHAETLKIIT   660
TPTKAYQLHS RPVPKLSPEM GSFGSLYTQN SSILDNDILN EPVPPEMNEQ AFEAISEELR   720
TVQEQMSALQ AKLDEEEHKN LKLQQHVDKL EHHSTQMQEL FSSERIDWTK QQEELLSQLN   780
VLEKQLQETQ TKNDFLKSEV HDLRVVLHSA DKELSSVKLE YSSFKTNQEK EFNKLSERHM   840
HVQLQLDNLR LENEKLLESK ACLQDSYDNL QEIMKFEIDQ LSRNLQNFKK ENETLKSDLN   900
NLMELLEAEK ERNNKLSLQF EEDKENSSKE ILKVLEAVRQ EKQKETAKCE QQMAKVQKLE   960
ESLLATEKVI SSLEKSRDSD KKVVADLMNQ IQELRTSVCE KTETIDTLKQ ELKDINCKYN   1020
SALVDREESR VLIKKQEVDI LDLKETLRLR ILSEDIERDM LCEDLAHATE QLNMLTEASK   1080
KHSGLLQSAQ EELTKKEALI QELQHKLNQK KEEVEQKKNE YNFKMRQLEH VMDSAAEDPQ   1140
SPKTPPHFQT HLAKLLETQE QEIEDGRASK TSLEHLVTKL NEDREVKNAE ILRMKEQLRE   1200
MENLRLESQQ LIEKNWLLQG QLDDIKRQKE NSDQNHPDNQ QLKNEQEESI KERLAKSKIV   1260
EEMLKMKADL EEVQSALYNK EMECLRMTDE VERTQTLESK AFQEKEQLRS KLEEMYEERE   1320
RTSQEMEMLR KQVECLAEEN GKLVGHQNLH QKIQYVVRLK KENVRLAEET EKLRAENVFL   1380
KEKKRSES
```

Seq ID NO: 165 DNA Sequence
Nucleic Acid Accession #: CAT cluster

```
1          11         21         31         41         51
|          |          |          |          |          |
TTTTTTTTTT TTTTTTCACA TGCTGATGTT GCTGCCGATG ATTTCAACGC CTGGCTTTGA   60
GATTCCGTGA GTAGTCTTGA ATAATTTAAA ATTCGAAAAT CAAATTCTAC TTATTTTCTC   120
TTAATGCTAT TGTATTTCCT AATTCTCAGC TTTAACATGT AAGAAAGTAC TTTCGCTAGG   180
GGTCTTAATT GAATGGTGGG GTCGAGATGA CTGCGTCAGA ATTAAATCTC TGGAAGACCT   240
CTGAGCTCCT TTTAAAATCA TCAACAAGCG AAAATCCTTA TCAATAGCGA TGTGGGAATG   300
CATTAGGTAC AGTATTTTAA ACATACAAAA CCTAGGCATA TTAAAAAGCA CTCCTCTGGT   360
AATTTAATAA GGAATAATGA TGTCCTTAAG TTTATTTTAA TCAGCAAGTA TGACTCAATT   420
TGAAAATATG AGAACAAATA GATTTAAATA GGAACACCCA GTAAACTATG GTATGCAAAT   480
AAACTCAGAG GTAAACTTGT GAATACATAA ATCTAAATAA GTCAGTTACC ATCAAAATAT   540
TACGTGATCC TATATTTTTC TGTCCACGTC TTAAAAGTAT TTTTTACCTT GGGGCTTTAT   600
TTTCTTTCCC TCTTCCCAAG ATTATCCAAG GCAGTTCCAA TACGCGTTTT CAATAATGGT   660
AATTAAACTT TTGGAGGGTA ATCGCCAGCT GTTTCCAGAA AAATACTTTT AATAGGTGGT   720
AGTCCTCCCT GTAACTGGGT TTTCCCGGGA ATCCGGGGGG GGCATGTTGT TTTTATTGTC   780
GCCATTTTTG TTTCGTCTTT TTTGTTTTGT TGGTGGTCAG GTTTTCTTTT CATAGCGGGG   840
GAGAAGATTT TGGTCGGACT AGCGCCATCC AGCGGGTTTA GAGAAGGAGC ACACTTTTCC   900
CCGAATAGTG GCTTTTGGAT GAACAATGAA
```

Seq ID NO: 166 DNA Sequence
Nucleic Acid Accession #: NM_006953.1
Coding sequence: 33..896

```
1          11         21         31         41         51
|          |          |          |          |          |
CCGTTCCGCG CTCTGGCGGC TCCTCCCGGG CGATGCCTCC GCTCTGGGCC CTGCTGGCCC   60
TCGGCTGCCT GCGGTTCGGC TCGGCTGTGA ACCTGCAGCC CCAACTGGCC AGTGTGACTT   120
TCGCCACCAA CAACCCCACA CTTACCACTG TGGCCTTGGA AAAGCCTCTC TGCATGTTTG   180
ACAGCAAAGA GGCCCTCACT GGCACCCACG AGGTCTACCT GTATGTCCTG GTCGACTCAG   240
CCATTTCCAG GAATGCCTCA GTGCAAGACA GCACCAACAC CCCACTGGGC TCAACGTTCC   300
TACAAACAGA GGGTGGGAGG ACAGGTCCCT ACAAAGCTGT GGCCTTTGAC CTGATCCCCT   360
GCAGTGACCT GCCCAGCCTG GATGCCATTG GGGATGTGTC CAAGGCCTCA CAGATCCTGA   420
```

```
ATGCCTACCT GGTCAGGGTG GGTGCCAACG GGACCTGCCT GTGGGATCCC AACTTCCAGG   480
GCCTCTGTAA CGCACCCCTG TCGGCAGCCA CGGAGTACAG GTTCAAGTAT GTCCTGGTCA   540
ATATGTCCAC GGGCTTGGTA GAGGACCAGA CCCTGTGGTC GGACCCCATC CGCACCAACC   600
AGCTCACCCC ATACTCGACG ATCGACACGT GGCCAGGCCG GCGGAGCGGA GGCATGATCG   660
TCATCACTTC CATCCTGGGC TCCCTGCCCT TCTTTCTACT TGTGGGTTTT GCTGGCGCCA   720
TTGCCCTCAG CCTCGTGGAC ATGGGGAGTT CTGATGGGGA AACGACTCAC GACTCCCAAA   780
TCACTCAGGA GGCTGTTCCC AAGTCGCTGG GGGCCTCGGA GTCTTCCTAC ACGTCCGTGA   840
ACCGGGGGCC GCCACTGGAC AGGGCTGAGG TGTATTCCAG CAAGCTCCAA GACTGAGCCC   900
AGCACCACCC CTGGGCAGCA GCATCCTCCT CTCTGGCCTT GCCCCAGGCC CTGCAGCGGT   960
GGTTGTCACA CCCTGACTTC AGGGAAGGTG AAACAGGGCT TGTCCCTCCA ACTGCAGGAA   1020
AACCCTTAAT AAAATCTTCT GATGAGTTCT AAAAAAAAA
```

Seq ID NO: 167 Protein Sequence
Protein Accession #: NP_008884.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPPLWALLAL GCLRFGSAVN LQPQLASVTF ATNNPTLTTV ALEKPLCMFD SKEALTGTHE   60
VYLYVLVDSA ISRNASVQDS TNTPLGSTFL QTEGGRTGPY KAVAFDLIPC SDLPSLDAIG   120
DVSKASQILN AYLVRVGANG TCLWDPNFQG LCNAPLSAAT EYRFKYVLVN MSTGLVEDQT   180
LWSDPIRTNQ LTPYSTIDTW PGRRSGGMIV ITSILGSLPF FLLVGFAGAI ALSLVDMGSS   240
DGETTHDSQI TQEAVPKSLG ASESSYTSVN RGPPLDRAEV YSSKLQD
```

Seq ID NO: 168 DNA Sequence
Nucleic Acid Accession #: NM_005672.1
Coding sequence: 18..389

```
1          11         21         31         41         51
|          |          |          |          |          |
AGGGAGAGGC AGTGACCATG AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GGCTTGGCCC   60
TGCAGCCAGG CACTGCCCTG CTGTGCTACT CCTGCAAAGC CCAGGTGAGC AACGAGGACT   120
GCCTGCAGGT GGAGAACTGC ACCCAGCTGG GGGAGCAGTG CTGGACCGCG CGCATCCGCG   180
CAGTTGGCCT CCTGACCGTC ATCAGCAAAG GCTGCAGCTT GAACTGCGTG GATGACTCAC   240
AGGACTACTA CGTGGGCAAG AAGAACATCA CGTGCTGTGA CACCGACTTG TGCAACGCCA   300
GCGGGGCCCA TGCCCTGCAG CCGGCTGCCG CCATCCTTGC GCTGCTCCCT GCACTCGGCC   360
TGCTGCTCTG GGGACCCGGC CAGCTATAGG CTCTGGGGGG CCCCGCTGCA GCCCACACTG   420
GGTGTGGTGC CCCAGGCCTT TGTGCCACTC CTCACAGAAC CTGGCCCAGT GGGAGCCTGT   480
CCTGGTTCCT GAGGCACATC CTAACGCAAG TTTGACCATG TATGTTTGCA CCCCTTTTCC   540
CCNAACCCTG ACCTTCCCAT GGGCCTTTTC CAGGATTCCN ACCNGGCAGA TCAGTTTTAG   600
TGANACANAT CCGCNTGCAG ATGGCCCCTC CAACCNTTTN TGTTGNTGTT TCCATGGCCC   660
AGCATTTTCC ACCCTTAACC CTGTGTTCAG GCACTTNTTC CCCCAGGAAG CCTTCCCTGC   720
CCACCCCATT TATGAATTGA GCCAGGTTTG GTCCGTGGTG TCCCCCGCAC CCAGCAGGGG   780
ACAGGCAATC AGGAGGGCCC AGTAAAGGCT GAGATGAAGT GGACTGAGTA GAACTGGAGG   840
ACAAGAGTTG ACGTGAGTTC CTGGGAGTTT CCAGAGATGG GGCCTGGAGG CCTGGAGGAA   900
GGGGCCAGGC CTCACATTTG TGGGGNTCCC GAATGGCAGC CTGAGCACAG CGTAGGCCCT   960
TAATAAACAC CTGTTGGATA AGCCAAAAAA
```

Seq ID NO: 169 Protein Sequence
Protein Accession #: NP_005663.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MKAVLLALLM AGLALQPGTA LLCYSCKAQV SNEDCLQVEN CTQLGEQCWT ARIRAVGLLT   60
VISKGCSLNC VDDSQDYYVG KKNITCCDTD LCNASGAHAL QPAAAILALL PALGLLLWGP   120
GQL
```

Seq ID NO: 170 DNA Sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

```
1          11         21         31         41         51
|          |          |          |          |          |
AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTTGC TTCCAGGGCC TGCTGATTTT   60
TGGAAATGTG ATTATTGGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT   120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG   180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCTGTCTG TTCTAGGCAT   240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT   300
AGTATATGCC TTTGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC   360
ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACAACAGCC CTCCAAACAA   420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA   480
CAATTGCTGT GGCGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC   540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA   600
AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTTATC ACAATCAGGG   660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG   720
ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG   780
AATTGAATAT TAAGAA
```

Seq ID NO: 171 Protein Sequence
Protein Accession #: NP_008883.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW    60
IGIFVGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL    120
FLKQMLERYQ NNSPPNNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN    180
DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAWFGFAI    240
LCWTFWVLLG TMFYWSRIEY
```

Seq ID NO: 172 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAGGCTCC AAAGACCCCG ACAGGCCCCG GCGGGTGGGA GGCGCGCGCC CCGGGGCGGG    60
CGGGGCTCCC CCTACCGGCC AGACCCGGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG    120
AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG    180
CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT    240
GCGAGACAAC GAGATCCAGA GGACTCCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG    300
TGTCATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAAATGG    360
ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTC CACGTTTTTT CATGGTTGCG    420
AAGCAGTGCT CCGCTGGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT    480
CTCCTGGAAG AGCCCATGCC CTTCTTTTAC CTCAAGTGTT GTAAAATTCG CTACTGCAAT    540
TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG    600
AGCTGTGGTG GGCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGGCCTC    660
AGCCTGTCTT GA
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Seq ID NO: 173 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MRLQRPRQAP AGGRRAPRGG RGSPYRPDPG RGARRLRRFQ KGGEGAPRAD PPWAPLGTMA    60
LLALLLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNRVW CHVCERENTF ECQNPRRCKW    120
TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEEPMPFFY LKCCKIRYCN    180
LEGPPINSSV FKEYAGSMGE SCGGLWLAIL LLLASIAAGL SLS
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Seq ID NO: 174 DNA Sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

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1          11         21         31         41         51
|          |          |          |          |          |
GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG    60
CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCCGCC TCCAGCTCCG    120
CGCTGCCCGG CAGCCGGGAG CCATGCGACC CCAGGGCCCC GCCGCCTCCC CGCAGCGGCT    180
CCGCGGCCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT    240
CCCCAAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG    300
AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG    360
CATTCCGGGT ACACCTGGGA TCCCAGGTCG GGATGGATTC AAAGGAGAAA AGGGGGAATG    420
TCTGAGGGAA AGCTTTGAGG AGTCCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC    480
ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC    540
AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACTTCGG CTAAAATGCA GAAATGCATG    600
CTGTCAGCGT TGGTATTTCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTGA    660
AGCTATAATT TATTTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG    720
CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT    780
CTGGGTTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT    840
TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC    900
TTTTTTTATT ATGCCTTGGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA    960
CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT    1020
TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTTTTAGT    1080
TGGTTAGAAT ACTTTCTTCA TAGTCACATT CTCTCAACCT ATAATTTGGA ATATTGTTGT    1140
GGTCTTTTGT TTTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAAGC TACCAATCTT    1200
TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA    1260
CAACCTTAAA AAAAAAAAAA AAAA
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Seq ID NO: 175 Protein Sequence
Protein Accession #: XP_057014

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1          11         21         31         41         51
|          |          |          |          |          |
MRPQGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKGKQKA QLRQREVVDL YNGMCLQGPA    60
GVPGRDGSPG ANGIPGTPGI PGRDGFKGEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL    120
GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIIYLDQ    180
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GSPEMNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIIEE   240
LPK
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Seq ID NO: 176 DNA Sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 1..2268

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1          11         21         31         41         51
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ATGGCGAGGA AGTTATCTGT AATCTTGATC CTGACCTTTG CCCTCTCTGT CACAAATCCC   60
CTTCATGAAC TAAAAGCAGC TGCTTTCCCC CAGACCACTG AGAAAATTAG TCCGAATTGG   120
GAATCTGGCA TTAATGTTGA CTTGGCAATT TCCACACGGC AATATCATCT ACAACAGCTT   180
TTCTACCGCT ATGGAGAAAA TAATTCTTTG TCAGTTGAAG GGTTCAGAAA ATTACTTCAA   240
AATATAGGCA TAGATAAGAT TAAAAGAATC CATATACACC ATGACCACGA CCATCACTCA   300
GACCACGAGC ATCACTCAGA CCATGAGCGT CACTCAGACC ATGAGCATCA CTCAGACCAC   360
GAGCATCACT CTGACCATGA TCATCACTCC CACCATAATC ATGCTGCTTC TGGTAAAAAT   420
AAGCGAAAAG CTCTTTGCCC AGACCATGAC TCAGATAGTT CAGGTAAAGA TCCTAGAAAC   480
AGCCAGGGGA AAGGAGCTCA CCGACCAGAA CATGCCAGTG GTAGAAGGAA TGTCAAGGAC   540
AGTGTTAGTG CTAGTGAAGT GACCTCAACT GTGTACAACA CTGTCTCTGA AGGAACTCAC   600
TTTCTAGAGA CAATAGAGAC TCCAAGACCT GGAAAACTCT TCCCCAAAGA TGTAAGCAGC   660
TCCACTCCAC CCAGTGTCAC ATCAAAGAGC CGGGTGAGCC GGCTGGCTGG TAGGAAAACA   720
AATGAATCTG TGAGTGAGCC CCGAAAAGGC TTTATGTATT CCAGAAACAC AAATGAAAAT   780
CCTCAGGAGT GTTTCAATGC ATCAAAGCTA CTGACATCTC ATGGCATGGG CATCCAGGTT   840
CCGCTGAATG CAACAGAGTT CAACTATCTC TGTCCAGCCA TCATCAACCA AATTGATGCT   900
AGATCTTGTC TGATTCATAC AAGTGAAAAG AAGGCTGAAA TCCCTCCAAA GACCTATTCA   960
TTACAAATAG CCTGGGTTGG TGGTTTTATA GCCATTTCCA TCATCAGTTT CCTGTCTCTG   1020
CTGGGGGTTA TCTTAGTGCC TCTCATGAAT CGGGTGTTTT TCAAATTTCT CCTGAGTTTC   1080
CTTGTGGCAC TGGCCGTTGG GACTTTGAGT GGTGATGCTT TTTTACACCT TCTTCCACAT   1140
TCTCATGCAA GTCACCACCA TAGTCATAGC CATGAAGAAC CAGCAATGGA AATGAAAAGA   1200
GGACCACTTT TCAGTCATCT GTCTTCTCAA AACATAGAAG AAAGTGCCTA TTTTGATTCC   1260
ACGTGGAAGG GTCTAACAGC TCTAGGAGGC CTGTATTTCA TGTTTCTTGT TGAACATGTC   1320
CTCACATTGA TCAAACAATT TAAAGATAAG AAGAAAAAGA ATCAGAAGAA ACCTGAAAAT   1380
GATGATGATG TGGAGATTAA GAAGCAGTTG TCCAAGTATG AATCTCAACT TTCAACAAAT   1440
GAGGAGAAAG TAGATACAGA TGATCGAACT GAAGGCTATT TACGAGCAGA CTCACAAGAG   1500
CCCTCCCACT TTGATTCTCA GCAGCCTGCA GTCTTGGAAG AAGAAGAGGT CATGATAGCT   1560
CATGCTCATC CACAGGAAGT CTACAATGAA TATGTACCCA GAGGGTGCAA GAATAAATGC   1620
CATTCACATT TCCACGATAC ACTCGGCCAG TCAGACGATC TCATTCACCA CCATCATGAC   1680
TACCATCATA TTCTCCATCA TCACCACCAC CAAAACCACC ATCCTCACAG TCACAGCCAG   1740
CGCTACTCTC GGGAGGAGCT GAAAGATGCC GGCGTCGCCA CTTTGGCCTG GATGGTGATA   1800
ATGGGTGATG GCCTGCACAA TTTCAGCGAT GGCCTAGCAA TTGGTGCTGC TTTTACTGAA   1860
GGCTTATCAA GTGGTTTAAG TACTTCTGTT GCTGTGTTCT GTCATGAGTT GCCTCATGAA   1920
TTAGGTGACT TTGCTGTTCT ACTAAAGGCT GGCATGACCG TTAAGCAGGC TGTCCTTTAT   1980
AATGCATTGT CAGCCATGCT GGCGTATCTT GGAATGGCAA CAGGAATTTT CATTGGTCAT   2040
TATGCTGAAA ATGTTTCTAT GTGGATATTT GCACTTACTG CTGGCTTATT CATGTATGTT   2100
GCTCTGGTTG ATATGGTACC TGAAATGCTG CACAATGATG CTAGTGACCA TGGATGTAGC   2160
CGCTGGGGGT ATTTCTTTTT ACAGAATGCT GGGATGCTTT TGGGTTTTGG AATTATGTTA   2220
CTTATTTCCA TATTTGAACA TAAAATCGTG TTTCGTATAA ATTTCTAG
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Seq ID NO: 177 Protein Sequence
Protein Accession #: XP_084007

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1          11         21         31         41         51
|          |          |          |          |          |
MARKLSVILI LTFALSVTNP LHELKAAAFP QTTEKISPNW ESGINVDLAI STRQYHLQQL   60
FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHDHHS DHEHHSDHER HSDHEHHSDH   120
EHHSDHDHHS HHNHAASGKN KRKALCPDHD SDSSGKDPRN SQGKGAHRPE HASGRRNVKD   180
SVSASEVTST VYNTVSEGTH FLETIETPRP GKLFPKDVSS STPPSVTSKS RVSRLAGRKT   240
NESVSEPRKG FMYSRNTNEN PQECFNASKL LTSHGMGIQV PLNATEFNYL CPAIINQIDA   300
RSCLIHTSEK KAEIPPKTYS LQIAWVGGFI AISIISFLSL LGVILVPLMN RVFFKFLLSF   360
LVALAVGTLS GDAFLHLLPH SHASHHHSHS HEEPAMEMKR GPLFSHLSSQ NIEESAYFDS   420
TWKGLTALGG LYFMFLVEHV LTLIKQFKDK KKKNQKKPEN DDDVEIKKQL SKYESQLSTN   480
EEKVDTDDRT EGYLRADSQE PSHFDSQQPA VLEEEEVMIA HAHPQEVYNE YVPRGCKNKC   540
HSHFHDTLGQ SDDLIHHHHD YHHILHHHHH QNHHPHSHSQ RYSREELKDA GVATLAWMVI   600
MGDGLHNFSD GLAIGAAFTE GLSSGLSTSV AVFCHELPHE LGDFAVLLKA GMTVKQAVLY   660
NALSAMLAYL GMATGIFIGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS   720
RWGYFFLQNA GMLLGFGIML LISIFEHKIV FRINF
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Seq ID NO: 178 DNA Sequence
Nucleic Acid Accession #: BC010423
Coding sequence: 248..1780

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1          11         21         31         41         51
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CACAGCGTGG GAAGCAGCTC TGGGGGAGCT CGGAGCTCCC GATCACGGCT TCTTGGGGGT   60
AGCTACGGCT GGGTGTGTAG AACGGGGCCG GGGCTGGGGC TGGGTCCCCT AGTGGAGACC   120
CAAGTGCGAG AGGCAAGAAC TCTGCAGCTT CCTGCCTTCT GGGTCAGTTC CTTATTCAAG   180
TCTGCAGCCG GCTCCCAGGG AGATCTCGGT GGAACTTCAG AAACGCTGGG CAGTCTGCCT   240
TTCAACCATG CCCCTGTCCC TGGGAGCCGA GATGTGGGGG CCTGAGGCCT GGCTGCTGCT   300
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GCTGCTACTG CTGGCATCAT TTACAGGCCG GTGCCCCGCG GGTGAGCTGG AGACCTCAGA   360
CGTGGTAACT GTGGTGCTGG GCCAGGACGC AAAACTGCCC TGCTTCTACC GAGGGGACTC   420
CGGCGAGCAA GTGGGGCAAG TGGCATGGGC TCGGGTGGAC GCGGGCGAAG GCGCCCAGGA   480
ACTAGCGCTA CTGCACTCCA AATACGGGCT TCATGTGAGC CCGGCTTACG AGGGCCGCGT   540
GGAGCAGCCG CCGCCCCCAC GCAACCCCCT GGACGGCTCA GTGCTCCTGC GCAACGCAGT   600
GCAGGCGGAT GAGGGCGAGT ACGAGTGCCG GGTCAGCACC TTCCCCGCCG GCAGCTTCCA   660
GGCGCGGCTG CGGCTCCGAG TGCTGGTGCC TCCCCTGCCC TCACTGAATC CTGGTCCAGC   720
ACTAGAAGAG GGCCAGGGCC TGACCCTGGC AGCCTCCTGC ACAGCTGAGG GCAGCCCAGC   780
CCCCAGCGTG ACCTGGGACA CGGAGGTCAA AGGCACAACG TCCAGCCGTT CCTTCAAGCA   840
CTCCCGCTCT GCTGCCGTCA CCTCAGAGTT CCACTTGGTG CCTAGCCGCA GCATGAATGG   900
GCAGCCACTG ACTTGTGTGG TGTCCCATCC TGGCCTGCTC CAGGACCAAA GGATCACCCA   960
CATCCTCCAC GTGTCCTTCC TTGCTGAGGC CTCTGTGAGG GGCCTTGAAG ACCAAAATCT   1020
GTGGCACATT GGCAGAGAAG GAGCTATGCT CAAGTGCCTG AGTGAAGGGC AGCCCCCTCC   1080
CTCATACAAC TGGACACGGC TGGATGGGCC TCTGCCCAGT GGGGTACGAG TGGATGGGGA   1140
CACTTTGGGC TTTCCCCCAC TGACCACTGA GCACAGCGGC ATCTACGTCT GCCATGTCAG   1200
CAATGAGTTC TCCTCAAGGG ATTCTCAGGT CACTGTGGAT GTTCTTGACC CCCAGGAAGA   1260
CTCTGGGAAG CAGGTGGACC TAGTGTCAGC CTCGGTGGTG GTGGTGGGTG TGATCGCCGC   1320
ACTCTTGTTC TGCCTTCTGG TGGTGGTGGT GGTGCTCATG TCCCGATACC ATCGGCGCAA   1380
GGCCCAGCAG ATGACCCAGA AATATGAGGA GGAGCTGACC CTGACCAGGG AGAACTCCAT   1440
CCGGAGGCTG CATTCCCATC ACACGGACCC CAGGAGCCAG CCGGAGGAGA GTGTAGGGCT   1500
GAGAGCCGAG GGCCACCCTG ATAGTCTCAA GGACAACAGT AGCTGCTCTG TGATGAGTGA   1560
AGAGCCCGAG GGCCGCAGTT ACTCCACGCT GACCACGGTG AGGGAGATAG AAACACAGAC   1620
TGAACTGCTG TCTCCAGGCT CTGGGCGGGC CGAGGAGGAG GAAGATCAGG ATGAAGGCAT   1680
CAAACAGGCC ATGAACCATT TTGTTCAGGA GAATGGGACC CTACGGGCCA AGCCCACGGG   1740
CAATGGCATC TACATCAATG GGCGGGGACA CCTGGTCTGA CCCAGGCCTG CCTCCCTTCC   1800
CTAGGCCTGG CTCCTTCTGT TGACATGGGA GATTTTAGCT CATCTTGGGG GCCTCCTTAA   1860
ACACCCCCAT TTCTTGCGGA AGATGCTCCC CATCCCACTG ACTGCTTGAC CTTTACCTCC   1920
AACCCTTCTG TTCATCGGGA GGGCTCCACC AATTGAGTCT CTCCCACCAT GCATGCAGGT   1980
CACTGTGTGT GTGCATGTGT GCCTGTGTGA GTGTTGACTG ACTGTGTGTG TGTGGAGGGG   2040
TGACTGTCCG TGGAGGGGTG ACTGTGTCCG TGGTGTGTAT TATGCTGTCA TATCAGAGTC   2100
AAGTGAACTG TGGTGTATGT GCCACGGGAT TTGAGTGGTT GCGTGGGCAA CACTGTCAGG   2160
GTTTGGCGTG TGTGTCATGT GGCTGTGTGT GACCTCTGCC TGAAAAAGCA GGTATTTTCT   2220
CAGACCCCAG AGCAGTATTA ATGATGCAGA GGTTGGAGGA GAGAGGTGGA GACTGTGGCT   2280
CAGACCCAGG TGTGCGGGCA TAGCTGGAGC TGGAATCTGC CTCCGGTGTG AGGGAACCTG   2340
TCTCCTACCA CTTCGGAGCC ATGGGGGCAA GTGTGAAGCA GCCAGTCCCT GGGTCAGCCA   2400
GAGGCTTGAA CTGTTACAGA AGCCCTCTGC CCTCTGGTGG CCTCTGGGCC TGCTGCATGT   2460
ACATATTTTC TGTAAATATA CATGCGCCGG GAGCTTCTTG CAGGAATACT GCTCCGAATC   2520
ACTTTTAATT TTTTTCTTTT TTTTTTCTTG CCCTTTCCAT TAGTTGTATT TTTTATTTAT   2580
TTTTATTTTT ATTTTTTTTT AGAGTTTGAG TCCAGCCTGG ACGATATAGC CAGACCCTGT   2640
CTGTAAAAAA ACCAAAACCC AAAAAAAAAA AAAAAAAAAA
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Seq ID NO: 179 Protein Sequence
Protein Accession #: AAH10423

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1          11         21         31         41         51
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MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE   60
QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA   120
DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS   180
VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL   240
HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL   300
GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL   360
FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA   420
EGHPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ   480
AMNHFVQENG TLRAKPTGNG IYINGRGHLV
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Seq ID NO: 180 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 482..3007

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1          11         21         31         41         51
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TACAACCTAA GAAAGCAAGA GTGATCAATC TCAGCTCTGT TAAACATCTT GTTTACTTAC   120
TGCATTCAGC AGCTTGCAAA TGGTTAACTA TATGCAAAAA AGTCAGCATA GCTGTGAAGT   180
ATGCCGTGAA TTTTAATTGA GGGAAAAAGG GACAATTGCT TCAGGATGCT CTAGTATGCA   240
CTCTGCTTGA AATATTTTCA ATGAAATGCT CAGTATTCTA TCTTTGACCA GAGGTTTTAA   300
CTTTATGAAG CTATGGGACT TGACAAAAAG TGATATTTGA GAAGAAAGTA CGCAGTGGTT   360
GGTGTTTTCT TTTTTTTAAT AAAGGAATTG AATTACTTTG AACACCTCTT CCAGCTGTGC   420
ATTACAGATA ACGTCAGGAA GAGTCTCTGC TTTACAGAAT CGGATTTCAT CACATGACAA   480
CATGAAGCTG TGGATTCATC TCTTTTATTC ATCTCTCCTT GCCTGTATAT CTTTACACTC   540
CCAAACTCCA GTGCTCTCAT CCAGAGGCTC TTGTGATTCT CTTTGCAATT GTGAGGAAAA   600
AGATGGCACA ATGCTAATAA ATTGTGAAGC AAAAGGTATC AAGATGGTAT CTGAAATAAG   660
TGTGCCACCA TCACGACCTT TCCAACTAAG CTTATTAAAT AACGGCTTGA CGATGCTTCA   720
CACAAATGAC TTTTCTGGGC TTACCAATGC TATTTCAATA CACCTTGGAT TTAACAATAT   780
TGCAGATATT GAGATAGGTG CATTTAATGG CCTTGGCCTC CTGAAACAAC TTCATATCAA   840
TCACAATTCT TTAGAAATTC TTAAAGAGGA TACTTTCCAT GGACTGGAAA ACCTGGAATT   900
CCTGCAAGCA GATAACAATT TTATCACAGT GATTGAACCA AGTGCCTTTA GCAAGCTCAA   960
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CAGACTCAAA GTGTTAATTT TAAATGACAA TGCTATTGAG AGTCTTCCTC CAAACATCTT   1020
CCGATTTGTT CCTTTAACCC ATCTAGATCT TCGTGGAAAT CAATTACAAA CATTGCCTTA   1080
TGTTGGTTTT CTCGAACACA TTGGCCGAAT ATTGGATCTT CAGTTGGAGG ACAACAAATG   1140
GGCCTGCAAT TGTGACTTAT TGCAGTTAAA AACTTGGTTG GAGAACATGC CTCCACAGTC   1200
TATAATTGGT GATGTTGTCT GCAACAGCCC TCCATTTTTT AAAGGAAGTA TACTCAGTAG   1260
ACTAAAGAAG GAATCTATTT GCCCTACTCC ACCAGTGTAT GAAGAACATG AGGATCCTTC   1320
AGGATCATTA CATCTGGCAG CAACATCTTC AATAAATGAT AGTCGCATGT CAACTAAGAC   1380
CACGTCCATT CTAAAACTAC CCACCAAAGC ACCAGGTTTG ATACCTTATA TTACAAAGCC   1440
ATCCACTCAA CTTCCAGGAC CTTACTGCCC TATTCCTTGT AACTGCAAAG TCCTATCCCC   1500
ATCAGGACTT CTAATACATT GTCAGGAGCG CAACATTGAA AGCTTATCAG ATCTGAGACC   1560
TCCTCCGCAA AATCCTAGAA AGCTCATTCT AGCGGGAAAT ATTATTCACA GTTTAATGAA   1620
GTCTGATCTA GTGGAATATT TCACTTTGGA AATGCTTCAC TTGGGAAACA ATCGTATTGA   1680
AGTTCTTGAA GAAGGATCGT TTATGAACCT AACGAGATTA CAAAAACTCT ATCTAAATGG   1740
TAACCACCTG ACCAAATTAA GTAAAGGCAT GTTCCTTGGT CTCCATAATC TTGAATACTT   1800
ATATCTTGAA TACAATGCCA TTAAGGAAAT ACTGCCAGGA ACCTTTAATC CAATGCCTAA   1860
ACTTAAAGTC CTGTATTTAA ATAACAACCT CCTCCAAGTT TTACCACCAC ATATTTTTTC   1920
AGGGGTTCCT CTAACTAAGG TAAATCTTAA AACAAACCAG TTTACCCATC TACCTGTAAG   1980
TAATATTTTG GATGATCTTG ATTTACTAAC CCAGATTGAC CTTGAGGATA ACCCCTGGGA   2040
CTGCTCCTGT GACCTGGTTG GACTGCAGCA ATGGATACAA AAGTTAAGCA AGAACACAGT   2100
GACAGATGAC ATCCTCTGCA CTTCCCCCGG GCATCTCGAC AAAAAGGAAT TGAAAGCCCT   2160
AAATAGTGAA ATTCTCTGTC CAGGTTTAGT AAATAACCCA TCCATGCCAA CACAGACTAG   2220
TTACCTTATG GTCACCACTC CTGCAACAAC AACAAATACG GCTGATACTA TTTTACGATC   2280
TCTTACGGAC GCTGTGCCAC TGTCTGTTCT AATATTGGGA CTTCTGATTA TGTTCATCAC   2340
TATTGTTTTC TGTGCTGCAG GGATAGTGGT TCTTGTTCTT CACCGCAGGA GAAGATACAA   2400
AAAGAAACAA GTAGATGAGC AAATGAGAGA CAACAGTCCT GTGCATCTTC AGTACAGCAT   2460
GTATGGCCAT AAAACCACTC ATCACACTAC TGAAAGACCC TCTGCCTCAC TCTATGAACA   2520
GCACATGGTG AGCCCCATGG TTCATGTCTA TAGAAGTCCA TCCTTTGGTC CAAAGCATCT   2580
GGAAGAGGAA GAAGAGAGGA ATGAGAAAGA AGGAAGTGAT GCAAAACATC TCCAAAGAAG   2640
TCTTTTGGAA CAGGAAAATC ATTCACCACT CACAGGGTCA AATATGAAAT ACAAAACCAC   2700
GAACCAATCA ACAGAATTTT TATCCTTCCA AGATGCCAGC TCATTGTACA GAAACATTTT   2760
AGAAAAAGAA AGGGAACTTC AGCAACTGGG AATCACAGAA TACCTAAGGA AAAACATTGC   2820
TCAGCTCCAG CCTGATATGG AGGCACATTA TCCTGGAGCC CACGAAGAGC TGAAGTTAAT   2880
GGAAACATTA ATGTACTCAC GTCCAAGGAA GGTATTAGTG GAACAGACAA AAAATGAGTA   2940
TTTTGAACTT AAAGCTAATT TACATGCTGA ACCTGACTAT TTAGAAGTCC TGGAGCAGCA   3000
AACATAGATG GAGAGTTTGA GGGCTTTCGC AGAAATGCTG TGATTCTGTT TTAAGTCCAT   3060
ACCTTGTAAA TAAGTGCCTT ACGTGAGTGT GTCATCAATC AGAACCTAAG CACAGCAGTA   3120
AACTATGGGG AAAAAAAAAG AAGAAGAAAA GAAACTCAGG GATCACTGGG AGAAGCCATG   3180
GCATTATCTT CAGGCAATTT AGTCTGTCCC AAATAAAATC AATCCTTGCA TGTAAATC     3238
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Seq ID NO: 181 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MKLWIHLFYS SLLACISLHS QTPVLSSRGS CDSLCNCEEK DGTMLINCEA KGIKMVSEIS   60
VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIHLGFNNI ADIEIGAFNG LGLLKQLHIN   120
HNSLEILKED TFHGLENLEF LQADNNFITV IEPSAFSKLN RLKVLILNDN AIESLPPNIF   180
RFVPLTHLDL RGNQLQTLPY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS   240
IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT   300
TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP   360
PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGSFMNL TRLQKLYLNG   420
NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI LPGTFNPMPK LKVLYLNNNL LQVLPPHIFS   480
GVPLTKVNLK TNQFTHLPVS NILDDLDLLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV   540
TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTTPATT TNTADTILRS   600
LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM   660
YGHKTTHHTT ERPSASLYEQ HMVSPMVHVY RSPSFGPKHL EEEEERNEKE GSDAKHLQRS   720
LLEQENHSPL TGSNMKYKTT NQSTEFLSFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA   780
QLQPDMEAHY PGAHEELKLM ETLMYSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEQQ   840
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Seq ID NO: 182 DNA Sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 1..1524

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ATGGCGGGTG CGGGCCCGAA GCGGCGCGCG CTAGCGGCGC CGGCGGCCGA GGAGAAGGAA   60
GAGGCGCGGG AGAAGATGCT GGCCGCCAAG AGCGCGGACG GCTCGGCGCC GGCAGGCGAG   120
GGCGAGGGCG TGACCCTGCA GCGGAACATC ACGCTGCTCA ACGGCGTGGC CATCATCGTG   180
GGGACCATTA TCGGCTCGGG CATCTTCGTG ACGCCCACGG GCGTGCTCAA GGAGGCAGGC   240
TCGCCGGGGC TGGCGCTGGT GGTGTGGGCC GCGTGCGGCG TCTTCTCCAT CGTGGGCGCG   300
CTCTGCTACG CGGAGCTCGG CACCACCATC TCCAAATCGG GCGGCGACTA CGCCTACATG   360
CTGGAGGTCT ACGGCTCGCT GCCCGCCTTC CTCAAGCTCT GGATCGAGCT GCTCATCATC   420
CGGCCTTCAT CGCAGTACAT CGTGGCCCTG GTCTTCGCCA CCTACCTGCT CAAGCCGCTC   480
TTCCCCACCT GCCCGGTGCC CGAGGAGGCA GCCAAGCTCG TGGCCTGCCT CTGCGTGCTG   540
CTGCTCACGG CCGTGAACTG CTACAGCGTG AAGGCCGCCA CCCGGGTCCA GGATGCCTTT   600
GCCGCCGCCA AGCTCCTGGC CCTGGCCCTG ATCATCCTGC TGGGCTTCGT CCAGATCGGA   660
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AAGGGTGATG TGTCCAATCT AGATCCCAAC TTCTCATTTG AAGGCACCAA ACTGGATGTG    720
GGGAACATTG TGCTGGCATT ATACAGCGGC CTCTTTGCCT ATGGAGGATG GAATTACTTG    780
AATTTCGTCA CAGAGGAAAT GATCAACCCC TACAGAAACC TGCCCCTGGC CATCATCATC    840
TCCCTGCCCA TCGTGACGCT GGTGTACGTG CTGACCAACC TGGCCTACTT CACCACCCTG    900
TCCACCGAGC AGATGCTGTC GTCCGAGGCC GTGGCCGTGG ACTTCGGGAA CTATCACCTG    960
GGCGTCATGT CCTGGATCAT CCCCGTCTTC GTGGGCCTGT CCTGCTTCGG CTCCGTCAAT   1020
GGGTCCCTGT TCACATCCTC CAGGCTCTTC TTCGTGGGGT CCCGGGAAGG CCACCTGCCC   1080
TCCATCCTCT CCATGATCCA CCCACAGCTC CTCACCCCCG TGCCGTCCCT CGTGTTCACG   1140
TGTGTGATGA CGCTGCTCTA CGCCTTCTCC AAGGACATCT TCTCCGTCAT CAACTTCTTC   1200
AGCTTCTTCA ACTGGCTCTG CGTGGCCCTG GCCATCATCG GCATGATCTG GCTGCGCCAC   1260
AGAAAGCCTG AGCTTGAGCG GCCCATCAAG GTGAACCTGG CCCTGCCTGT GTTCTTCATC   1320
CTGGCCTGCC TCTTCCTGAT CGCCGTCTCC TTCTGGAAGA CACCCGTGGA GTGTGGCATC   1380
GGCTTCACCA TCATCCTCAG CGGGCTGCCC GTCTACTTCT TCGGGGTCTG GTGGAAAAAC   1440
AAGCCCAAGT GGCTCCTCCA GGGCATCTTC TCCACGACCG TCCTGTGTCA GAAGCTCATG   1500
CAGGTGGTCC CCCAGGAGAC ATAG
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Seq ID NO: 183 Protein Sequence
Protein Accession #: XP_035292.2

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1          11         21         31         41         51
|          |          |          |          |          |
MAGAGPKRRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV    60
GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYAELGTTI SKSGGDYAYM    120
LEVYGSLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCVL    180
LLTAVNCYSV KAATRVQDAF AAAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV    240
GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL    300
STEQMLSSEA VAVDFGNYHL GVMSWIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP    360
SILSMIHPQL LTPVPSLVFT CVMTLLYAFS KDIFSVINFF SFFNWLCVAL AIIGMIWLRH    420
RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWWKN    480
KPKWLLQGIF STTVLCQKLM QVVPQET
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Seq ID NO: 184 DNA Sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 1..822

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAACTGGA GTATCTTTGA GGGACTCCTG AGTGGGGTCA ACAAGTACTC CACAGCCTTT    60
GGGCGCATCT GGCTGTCTCT GGTCTTCATC TTCCGCGTGC TGGTGTACCT GGTGACGGCC    120
GAGCGTGTGT GGAGTGATGA CCACAAGGAC TTCGACTGCA ATACTCGCCA GCCCGGCTGC    180
TCCAACGTCT GCTTTGATGA GTTCTTCCCT GTGTCCCATG TGCGCCTCTG GGCCCTGCAG    240
CTTATCCTGG TGACATGCCC CTCACTGCTC GTGGTCATGC ACGTGGCCTA CCGGGAGGTT    300
CAGGAGAAGA GGCACCGAGA AGCCCATGGG GAGAACAGTG GGCGCCTCTA CCTGAACCCC    360
GGCAAGAAGC GGGGTGGGCT CTGGTGGACA TATGTCTGCA GCCTAGTGTT CAAGGCGAGC    420
GTGGACATCG CCTTTCTCTA TGTGTTCCAC TCATTCTACC CCAAATATAT CCTCCCTCCT    480
GTGGTCAAGT GCCACGCAGA TCCATGTCCC AATATAGTGG ACTGCTTCAT CTCCAAGCCC    540
TCAGAGAAGA ACATTTTCAC CCTCTTCATG GTGGCCACAG CTGCCATCTG CATCCTGCTC    600
AACCTCGTGG AGCTCATCTA CCTGGTGAGC AAGAGATGCC ACGAGTGCCT GGCAGCAAGG    660
AAAGCTCAAG CCATGTGCAC AGGTCATCAC CCCCACGGTA CCACCTCTTC CTGCAAACAA    720
GACGACCTCC TTTCGGGTGA CCTCATCTTT CTGGGCTCAG ACAGTCATCC TCCTCTCTTA    780
CCAGACCGCC CCCGAGACCA TGTGAAGAAA ACCATCTTGT GA
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Seq ID NO: 185 Protein Sequence
Protein Accession #: NP_005259.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MNWSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVTA ERVWSDDHKD FDCNTRQPGC    60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP    120
GKKRGGLWWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP    180
SEKNIFTLFM VATAAICILL NLVELIYLVS KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ    240
DDLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL
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Seq ID NO: 186 DNA Sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 25..457

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1          11         21         31         41         51
|          |          |          |          |          |
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCCTCC TCACCCTCCT    60
CGCCCTGCTG GCGCTCACCT CCGCGGTCGC CAAAAAGAAA GATAAGGTGA AGAAGGGCGG    120
CCCGGGGAGC GAGTGCGCTG AGTGGGCCTG GGGGCCCTGC ACCCCCAGCA GCAAGGATTG    180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGCCCAGACC CAGCGCATCC GGTGCAGGGT    240
GCCCTGCAAC TGGAAGAAGG AGTTTGGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG    300
TGCGTGTGAT GGGGGCACAG GCACCAAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA    360
CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCCA AGACCAAAGC    420
AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA    480
GCCCCTGGTG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC    540
```

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CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC   600
ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT   660
TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC   720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTTCCCCC CAATAAAAGC TCTTCTTTTT   780
TAATAT
```

Seq ID NO: 187 Protein Sequence
Protein Accession #: NP_002382.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQHRGFLLLT LLALLALTSA VAKKKDKVKK GGPGSECAEW AWGPCTPSSK DCGVGFREGT    60
CGAQTQRIRC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLKKA RYNAQCQETI   120
RVTKPCTPKT KAKAKAKKGK GKD
```

Seq ID NO: 188 DNA Sequence
Nucleic Acid Accession #: NM_015507
Coding sequence: 241-1902

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1          11         21         31         41         51
|          |          |          |          |          |
CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GGCGCCCCCA GCCCCTCCCC AGGCCGCGAG    60
CGCCCCTGCC GCGGTGCCTG GCCTCCCCTC CCAGACTGCA GGGACAGCAC CCGGTAACTG   120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG   180
GGGTCCGGCC GGCGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCGAGA   240
ATGCCTCTGC CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC   300
GGGAACGCGG CCAGTGCAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC   360
TGTCACTATG GAACTAAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC   420
TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC   480
AGATGCTTTC CAGGATACAC CGGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG   540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC   600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG   660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC   720
TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT   780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC   840
AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA   900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA   960
GGGTCCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT  1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC  1080
AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAAATTAA AAATGTTACC  1140
CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACTTGC AGCCCTTCAA CTATGAAGAG  1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA  1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA  1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT  1380
CTGGTCCAAA GGAAAGCGCT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT  1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC  1500
TGGAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGGCA  1560
GGTCACAAGA AAGACATTGG CCGATTGAAA CTTCTCCTAC CTGACCTGCA ACCCCAAAGC  1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCGGAGACA AAGTCGGGAA ACTTCGAGTG  1680
TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG  1740
TGGAAGACAG GGAAAATTCA GTTGTATCAA GGAACTGATG CTACCAAAAG CATCATTTTT  1800
GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTTGCTTGTT  1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT  1920
TTGACTTTGT ATGTCAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT  1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT  2040
TCTTGTATAA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA  2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCCTCCT  2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA  2220
TAGAAAAAAA AGCACAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC  2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT  2340
TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAAAAA AAAAAAA
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Seq ID NO: 189 Protein Sequence
Protein Accession #: NP_056322.2

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1          11         21         31         41         51
|          |          |          |          |          |
MPLPWSLALP LLLSWVAGGP GNAASARHHG LLASARQPGV CHYGTKLACC YGWRRNSKGV    60
CEATCEPGCK FGECVGPNKC RCPPGYTGKT CSQDVNECGM KPRPCQHRCV NTHGSYKCFC   120
LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS   180
GKVICPYNRR CVNTFGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFNTQ   240
GSFKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLLAHKNSM KKKAKIKNVT   300
PEPTRTPTPK VNLQPFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER   360
SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD   420
WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFDYRL AGDKVGKLRV   480
FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGKTG EIAVDGVLLV   540
SGLCPDSLLS VDD
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Seq ID NO: 190 DNA Sequence
Nucleic Acid Accession #: NM_006475
Coding sequence: 12..2522

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1          11         21         31         41         51
|          |          |          |          |          |
AGAGACTCAA GATGATTCCC TTTTTACCCA TGTTTTCTCT ACTATTGCTG CTTATTGTTA     60
ACCCTATAAA CGCCAACAAT CATTATGACA AGATCTTGGC TCATAGTCGT ATCAGGGGTC    120
GGGACCAAGG CCCAAATGTC TGTGCCCTTC AACAGATTTT GGGCACCAAA AAGAAATACT    180
TCAGCACTTG TAAGAACTGG TATAAAAAGT CCATCTGTGG ACAGAAAACG ACTGTTTTAT    240
ATGAATGTTG CCCTGGTTAT ATGAGAATGG AAGGAATGAA AGGCTGCCCA GCAGTTTTGC    300
CCATTGACCA TGTTTATGGC ACTCTGGGCA TCGTGGGAGC CACCACAACG CAGCGCTATT    360
CTGACGCCTC AAAACTGAGG GAGGAGATCG AGGGAAAGGG ATCCTTCACT TACTTTGCAC    420
CGAGTAATGA GGCTTGGGAC AACTTGGATT CTGATATCCG TAGAGGTTTG GAGAGCAACG    480
TGAATGTTGA ATTACTGAAT GCTTTACATA GTCACATGAT TAATAAGAGA ATGTTGACCA    540
AGGACTTAAA AAATGGCATG ATTATTCCTT CAATGTATAA CAATTTGGGG CTTTTCATTA    600
ACCATTATCC TAATGGGGTT GTCACTGTTA ATTGTGCTCG AATCATCCAT GGGAACCAGA    660
TTGCAACAAA TGGTGTTGTC CATGTCATTG ACCGTGTGCT TACACAAATT GGTACCTCAA    720
TTCAAGACTT CATTGAAGCA GAAGATGACC TTTCATCTTT TAGAGCAGCT GCCATCACAT    780
CGGACATATT GGAGGCCCTT GGAAGAGACG GTCACTTCAC ACTCTTTGCT CCCACCAATG    840
AGGCTTTTGA GAAACTTCCA CGAGGTGTCC TAGAAAGGTT CATGGGAGAC AAAGTGGCTT    900
CCGAAGCTCT TATGAAGTAC CACATCTTAA ATACTCTCCA GTGTTCTGAG TCTATTATGG    960
GAGGAGCAGT CTTTGAGACG CTGGAAGGAA ATACAATTGA GATAGGATGT GACGGTGACA   1020
GTATAACAGT AAATGGAATC AAAATGGTGA ACAAAAAGGA TATTGTGACA AATAATGGTG   1080
TGATCCATTT GATTGATCAG GTCCTAATTC CTGATTCTGC CAAACAAGTT ATTGAGCTGG   1140
CTGGAAAACA GCAAACCACC TTCACGGATC TTGTGGCCCA ATTAGGCTTG GCATCTGCTC   1200
TGAGGCCAGA TGGAGAATAC ACTTTGCTGG CACCTGTGAA TAATGCATTT TCTGATGATA   1260
CTCTCAGCAT GGTTCAGCGC CTCCTTAAAT TAATTCTGCA GAATCACATA TTGAAAGTAA   1320
AAGTTGGCCT TAATGAGCTT TACAACGGGC AAATACTGGA AACCATCGGA GGCAAACAGC   1380
TCAGAGTCTT CGTATATCGT ACAGCTGTCT GCATTGAAAA TTCATGCATG GAGAAAGGGA   1440
GTAAGCAAGG GAGAAACGGT GCGATTCACA TATTCCGCGA GATCATCAAG CCAGCAGAGA   1500
AATCCCTCCA TGAAAAGTTA AAACAAGATA AGCGCTTTAG CACCTTCCTC AGCCTACTTG   1560
AAGCTGCAGA CTTGAAAGAG CTCCTGACAC AACCTGGAGA CTGGACATTA TTTGTGCCAA   1620
CCAATGATGC TTTTAAGGGA ATGACTAGTG AAGAAAAAGA AATTCTGATA CGGGACAAAA   1680
ATGCTCTTCA AAACATCATT CTTTATCACC TGACACCAGG AGTTTTCATT GGAAAAGGAT   1740
TTGAACCTGG TGTTACTAAC ATTTTAAAGA CCACACAAGG AAGCAAAATC TTTCTGAAAG   1800
AAGTAAATGA TACACTTCTG GTGAATGAAT TGAAATCAAA AGAATCTGAC ATCATGACAA   1860
CAAATGGTGT AATTCATGTT GTAGATAAAC TCCTCTATCC AGCAGACACA CCTGTTGGAA   1920
ATGATCAACT GCTGGAAATA CTTAATAAAT TAATCAAATA CATCCAAATT AAGTTTGTTC   1980
GTGGTAGCAC CTTCAAAGAA ATCCCCGTGA CTGTCTATAC AACTAAAATT ATAACCAAAG   2040
TTGTGGAACC AAAAATTAAA GTGATTGAAG GCAGTCTTCA GCCTATTATC AAAACTGAAG   2100
GACCCACACT AACAAAAGTC AAAATTGAAG GTGAACCTGA ATTCAGACTG ATTAAAGAAG   2160
GTGAAACAAT AACTGAAGTG ATCCATGGAG AGCCAATTAT TAAAAAATAC ACCAAAATCA   2220
TTGATGGAGT GCCTGTGGAA ATAACTGAAA AAGAGACACG AGAAGAACGA ATCATTACAG   2280
GTCCTGAAAT AAAATACACT AGGATTTCTA CTGGAGGTGG AGAAACAGAA GAAACTCTGA   2340
AGAAATTGTT ACAAGAAGAG GTCACCAAGG TCACCAAATT CATTGAAGGT GGTGATGGTC   2400
ATTTATTTGA AGATGAAGAA ATTAAAAGAC TGCTTCAGGG AGACACACCC GTGAGGAAGT   2460
TGCAAGCCAA CAAAAAAGTT CAAGGTTCTA GAAGACGATT AAGGGAAGGT CGTTCTCAGT   2520
GAAAATCCAA AAACCAGAAA AAAATGTTTA TACAACCCTA AGTCAATAAC CTGACCTTAG   2580
AAAATTGTGA GAGCCAAGTT GACTTCAGGA ACTGAAACAT CAGCACAAAG AAGCAATCAT   2640
CAAATAATTC TGAACACAAA TTTAATATTT TTTTTTCTGA ATGAGAAACA TGAGGGAAAT   2700
TGTGGAGTTA GCCTCCTGTG GTAAAGGAAT TGAAGAAAAT ATAACACCTT ACACCCTTTT   2760
TCATCTTGAC ATTAAAAGTT CTGGCTAACT TTGGAATCCA TTAGAGAAAA ATCCTTGTCA   2820
CCAGATTCAT TACAATTCAA ATCGAAGAGT TGTGAACTGT TATCCCATTG AAAAGACCGA   2880
GCCTTGTATG TATGTTATGG ATACATAAAA TGCACGCAAG CCATTATCTC TCCATGGGAA   2940
GCTAAGTTAT AAAAATAGGT GCTTGGTGTA CAAAACTTTT TATATCAAAA GGCTTTGCAC   3000
ATTTCTATAT GAGTGGGTTT ACTGGTAAAT TATGTTATTT TTTACAACTA ATTTTGTACT   3060
CTCAGAATGT TTGTCATATG CTTCTTGCAA TGCATATTTT TTAATCTCAA ACGTTTCAAT   3120
AAAACCATTT TTCAGATATA AAGAGAATTA CTTCAAATTG AGTAATTCAG AAAAACTCAA   3180
GATTTAAGTT AAAAAGTGGT TTGGACTTGG GAA
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Seq ID NO: 191 Protein Sequence
Protein Accession #: BAA02836.1

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1          11         21         31         41         51
|          |          |          |          |          |
MIPFLPMFSL LLLLIVNPIN ANNHYDKILA HSRIRGRDQG PNVCALQQIL GTKKKYFSTC     60
KNWYKKSICG QKTTVLYECC PGYMRMEGMK GCPAVLPIDH VYGTLGIVGA TTTQRYSDAS    120
KLREEIEGKG SFTYFAPSNE AWDNLDSDIR RGLESNVNVE LLNALHSHMI NKRMLTKDLK    180
NGMIIPSMYN NLGLFINHYP NGVVTVNCAR IIHGNQIATN GVVHVIDRVL TQIGTSIQDF    240
IEAEDDLSSF RAAAITSDIL EALGRDGHFT LFAPTNEAFE KLPRGVLERF MGDKVASEAL    300
MKYHILNTLQ CSESIMGGAV FETLEGNTIE IGCDGDSITV NGIKMVNKKD IVTNNGVIHL    360
IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLLAPVN NAFSDDTLSM    420
VQRLLKLILQ NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG    480
RNGAIHIFRE IIKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA    540
FKGMTSEEKE ILIRDKNALQ NIILYHLTPG VFIGKGFEPG VTNILKTTQG SKIFLKEVND    600
TLLVNELKSK ESDIMTTNGV IHVVDKLLYP ADTPVGNDQL LEILNKLIKY IQIKFVRGST    660
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PKEIPVTVYT TKIITKVVEP KIKVIEGSLQ PIIKTEGPTL TKVKIEGEPE PRLIKEGETI   720
TEVIHGEPII KKYTKIIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ETEETLKKLL   780
QEEVTKVTKF IEGGDGHLFE DEEIKRLLQG DTPVRKLQAN KKVQGSRRRL REGRSQ
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Seq ID NO: 192 DNA Sequence
Nucleic Acid Accession #: NM_006670
Coding sequence: 85..1347

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1          11         21         31         41         51
|          |          |          |          |          |
CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCCAGCCC     60
AGCTCCGGGG AAACGCGAGC CGCGATGCCT GGGGGGTGCT CCCGGGGCCC CGCCGCCGGG    120
GACGGGCGTC TGCGGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCCTCGTCT    180
TCTCCCACCT CCTCGGCATC CTCCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCCGCCGTG    240
TCCGCCCAGC CCCCGCTGCC GGACCAGTGC CCCGCGCTGT GCGAGTGCTC CGAGGCAGCG    300
CGCACAGTCA AGTGCGTTAA CCGCAATCTG ACCGAGGTGC CCACGGACCT GCCCGCCTAC    360
GTGCGCAACC TCTTCCTTAC CGGCAACCAG CTGGCCGTGC TCCCTGCCGG CGCCTTCGCC    420
CGCCGGCCGC CGCTGGCGGA GCTGGCCGCG CTCAACCTCA GCGGCAGCCG CCTGGACGAG    480
GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC    540
CCACTGGCCG ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTCGGCCCCC    600
AGTCCCCTTG TGGAACTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC    660
CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCCGTGCACT GCAGGGGCTC    720
CGCCGCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA    780
CTGCCCAGCC TCAGGCACCT GGACTTAAGT AATAATTCGC TGGTGAGCCT GACCTACGTG    840
TCCTTCCGCA ACCTGACACA TCTAGAAAGC CTCCACCTGG AGGACAATGC CCTCAAGGTC    900
CTTCACAATG GCACCCTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGGT TTTCCTGGAC    960
AACAATCCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA   1020
GAGGTAGTGC AGGGCAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG   1080
GTCCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG   1140
CAAACCTCTT ATGTCTTCCT GGGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCCTCCTG   1200
GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC   1260
AGGGATCACA TGGAAGGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAACA   1320
AACCTCAGTT CTAACTCGGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG   1380
CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA   1440
TAGATACAAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCCTTG TTATGTAAAG   1500
TTTCTCGGTG TGTTCTGTTA ATGTAAGACG ATGAACAGTT GTGTATAGTG TTTTACCCTC   1560
TTCTTTTTCT TGGAACTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA   1620
TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC   1680
ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTTCGAG AAAAATACTT TATTCATAAA   1740
TATCAGTTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAT AATTGCATCC TATAAACTGC   1800
CTGCAGACGT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CCTGCATCCA   1860
AGAGCATGCT TACATTTTAC TGTTCTGCAT ATTACAAAAA ATAACTTGCA ACTTCATAAC   1920
TTCTTTGACA AAGTAAATTA CTTTTTTGAT TGCAGTTTAT ATGAAAATGT ACTGATTTTT   1980
TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAAAAA AAAAATAAAG   2040
ATTCTTAAAA GAA
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Seq ID NO: 193 Protein Sequence
Protein Accession #: CAA82324.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPGGCSRGPA AGDGRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD     60
QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLAVLPAGA FARRPPLAEL    120
AALNLSGSRL DEVRAGAFEH LPSLRQLDLS HNPLADLSPF AFSGSNASVS APSPLVELIL    180
NHIVPPEDER QNRSFEGMVV AALLAGRALQ GLRRLELASN HFLYLPRDVL AQLPSLRHLD    240
LSNNSLVSLT YVSFRNLTHL ESLHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVCDC    300
HMADMVTWLK ETEVVQGKDR LTCAYPEKMR NRVLLELNSA DLDCDPILPP SLQTSYVFLG    360
IVLALIGAIF LLVLYLNRKG IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV
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Seq ID NO: 194 DNA Sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86..1126

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1          11         21         31         41         51
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GACGCCAAGG GAGCAGGACG GAGCCATGGA CCCCGCCAGG AAAGCAGGTG CCCAGGCCAT    120
GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA    180
GTGCTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CCGAACAAGA TGAAGACAGT    240
GAAGTGCGCG CCGGGCGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA    300
CGGACAATTC TCGCTGGCAG TGCSGGGTTG CGGTTCGGGA CTCCCCGGCA AGAATGACCG    360
CGGCCTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG    420
CTGCAACGCC AAGCTCAACC TCACCTCGCG GGCGCTCGAC CCGGCAGGTA ATGAGAGTGC    480
ATACCCGCCC AACGGCGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA    540
GGGTACATCG CCGCCGGTCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG    600
CTTCGACGGC AACGTCACCT TGACGGCAGC TAATGTGACT GTGTCCTTGC CTGTCCGGGG    660
CTGTGTCCAG GATGAATTCT GCACTCGGGA TGGAGTAACA GGCCCAGGGT TCACGCTCAG    720
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TGGCTCCTGT TGCCAGGGGT CCCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC   780
CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCCTCCAGAG CCCACGACTG TGGCCTCAAC   840
CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAAACCCAT   900
GCCAGCGCCA ACCAGTCAGA CTCCGAGACA GGGAGTAGAA CACGAGGCCT CCCGGGATGA   960
GGAGCCCAGG TTGACTGGAG GCGCCGCTGG CCACCAGGAC CGCAGCAATT CAGGGCAGTA  1020
TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG  1080
ATTGGCAGCC CTTCTGTTGG CCGTGGCTGC TGGTGTCCTA CTGTGAGCTT CTCCACCTGG  1140
AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCCTGTT  1200
CCCACCACTG GACTGGGCTG GCCCAGCCCC TGTTTTTCCA ACATTCCCCA GTATCCCCAG  1260
CTTCTGCTGC GCTGGTTTGC GGCTTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG  1320
GGGTGTTCTA GCTTTTTGAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG  1380
TCCTCTTGTG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG  1440
AGGATGCTAA GCTTCCTACT CACTTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG  1500
GGTGGGACAA TGGCTCCCCA CTCTAAGCAC TGCCTCCCCT ACTCCCCGCA TCTTTGGGGA  1560
ATCGGTTCCC CATATGTCTT CCTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC  1620
CTTATGTCTG TGTGTGATCA GTTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT  1680
TTGTATAGTG AAAAAAAA
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Seq ID NO: 195 Protein Sequence
Protein Accession #: NP_055215

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1          11         21         31         41         51
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MDPARKAGAQ AMIWTAGWLL LLLLRGGAQA LECYSCVQKA DDGCSPNKMK TVKCAPGVDV    60
CTEAVGAVET IHGQFSLAVX GCGSGLPGKN DRGLDLHGLL AFIQLQQCAQ DRCNAKLNLT   120
SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVTLT   180
AANVTVSLPV RGCVQDEFCT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY FSPRIPPLVR   240
LPPPEPTTVA STTSVTTSTS APVRPTSTTK PMPAPTSQTP RQGVEHEASR DEEPRLTGGA   300
AGHQDRSNSG QYPAKGGPQQ PHNKGCVAPT AGLAALLLAV AAGVLL
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Seq ID NO: 196 DNA Sequence
Nucleic Acid Accession #: NM_006536
Coding sequence: 109..2940

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1          11         21         31         41         51
|          |          |          |          |          |
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ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG   120
AGCATTGCAG GTCCTATTTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA   180
GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC   240
ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG   300
ATAACTGAAG CTTCATTTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTCAGAAAT   360
ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA   420
TCATATGAAA AGGCAAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA   480
TACACCCTAC AATACAGAGG GTGTGGAAAA GAGGGAAAAT ACATTCATTT CACACCTAAT   540
TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT   600
GAATGGGCCC ACCTCCGTTG GGGTGTGTTC GATGAGTATA ACAATGACAA ACCTTTCTAC   660
ATAAATGGGC AAAATCAAAT TAAAGTGACA AGGTGTTCAT CTGACATCAC AGGCATTTTT   720
GTGTGTGAAA AAGGTCCTTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA   780
GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA   840
AGTTTATCTT CTGTGGTTGA ATTTTGTAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC   900
CTACAGAACC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCACAGA CTCTGCTGAC   960
TTTCACCACA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCCTCCCAC ATTCTCGCTT  1020
GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG  1080
GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAATTTT ATTTGATGCA GATTGTTGAA  1140
ATTCATACCT TCGTGGGCAT TGCCAGTTTC GACAGCAAAG GAGAGATCAG AGCCCAGCTA  1200
CACCAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA  1260
TCAGCTAAAA CAGACATCAG CATTTGTTCA GGGCTTAAGA AAGGATTTGA GGTGGTTGAA  1320
AAACTGAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG  1380
CTTCTTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCCATTGCC  1440
CTGGGTTCAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG  1500
TTCTTTGTTC CAGATATATC AAACTCCAAT AGCATGATTG ATGCTTTCAG TAGAATTTCC  1560
TCTGGAACTG GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAAAATGTC  1620
AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT  1680
ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTATT TGATCCTGAT  1740
GGACGAAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT  1800
TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAACAA TACCCATCAT  1860
TCTCTGCAAG CCCTGAAAGT GACAGTGACC TCTCGCGCCT CCAACTCAGC TGTGCCCCCA  1920
GCCACTGTGG AAGCCTTTGT GGAAAGAGAC AGCCTCCATT TTCCTCATCC TGTGATGATT  1980
TATGCCAATG TGAAACAGGG ATTTTATCCC ATTCTTAATG CCACTGTCAC TGCCACAGTT  2040
GAGCCAGAGA CTGGAGATCC TGTTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT  2100
GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTTTCT CCTTTGCTGC AAATGGTAGA  2160
TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCCAGC CCACTCTATT  2220
CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT  2280
GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC  2340
AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCCACCC TGATGTGTTT  2400
CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT  2460
TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG  2520
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AGTAAAAGTC TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA  2580
AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTCC  2640
ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT  2700
GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCCAGGCG  2760
CCTCTGTTTA TTCCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA  2820
GGAGTTTTAA CAGCAATGGG TTTGATAGGA ATCATTTGCC TTATTATAGT TGTGACACAT  2880
CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA  2940
ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA  3000
CATACTAACA AAGTCAAATT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTTGTACA  3060
ATACAGATAA GATTTTTACA TGGTAGATCA ACAATTCTTT TTGGGGGTAG ATTAGAAAAC  3120
CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAAGTAAT GTCTTTAAAG  3180
GCAAAGGGAA GGGTAAAGTC GGACCAGTGT CAAGGAAAGT TTGTTTTATT GAGGTGGAAA  3240
AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA  3300
TCATTTAGTT ACTTTGATTA ATTTTTCTTT TCTCCTTATC TGTGCAGTAC AGGTTGCTTG  3360
TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAAG CTCTTTACCT  3420
CTTGCTATTT TGTTATATAT ATTTCAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT  3480
TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT  3540
TTTATGACAA AGGTCTATTG AATTTATTTG TNTGTAAGTT TCTACTCCCA TCAAAGCAGC  3600
TTTCTAAGTT TATTGCCTTG GGTTATTATG GAATGATAGT TATAGCCCCN TATAATGCCT  3660
TACCTAGGAA A
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Seq ID NO: 197 Protein Sequence
Protein Accession #: NP_006527

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1          11         21         31         41         51
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MTQRSIAGPI CNLKFVTLLV ALSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLISN    60
IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAH   120
GDDPYTLQYR GCGKEGKYIH FTPNFLLNDN LTAGYGSRGR VFVHEWAHLR WGVFDEYNND   180
KPFYINGQNQ IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI   240
MFMQSLSSVV EFCNASTHNQ EAPNLQNQMC SLRSAWDVIT DSADFHHSFP MNGTELPPPP   300
TFSLVQAGDK VVCLVLDVSS KMAEADRLLQ LQQAAEFYLM QIVEIHTFVG IASFDSKGEI   360
RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF EVVEKLNGKA YGSVMILVTS   420
GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRLT GGLKFFVPDI SNSNSMIDAF   480
SRISSGTGDI FQQHIQLEST GENVKPHHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL   540
FDPDGRKYYT NNFITNLTFR TASLWIPGTA KPGHWTYTLN NTHHSLQALK VTVTSRASNS   600
AVPPATVEAF VERDSLHFPH PVMIYANVKQ GFYPILNATV TATVEPETGD PVTLRLLDDG   660
AGADVIKNDG IYSRYFFSFA ANGRYSLKVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN   720
IQMNAPRKSV GRNEEERKWG FSRVSSGGSF SVLGVPAGPH PDVFPPCKII DLEAVKVEEE   780
LTLSWTAPGE DFDQGQATSY EIRMSKSLQN IQDDFNNAIL VNTSKRNPQQ AGIREIFTFS   840
PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY   900
LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENGT KLL
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Seq ID NO: 198 DNA Sequence
Nucleic Acid Accession #: NM_001944
Coding sequence: 84..3083

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TTTCACCAGG GAAATCAGAG ACAATGATGG GGCTCTTCCC CAGAACTACA GGGGCTCTGG   120
CCATCTTCGT GGTGGTCATA TTGGTTCATG GAGAATTGCG AATAGAGACT AAAGGTCAAT   180
ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAAAGAAG GCAAAAACGT GAATGGGTGA   240
AATTTGCCAA ACCCTGCAGA GAAGGAGAAG ATAACTCAAA AAGAAACCCA ATTGCCAAGA   300
TTACTTCAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG   360
ATCAGCCGCC TTTTGGAATC TTTGTTGTTG ACAAAAACAC TGGAGATATT AACATAACAG   420
CTATAGTCGA CCGGGAGGAA ACTCCAAGCT TCCTGATCAC ATGTCGGGCT CTAAATGCCC   480
AAGGACTAGA TGTAGAGAAA CCACTTATAC TAACGGTTAA AATTTTGGAT ATTAATGATA   540
ATCCTCCAGT ATTTTCACAA CAAATTTTCA TGGGTGAAAT TGAAGAAAAT AGTGCCTCAA   600
ACTCACTGGT GATGATACTA AATGCCACAG ATGCAGATGA ACCAAACCAC TTGAATTCTA   660
AAATTGCCTT CAAAATTGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTC CTCCTAAGCA   720
GAAACACTGG GGAAGTCCGT ACTTTGACCA ATTCTCTTGA CCGAGAGCAA GCTAGCAGCT   780
ATCGTCTGGT TGTGAGTGGT GCAGACAAAG ATGGAGAAGG ACTATCAACT CAATGTGAAT   840
GTAATATTAA AGTGAAAGAT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT   900
CAGCACGTAT TGAAGAAAAT ATTTTAAGTT CTGAATTACT TCGATTTCAA GTAACAGATT   960
TGGATGAAGA GTACACAGAT AATTGGCTTG CAGTATATTT CTTTACCTCT GGGAATGAAG  1020
GAAATTGGTT TGAAATACAA ACTGATCCTA GAACTAATGA AGGCATCCTG AAAGTGGTGA  1080
AGGCTCTAGA TTATGAACAA CTACAAAGCG TGAAACTTAG TATTGCTGTC AAAAACAAAG  1140
CTGAATTTCA CCAATCAGTT ATCTCTCGAT ACCGAGTTCA GTCAACCCCA GTCACAATTC  1200
AGGTAATAAA TGTAAGAGAA GGAATTGCAT TCCGTCCTGC TTCCAAGACA TTTACTGTGC  1260
AAAAAGGCAT AAGTAGCAAA AAATTGGTGG ATTATATCCT GGGAACATAT CAAGCCATCG  1320
ATGAGGACAC TAACAAAGCT GCCTCAAATG TCAAATATGT CATGGGACGT AACGATGGTG  1380
GATACCTAAT GATTGATTCA AAAACTGCTG AAATCAAATT TGTCAAAAAT ATGAACCGAG  1440
ATTCTACTTT CATAGTTAAC AAAACAATCA CAGCTGAGGT TCTGGCCATA GATGAATACA  1500
CGGGTAAAAC TTCTACAGGC ACGGTATATG TTAGAGTACC CGATTTCAAT GACAATTGTC  1560
CAACAGCTGT CCTCGAAAAA GATGCAGTTT GCAGTTCTTC ACCTTCCGTG GTTGTCTCCG  1620
CTAGAACACT GAATAATAGA TACACTGGCC CCTATACATT TGCACTGGAA GATCAACCTG  1680
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TAAAGTTGCC TGCCGTATGG AGTATCACAA CCCTCAATGC TACCTCGGCC CTCCTCAGAG  1740
CCCAGGAACA GATACCTCCT GGAGTATACC ACATCTCCCT GGTACTTACA GACAGTCAGA  1800
ACAATCGGTG TGAGATGCCA CGCAGCTTGA CACTGGAAGT CTGTCAGTGT GACAACAGGG  1860
GCATCTGTGG AACTTCTTAC CCAACCACAA GCCCTGGGAC CAGGTATGGC AGGCCGCACT  1920
CAGGGAGGCT GGGGCCTGCC GCCATCGGCC TGCTGCTCCT TGGTCTCCTG CTGCTGCTGT  1980
TGGCCCCCCT TCTGCTGTTG ACCTGTGACT GTGGGGCAGG TTCTACTGGG GGAGTGACAG  2040
GTGGTTTTAT CCCAGTTCCT GATGGCTCAG AAGGAACAAT TCATCAGTGG GGAATTGAAG  2100
GAGCCCATCC TGAAGACAAG GAAATCACAA ATATTTGTGT GCCTCCTGTA ACAGCCAATG  2160
GAGCCGATTT CATGGAAAGT TCTGAAGTTT GTACAAATAC GTATGCCAGA GGCACAGCGG  2220
TGGAAGGCAC TTCAGGAATG GAAATGACCA CTAAGCTTGG AGCAGCCACT GAATCTGGAG  2280
GTGCTGCAGG CTTTGCAACA GGGACAGTGT CAGGAGCTGC TTCAGGATTC GGAGCAGCCA  2340
CTGGAGTTGG CATCTGTTCC TCAGGGCAGT CTGGAACCAT GAGAACAAGG CATTCCACTG  2400
GAGGAACCAA TAAGGACTAC GCTGATGGGG CGATAAGCAT GAATTTTCTG GACTCCTACT  2460
TTTCTCAGAA AGCATTTGCC TGTGCGGAGG AAGACGATGG CCAGGAAGCA AATGACTGCT  2520
TGTTGATCTA TGATAATGAA GGCGCAGATG CCACTGGTTC TCCTGTGGGC TCCGTGGGTT  2580
GTTGCAGTTT TATTGCTGAT GACCTGGATG ACAGCTTCTT GGACTCACTT GGACCCAAAT  2640
TTAAAAAACT TGCAGAGATA AGCCTTGGTG TTGATGGTGA AGGCAAAGAA GTTCAGCCAC  2700
CCTCTAAAGA CAGCGGTTAT GGGATTGAAT CCTGTGGCCA TCCCATAGAA GTCCAGCAGA  2760
CAGGATTTGT TAAGTGCCAG ACTTTGTCAG GAAGTCAAGG AGCTTCTGCT TTGTCCGCCT  2820
CTGGGTCTGT CCAGCCAGCT GTTTCCATCC CTGACCCTCT GCAGCATGGT AACTATTTAG  2880
TAACGGAGAC TTACTCGGCT TCTGGTTCCC TCGTGCAACC TTCCACTGCA GGCTTTGATC  2940
CACTTCTCAC ACAAAATGTG ATAGTGACAG AAAGGGTGAT CTGTCCCATT TCCAGTGTTC  3000
CTGGCAACCT AGCTGGCCCA ACGCAGCTAC GAGGGTCACA TACTATGCTC TGTACAGAGG  3060
ATCCTTGCTC CCGTCTAATA TGACCAGAAT GAGCTGGAAT ACCACACTGA CCAAATCTGG  3120
ATCTTTGGAC TAAAGTATTC AAAATAGCAT AGCAAAGCTC ACTGTATTGG GCTAATAATT  3180
TGGCACTTAT TAGCTTCTCT CATAAACTGA TCACGATTAT AAATTAAATG TTTGGGTTCA  3240
TACCCCAAAA GCAATATGTT GTCACTCCTA ATTCTCAAGT ACTATTCAAA TTGTAGTAAA  3300
TCTTAAAGTT TTTCAAAACC CTAAAATCAT ATTCGC
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Seq ID NO: 199 Protein Sequence
Protein Accession #: NP_001935

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MMGLFPRTTG ALAIFVVVIL VHGELRIETK GQYDEEEMTM QQAKRRQKRE WVKFAKPCRE    60
GEDNSKRNPI AKITSDYQAT QKITYRISGV GIDQPPFGIF VVDKNTGDIN ITAIVDREET   120
PSFLITCRAL NAQGLDVEKP LILTVKILDI NDNPPVFSQQ IFMGEIEENS ASNSLVMILN   180
ATDADEPNHL NSKIAFKIVS QEPAGTPMFL LSRNTGEVRT LTNSLDREQA SSYRLVVSGA   240
DKDGEGLSTQ CECNIKVKDV NDNFPMFRDS QYSARIEENI LSSELLRFQV TDLDEEYTDN   300
WLAVYFFTSG NEGNWFEIQT DPRTNEGILK VVKALDYEQL QSVKLSIAVK NKAEFHQSVI   360
SRYRVQSTPV TIQVINVREG IAFRPASKTF TVQKGISSKK LVDYILGTYQ AIDEDTNKAA   420
SNVKYVMGRN DGGYLMIDSK TAEIKFVKNM NRDSTFIVNK TITAEVLAID EYTGKTSTGT   480
VYVRVPDFND NCPTAVLEKD AVCSSSPSVV VSARTLNNRY TGPYTFALED QPVKLPAVWS   540
ITTLNATSAL LRAQEQIPPG VYHISLVLTD SQNNRCEMPR SLTLEVCQCD NRGICGTSYP   600
TTSPGTRYGR PHSGRLGPAA IGLLLLGLLL LLLAPLLLLT CDCGAGSTGG VTGGFIPVPD   660
GSEGTIHQWG IEGAHPEDKE ITNICVPPVT ANGADFMESS EVCTNTYARG TAVEGTSGME   720
MTTKLGAATE SGGAAGFATG TVSGAASGFG AATGVGICSS GQSGTMRTRH STGGTNKDYA   780
DGAISMNFLD SYFSQKAFAC AEEDDGQEAN DCLLIYDNEG ADATGSPVGS VGCCSFIADD   840
LDDSFLDSLG PKFKKLAEIS LGVDGEGKEV QPPSKDSGYG IESCGHPIEV QQTGFVKCQT   900
LSGSQGASAL SASGSVQPAV SIPDPLQHGN YLVTETYSAS GSLVQPSTAG FDPLLTQNVI   960
VTERVICPIS SVPGNLAGPT QLRGSHTMLC TEDPCSRLI
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Seq ID NO: 200 DNA Sequence
Nucleic Acid Accession #: NM_020411
Coding sequence: 86..526

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1          11         21         31         41         51
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AAGGCACGAG GGAACCTCAC TGCGCATGCT CCTTTGGTGC CCACCTCAGT GCGCATGTTC   120
ACTGGGCGTC TTCCCATCGG CCCCTTCGCC AGTGTGGGGA ACGCGGCGGA GCTGTGAGCC   180
GGCGACTCGG GTCCCTGAGG TCTGGATTCT TTCTCCGCTA CTGAGACACG GCGGACACAC   240
ACAAACACAG AACCACACAG CCAGTCCCAG GAGCCCAGTA ATGGAGAGCC CCAAAAAGAA   300
GAACCAGCAG CTGAAAGTCG GGATCCTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT   360
ACAGCTGAGA TCCCAGTGCG CGACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAAC   420
ACCGGGGATA AATCTGGATT TGGGTTCCGG CGTCAAGGTG AAGATAATAC CTAAAGAGGA   480
ACACTGTAAA ATGCCAGAAG CAGGTGAAGA GCAACCACAA GTTTAAATGA AGACAAGCTG   540
AAACAACGCA AGCTGGTTTT ATATTAGATA TTTGACTTAA ACTATCTCAA TAAAGTTTTG   600
CAGCTTTCAC CAAAAAAAAA AAAAAA
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Seq ID NO: 201 Protein Sequence
Protein Accession #: NP_065144.1

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1          11         21         31         41         51
|          |          |          |          |          |
MLLWCPPQCA CSLGVFPSAP SPVWGTRRSC EPATRVPEVW ILSPLLRHGG HTQTQNHTAS    60
PRSPVMESPK KKNQQLKVGI LHLGSRQKKI RIQLRSQCAT WKVICKSCIS QTPGINLDLG   120
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SGVKVKIIPK EEHCKMPEAG EEQPQV

Seq ID NO: 202 DNA Sequence
Nucleic Acid Accession #: AA172056
Coding sequence: 121..339

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1          11         21         31         41         51
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TGGATTTTGA AGAATTCTTA AGAAGCCATG TAAAGGGGGC TCTCTGGCCT TGAAATAGTG    120
ATGTTTTTTA TACAGAAAGG AGAATGCAGA ATGGTCAGAC TATCATGCAC TGTTAAATTT    180
GATTTCAAGA AATTACAGGA AAACTTTCCA AAGTTCCATC TCACAGAANN TTATTTTNCC    240
AAGAATTCCA AGATAAGTTT AGTTTTATGG AAGACTTTTA TGTGGTTTTT ACTCACTCTT    300
CATCTCAGAC ATCGACAGAT GATTACATCA CTTATAGTTC TAGTAAATTT ATTAATATAA    360
AACTCAGAGA CATTCCAATA TCCACATTGC TTACACCATT AGGCATAGAT TCAGTGTCAG    420
CTATGACAAT TGAAAATGAG CTGTTTTGTG ATTTAAAGGT TTAAATTTCT CTAACCAAAC    480
TGCTTGATCC AGATGCAGGA CTGCAAATGT TAATATTTGT TCTGGAAGAA CAATCAAATA    540
AGACTTAAGA GGAAAGGGAA TGGCCACAAT CCACCTGAAA TTTTTTCTTA AAAAGTGTGC    600
AGCCTACTAA ATCAGAATGA AAATAGAAGT ACAAGATTAT AAACAAAATG CAATCAAACT    660
TTTCTTAAGC TTACCTAAAG TTATTTCATC TGAAAATTTC AAGCAACTTT GTTCAACATT    720
AAATTGACAA TCTAAACTAA CAAGTCTTTT GAATTTATGC ATGGTAGTAA ACATTCTCTC    780
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TTCACTCATC AAAAAATAAA GTTTGTTACA TTTAGTATTT TCCCAATAAA ATTGGTCGTT    900
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GKGRCPFDPN FKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF   240
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PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV
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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

2. The method of Claim 1, wherein the biological sample comprises isolated nucleic acids.

3. The method of Claim 2:
  a) wherein the nucleic acids are mRNA; or
  b) further comprising the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

4. The method of Claim 1, wherein the polynucleotide:
  a) comprises a sequence as shown in Tables 1A-13; or
  b) is immobilized on a solid surface.

5. The method of Claim 1, wherein the patient is:
  a) undergoing a therapeutic regimen to treat bladder cancer; or
  b) suspected of having bladder cancer.

6. An isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-13.

7. The nucleic acid molecule of Claim 6, which is labeled.

8. An expression vector comprising the nucleic acid of Claim 7.

9. A host cell comprising the expression vector of Claim 8.

10. An isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

11. An antibody that specifically binds a polypeptide of Claim 10.

12. The antibody of Claim 11, further conjugated to an effector component.

13. The antibody of Claim 12, wherein the effector component is a fluorescent label.

14. The antibody of Claim 12, wherein the effector component is a radioisotope or a cytotoxic chemical.

15. The antibody of Claim 11, which is
   a) an antibody fragment; or
   b) a humanized antibody

16. A method of detecting a bladder cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody of Claim 11.

17. The method of Claim 16, wherein the antibody is further conjugated to an effector component.

18. The method of Claim 17, wherein the effector component is a fluorescent label.

19. A method for identifying a compound that modulates a bladder cancer-associated polypeptide, the method comprising the steps of:

a) contacting the compound with a bladder cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13; and

b) determining the functional effect of the compound upon the polypeptide.

20. A drug screening assay comprising the steps of

a) administering a test compound to a mammal having bladder cancer or a cell isolated therefrom;

b) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of bladder cancer.